

## 【表434】

partial sequence, homeobox PBX2 (HPBX) gene, receptor for advance glycosylation end products (RAGE) gene, complete cds, and 6 unidentifed cds, complete sequence.//1.6e-16:123:91//U89336  
 F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845  
 F-NT2RM4002452  
 F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988  
 F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690  
 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255  
 F-NT2RM4002482//Homo sapiens mRNA for KIA0691 protein, complete cds.//2.3e-93:464:91//AB014591  
 F-NT2RM4002493  
 F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484  
 F-NT2RM4002504//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, E STS, GSSs, complete sequence.//3.8e-31:233:87//AL031577  
 F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162  
 F-NT2RM4002532  
 F-NT2RM4002534  
 F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759  
 F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:90:2:89//AF022962  
 F-NT2RM4002567//CITBI-E1-2503J7, TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402  
 F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344  
 F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875  
 F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone D508B79, complete sequence.//3.7e-44:768:64//AC005454  
 F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L: Region 36B1-36B3; P1 clone D50528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122  
 F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385  
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP), partial cds.//1.1e-153:747:96//AJ012449  
 F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047  
 F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784  
 F-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12.//2.8e-183:548:91//X88834  
 F-NT2RP1000101//H. sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.11a.//6.0e-27:163:95//Z60555  
 F-NT2RP1000111//CIT-HSP-2307014, TR CIT-HSP Homo sapiens genomic clone 2307014, genomic survey sequence.//1.2e-11:128:81//AQ016069  
 F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:32:4:81//M86699  
 F-NT2RP1000124//Plasmodium falciparum DNA seq SEQUENCING IN PROGRESS from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557  
 F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:68//E08546  
 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792  
 F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.9e-20:431:64//AC006030  
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97//AF070535  
 F-NT2RP1000191  
 F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496  
 F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 D505273 (D80)), complete sequence.//4.7e-51:508:69//AC004373  
 F-NT2RP1000259  
 F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeat s mRNA, complete cds.//7.8e-142:866:88//AF042383  
 F-NT2RP1000324//RPC111-81021, TJ RPC111 Homo sapiens genomic clone R-81021, genomic survey sequence.//2.8e-29:182:92//AQ285136  
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene e

ncoding mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551  
 F-NT2RP1000333//Caenorhabditis elegans cosmid C0306, complete sequence.//1.4e-08:281:61//Z75525  
 F-NT2RP1000348//H. sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.rtlc.//1.7e-09:71:100//Z56610  
 F-NT2RP1000357  
 F-NT2RP1000358  
 5.7e-16:403:61//AC005456  
 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538  
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594  
 F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558  
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159  
 F-NT2RP1000416  
 F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//1.0:198:60//L40178  
 F-NT2RP1000439//HS\_2182\_A1\_D06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence.//2.1e-68:441:87//AQ024305  
 F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047  
 F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.7e-132:204:99//AC004453  
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R2709 D, genomic sequence, complete sequence.//4.9e-80:196:95//AC002985  
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.//1.9e-55:440:80//U47634  
 F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/c chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs.//2.6e-92:562:88//Z99297  
 F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:98//D87686  
 F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's.//0.11:360:58//M81648  
 F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.9e-34:209:93//AC004895  
 F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein Chp24 mRNA, partial cds.//1.2e-08:331:63//U26264  
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418  
 F-NT2RP1000577//HS\_2228\_B2\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128  
 F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620  
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2 69730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770  
 F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419  
 F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989  
 F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943  
 F-NT2RP1000688//H. sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907  
 F-NT2RP1000695  
 F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//130536  
 F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932  
 F-NT2RP1000730  
 F-NT2RP1000733//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742  
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434  
 F-NT2RP1000746//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//1.5e-83:466:92//AQ186344  
 F-NT2RP1000767//Homo sapiens full length insert cDNA clone Z081B0 4.//2.8e-21:144:91//AF086442  
 F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

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F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//MT1213	F-NT2RP1001286//Homo sapiens chromosome X region from tilamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's.//0.54:292:63//L44140
F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244	F-NT2RP1001294
F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837	F-NT2RP1001302
F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020	F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750
F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398	F-NT2RP1001311//RPC111-67014.TK RPC111 Homo sapiens genomic clone R-67014, genomic survey sequence.//0.26:80:75//AQ239291
F-NT2RP1000846//Human chromosome 8 BAC clone CIT9875K-2A8 complete sequence.//3.3e-15:196:76//U96629	F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pJ519013 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228
F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812	F-NT2RP1001361//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647
F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840	F-NT2RP1001385
F-NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.//6.7e-106:551:95//AF064094	F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316
F-NT2RP1000902//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 31605, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199	F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257120 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6 (D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878
F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761	F-NT2RP1001424
F-NT2RP1000916	F-NT2RP1001432
F-NT2RP1000943//Hyllobates lar huntingtin gene, partial exon.//0.19:103:72//L49362	F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:22:97//AF052149
F-NT2RP1000944//HS_2179_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=16 Row=F, genomic survey sequence.//0.032:140:63//AQ055269	F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737
F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483	F-NT2RP1001466//HS_3006_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336
F-NT2RP1000954//cSRL-143C4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143C4, genomic survey sequence.//0.030:89:78//BD1950	F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375
F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068	F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//4.0e-87:563:85//L11316
F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263	F-NT2RP1001494
F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:98//M60858	F-NT2RP1001543//Drosophila melanogaster DNA sequence (Pi DSD1142 (D148)), complete sequence.//1.9e-27:387:67//AC004280
F-NT2RP1000980//CIT-HSP-2314810, TF CIT-HSP Homo sapiens genomic clone 2314810, genomic survey sequence.//0.32:137:68//AQ017126	F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840
F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435	F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343
F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mai-41) gene, complete cds, and THI gene, partial cds.//1.3e-31:497:65//U34925	F-NT2RP1001616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913
F-NT2RP1001013//HS_3068_B1_B09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667	F-NT2RP1001665//CIT-HSP-2059N5, TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912
F-NT2RP1001014//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711	F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081
F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.//1.3e-134:241:99//AC004686	F-NT2RP2000006//HS_3061_B2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856
F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993	F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390
F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267	F-NT2RP2000008//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424
F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938	F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75//AC005066
F-NT2RP1001113	F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//Z88655
F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:68//U79139	F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290
F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039	F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749
F-NT2RP1001199	F-NT2RP2000054//CIT-HSP-2328J24, TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence.//3.3e-39:236:91//AQ043092
F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508	F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610
F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pJ356d6, complete sequence.//7.3e-50:128:99//AC002036	F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485
F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4.3e-91:344:93//AF029914	F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754
	F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037
	F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079
	F-NT2RP2000079//H.sapiens CpG island DNA genomic MseI fragment, clone 40c2, forward read cpg40c2.fttk.//3.2e-33:197:95//Z55440
	F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338
	F-NT2RP2000091//HS_2228_A2_B02_MR CIT Approved Human Genomic Sperm

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【表436】

Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363  
 F-NT2RP2000097  
 F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961  
 F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973  
 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356  
 F-NT2RP2000120//HS\_3000\_B1\_E03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177  
 F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827  
 F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419  
 F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Morrie Disease (Pseudoglioma)) gene and a CCI-3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370  
 F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924  
 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295  
 F-NT2RP2000195//Human DNA sequence from clone 4514 on chromosome 6 q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581  
 F-NT2RP2000205  
 F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmid R2 9828 and F25496, complete sequence.//7.2e-80:170:90//AC003030  
 F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-15 ZES, complete sequence.//5.5e-64:400:85//AC004382  
 F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome X q26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3) (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632  
 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//8.8e-30:508:67//U88401  
 F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:87//AC004056  
 F-NT2RP2000248  
 F-NT2RP2000257//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone YIE3, WORKING DRAFT SEQUENCE.//0.0078:286:60//AL021388  
 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence.//5.7e-82:416:97//AQ059184  
 F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC30 1323), complete sequence.//4.5e-29:310:73//AC006116  
 F-NT2RP2000274  
 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6.3e-20:260:73//X74904  
 F-NT2RP2000288  
 F-NT2RP2000289  
 F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//4.6e-69:744:70//M27877  
 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL021530  
 F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173:76//AC006082  
 F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.3e-144:731:95//AL022398  
 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.9e-102:555:90//AL034430  
 F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//6.4e-105:639:87//M25757  
 F-NT2RP2000337//HS\_2060\_B1\_E01\_MR CIT Approved Human Genomic Sperm

Library D Homo sapiens genomic clone Plate=2050 Col=1 Row=J, genomic survey sequence.//0.78:218:60//AQ243333  
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds.//3.6e-129:627:97//U83981  
 F-NT2RP2000369//HS\_2182\_B1\_B11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835  
 F-NT2RP2000412//Human DNA sequence from PAC 12409 on chromosome 6q 21. Contains DNAJ2 (MDJ1) like pseudogene, ESTs, STSs and GSSs.//0.72:170:65//AL021327  
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:93//L28010  
 F-NT2RP2000420//Homo sapiens full length insert cDNA YQ86E07.//9.2e-77:423:93//AF075093  
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:96//AF102265  
 F-NT2RP2000438//CITBI-EI-2519019.TR CITBI-EI Homo sapiens genomic clone 2519019, genomic survey sequence.//0.96:61:78//AQ276878  
 F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.1e-17:341:67//AC004691  
 F-NT2RP2000459//H.sapiens mRNA for isogen 38.//5.7e-21:158:87//Z68747  
 F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:73//Z92844  
 F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//0.0031:187:66//AC005229  
 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence.//8.8e-07:179:64//AL026277  
 F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tc:tex2) gene, wild type, promoter sequence.//0.19:72:81//U21671  
 F-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//5.0e-115:570:96//AL022318  
 F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//8.4e-37:196:98//AB005543  
 F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//AC005321  
 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514  
 F-NT2RP2000644//HS\_3211\_A1\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486  
 F-NT2RP2000656  
 F-NT2RP2000658//CITBI-EI-2518N15.TF CITBI-EI Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386  
 F-NT2RP2000668  
 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916  
 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913  
 F-NT2RP2000710//Drosophila melanogaster: Chromosome 2L: Region 36B 1-36B3: P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122  
 F-NT2RP2000715//Homo sapiens PAC clone DJ1056K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540  
 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965  
 F-NT2RP2000758//Human LIM-kinase and alternatively spliced LIM-kinase (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293  
 F-NT2RP2000764//HS\_2254\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=M, genomic survey sequence.//0.071:45:95//AQ068887  
 F-NT2RP2000809  
 F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698  
 F-NT2RP2000814  
 F-NT2RP2000816  
 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292  
 F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479  
 F-NT2RP2000845  
 F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284  
 F-NT2RP2000892  
 F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete c

【表437】

ds.//3.4e-129:610:98//AB018266	one 4ell, forward read cpg4ell.fla.//1.7e-12:98:92//Z61305
F-NTZRP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014	F-NTZRP2001378//HS_3054_B2_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=8, genomic survey sequence.//9.8e-17:131:89//AQ100721
F-NTZRP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16 p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890	F-NTZRP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371
F-NTZRP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298	F-NTZRP2001392//S.pristinaespiralis snbC gene & snbDE gene.//0.019:267:59//Y11548
F-NTZRP2000955	F-NTZRP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS. CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242
F-NTZRP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393	F-NTZRP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219
F-NTZRP2000985//Homo sapiens chromosome 17, clone hRPK.597_M12, complete sequence.//1.6e-72:498:82//AC005277	F-NTZRP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759
F-NTZRP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-121:171:77//AC002394	F-NTZRP2001423//Xenopus laevis ERI mRNA, complete cds.//3.7e-34:269:85//AF015454
F-NTZRP2001036//Homo sapiens chromosome 17, clone hRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167	F-NTZRP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065
F-NTZRP2001044//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224	F-NTZRP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702
F-NTZRP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957	F-NTZRP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350
F-NTZRP2001065	F-NTZRP2001445//P. falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275
F-NTZRP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561	F-NTZRP2001449//B. taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931
F-NTZRP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423	F-NTZRP2001450
F-NTZRP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063	F-NTZRP2001467
F-NTZRP2001119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596	F-NTZRP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561
F-NTZRP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072	F-NTZRP2001511//Dryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355
F-NTZRP2001137//HS_2193_B2_O12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=M, genomic survey sequence.//1.8e-11:136:78//AQ032187	F-NTZRP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALARI.//2.0e-136:657:97//Y14494
F-NTZRP2001149//Homo sapiens chromosome 22q11.2 Cosmid Clone 2h In DCCR Region, complete sequence.//6.2e-29:247:78//AC000076	F-NTZRP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-37:357:64//AC004596
F-NTZRP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (AF-6, Atadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178	F-NTZRP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586
F-NTZRP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949	F-NTZRP2001560
F-NTZRP2001174//RPC111-5BL2.TK RPC111 Homo sapiens genomic clone R-5BL2, genomic survey sequence.//7.6e-07:196:64//AQ237306	F-NTZRP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//AB007957
F-NTZRP2001196	F-NTZRP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943
F-NTZRP2001218	F-NTZRP2001581//Mus musculus semaphorin 5A mRNA, complete cds.//6.5e-09:222:66//AF030430
F-NTZRP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893	F-NTZRP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648
F-NTZRP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760	F-NTZRP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340
F-NTZRP2001245//HS_3062_B1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177	F-NTZRP2001613
F-NTZRP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353	F-NTZRP2001628//H. sapiens (xsl28) mRNA, 380bp.//1.7e-15:279:68//Z36784
F-NTZRP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430	F-NTZRP2001634//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds.//5.4e-123:606:96//AF030233
F-NTZRP2001290//M. musculus mRNA for 147 clone.//8.6e-102:641:86//X61455	F-NTZRP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-14:4:687:97//AF058718
F-NTZRP2001295//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594	F-NTZRP2001663//H. sapiens mRNA for 2-phosphopyruvate-hydratase-alphha-enolase.//1.0e-36:372:74//X84907
F-NTZRP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//W22967	F-NTZRP2001675//S. pombe chromosome 1 cosmid c2G11.//0.070:507:59//Z54354
F-NTZRP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//W80783	F-NTZRP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259
F-NTZRP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539	F-NTZRP2001678//HS_2007_A2_A04_TT CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699
F-NTZRP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147	F-NTZRP2001699//RPC111-57B17.TK RPC111 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592
F-NTZRP2001366//H. sapiens CpG island DNA genomic MseI fragment, cl	F-NTZRP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079

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18:151:86//D14697	F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783	F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0.258:63//D85923
F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378	F-NT2RP2001839//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347	F-NT2RP2002172//HS_3020_B1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169
F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610	F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219	F-NT2RP2002185//RPC111-67B15.TJ RPC111 Homo sapiens genomic clone R-67B15, genomic survey sequence.//2.8e-18:109:100//AQ201833
F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309	F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein n, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//1.8e-87:496:92//AL031864	F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl) mRNA, complete cds.//2.7e-36:363:78//U09215
F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (Sptase) mRNA, 3' end.//9.2e-112:633:90//M74161	F-NT2RP2001900//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone ROB45, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281	F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-82:477:89//AF032872
F-NT2RP2001907//H. sapiens CpG island DNA genomic MseI fragment, clone 97111, forward read cpg97111.ftla.//4.2e-26:206:84//Z64125	F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688	F-NT2RP2002208
F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856	F-NT2RP2001943//Drosophila melanogaster cosmid 25EB, //0.00036:248:60//AL009196	F-NT2RP2002219//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//1.0:378:58//AL034557
F-NT2RP2001946//Homo sapiens clone N0D140K04, complete sequence.//3.8e-78:232:99//AC005033	F-NT2RP2001947//Homo sapiens full length insert cDNA clone ZD81B04, //2.0e-28:172:94//AF086442	F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308
F-NT2RP2001969//H. sapiens CpG island DNA genomic MseI fragment, clone 152a8, reverse read cpg152a8.ftla.//1.0e-20:123:99//Z59378	F-NT2RP2001976	F-NT2RP2002235//P. falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998
F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117	F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117	F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394
F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022	F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299	F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418
F-NT2RP2002032//Homo sapiens chromosome 5, BAC clone Sm9 (LBNL H220), complete sequence.//0.76:189:65//AC005895	F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825	F-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//9.7e-67:340:89//AL033527
F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029	F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//2.2e-86:722:77//AC004552	F-NT2RP2002270//RPC111-77C23.TV RPC111 Homo sapiens genomic clone R-77C23, genomic survey sequence.//2.9e-18:79:93//AQ268098
F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6 q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375	F-NT2RP2002058//S. cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301	F-NT2RP2002282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033
F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//U87306	F-NT2RP2002070//beta-ADD=adducin beta subunit 63 kDa isoform/membrane skeleton protein, beta-ADD=adducin beta subunit 63 kDa isoform/membrane skeleton protein (alternatively spliced, exon 10 to 13 region) [human, Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083	F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//AF069532
F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917	F-NT2RP2002099//Homo sapiens mRNA for E18-55kDa-associated protein.//9.8e-111:533:97//A007509	F-NT2RP2002316//HS_2171_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673
F-NT2RP2002105//H. sapiens CpG island DNA genomic MseI fragment, clone 10H8, forward read cpg10H8.ftla.//2.4e-29:178:94//Z58857	F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey sequence.//2.5e-32:202:92//B64468	F-NT2RP2002325//Homo sapiens mRNA for Pex1lp, complete cds.//3.9e-123:640:95//AB015594
F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//M25874	F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0.258:63//D85923	F-NT2RP2002333
	F-NT2RP2002172//HS_3020_B1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169	F-NT2RP2002373//F. rubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//Z87330
	F-NT2RP2001839//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347	F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958
	F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610	F-NT2RP2002394//P. falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275
	F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219	F-NT2RP2002408//F. rubripes GSS sequence, clone 08DG11aB8, genomic survey sequence.//5.7e-15:220:71//AL015615
	F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309	F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ223742
	F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein n, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//1.8e-87:496:92//AL031864	F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682
	F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (Sptase) mRNA, 3' end.//9.2e-112:633:90//M74161	F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169
	F-NT2RP2001900//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone ROB45, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281	F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//1.9e-06:281:66//AC004381
	F-NT2RP2001943//Drosophila melanogaster cosmid 25EB, //0.00036:248:60//AL009196	F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:63//D42045
	F-NT2RP2001946//Homo sapiens clone N0D140K04, complete sequence.//3.8e-78:232:99//AC005033	F-NT2RP2002475
	F-NT2RP2001947//Homo sapiens full length insert cDNA clone ZD81B04, //2.0e-28:172:94//AF086442	F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289
	F-NT2RP2001969//H. sapiens CpG island DNA genomic MseI fragment, clone 152a8, reverse read cpg152a8.ftla.//1.0e-20:123:99//Z59378	F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300
	F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117	F-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence.//7.2e-18:134:90//AC006213
	F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022	F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334
	F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299	F-NT2RP2002520
	F-NT2RP2002032//Homo sapiens chromosome 5, BAC clone Sm9 (LBNL H220), complete sequence.//0.76:189:65//AC005895	F-NT2RP2002537
	F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825	F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127
	F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029	F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC005317
	F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//2.2e-86:722:77//AC004552	F-NT2RP2002591//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304
	F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6 q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375	F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR012155
	F-NT2RP2002058//S. cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301	F-NT2RP2002606//Rattus norvegicus Rab3n mRNA, complete cds.//1.9e-43:282:87//U19181
	F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//U87306	F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310
	F-NT2RP2002070//beta-ADD=adducin beta subunit 63 kDa isoform/membrane skeleton protein, beta-ADD=adducin beta subunit 63 kDa isoform/membrane skeleton protein (alternatively spliced, exon 10 to 13 region) [human, Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083	
	F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917	
	F-NT2RP2002099//Homo sapiens mRNA for E18-55kDa-associated protein.//9.8e-111:533:97//A007509	
	F-NT2RP2002105//H. sapiens CpG island DNA genomic MseI fragment, clone 10H8, forward read cpg10H8.ftla.//2.4e-29:178:94//Z58857	
	F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey sequence.//2.5e-32:202:92//B64468	
	F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//M25874	

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F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//5.6e-27:460:63//Y10806  
F-NT2RP2002621  
F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397  
F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384  
F-NT2RP2002701//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380  
F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980  
F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572  
F-NT2RP2002721//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107  
F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388  
F-NT2RP2002740//Absidia glauca ORF, 3' end: (+) mating type surface protein (PSSP15) gene, complete cds: ORF, 5' end.//0.0073:274:66//M94861  
F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D90916  
F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296  
F-NT2RP2002752//Human BAC clone RG317MD2 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433  
F-NT2RP2002753//Human DNA sequence from cosmid B1187 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171  
F-NT2RP2002769//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylC) gene, complete cds.//0.0016:412:60//U78289  
F-NT2RP2002778//CIT-HSP-2059C5, TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837  
F-NT2RP2002800  
F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p1.2 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:94//AC006078  
F-NT2RP2002851//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone TRB-4.//0.85:93:68//M18845  
F-NT2RP2002862//HS\_3084\_A1\_H03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//5.0e-67:390:91//AQ186344  
F-NT2RP2002880  
F-NT2RP2002891//CIT-HSP-2310D14, TF CIT-HSP Homo sapiens genomic clone 2310D14, genomic survey sequence.//0.11:53:90//AQ019792  
F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511  
F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392  
F-NT2RP2002929//F.rubripes GSS sequence, clone 123123a1, genomic survey sequence.//3.9e-06:66:83//AL017246  
F-NT2RP2002939  
F-NT2RP2002954  
F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483  
F-NT2RP2002979//CIT-HSP-2340D12, TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence.//4.6e-96:476:97//AQ057233  
F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230  
F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569  
F-NT2RP2002987//Homo sapiens (subclone 6\_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958  
F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424  
F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765  
F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849\_M\_15, complete sequence.//4.2e-23:202:82//AC005703  
F-NT2RP2003073//Human DNA sequence from PAC 305D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822  
F-NT2RP2003099//HS\_3008\_B2\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786  
F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362  
F-NT2RP2003117//HS\_2034\_B2\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797  
F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765  
F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329  
F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915  
F-NT2RP2003137//CIT-HSP-2300J6, TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976  
F-NT2RP2003157//Human DNA sequence from cDNA 16pHCQ:16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716  
F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025  
F-NT2RP2003161//CITBI-E1-2506E20, TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657  
F-NT2RP2003164  
F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328  
F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040  
F-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597  
F-NT2RP2003206  
F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794  
F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:86//AF023657  
F-NT2RP2003237//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447  
F-NT2RP2003243//RPC111-36J1, TP RPC111 Homo sapiens genomic clone RPC111-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107  
F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NG05) mRNA, complete cds.//6.0e-114:696:87//L38481  
F-NT2RP2003272//RPC111-67B15, TJ RPC111 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833  
F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525  
F-NT2RP2003280//RPC111-1412, TVB RPC111 Homo sapiens genomic clone RPC111-1412, genomic survey sequence.//6.4e-77:400:95//B85286  
F-NT2RP2003286//CIT-HSP-2336D3, TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024  
F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973  
F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572  
F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722  
F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666  
F-NT2RP2003308//D.melanogaster crn mRNA.//1.1e-63:697:70//X58374  
F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131\_K\_11, complete sequence.//0.040:145:64//AC005288  
F-NT2RP2003339  
F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559  
F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510  
F-NT2RP2003391  
F-NT2RP2003393//HS\_3218\_A2\_B09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356  
F-NT2RP2003394  
F-NT2RP2003401  
F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630  
F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023  
F-NT2RP2003446  
F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome: segment 3/4.//0.0018:366:60//AJ235272  
F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311a8 (BC2 69730) containing the HFE1 gene, complete sequence.//7.5e-16:189:68//AC004770  
F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977  
F-NT2RP2003499  
2.1e-08:408:61//AB000826  
F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUEN

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CE, 12 unordered pieces.//1.9e-33:192:96//AC005236  
 F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB1, partial cds.//1.0:328:60//AB013801  
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-7  
 6:403:93//D87460  
 F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:  
 151:95//X03702  
 F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5'  
 end.//1.3e-101:564:91//M21977  
 F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome  
 6.//2.0e-40:315:75//Z80899  
 F-NT2RP2003543  
 F-NT2RP2003559//H.sapiens CpG island DNA genomic MseI fragment, cl  
 one 90a5, reverse read cpg90a5.rtl.//1.1e-20:122:99//Z56144  
 F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complet  
 e cds.//8.8e-27:664:63//M34551  
 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cd  
 s.//4.1e-113:541:98//AB007931  
 F-NT2RP2003581  
 F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic  
 survey sequence.//1.9e-11:210:65//AL012756  
 F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNA1)  
 mRNA, complete cds.//1.9e-123:587:98//AF030233  
 F-NT2RP2003629  
 F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid  
 synthetase.//7.8e-88:582:84//AJ006215  
 F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENC  
 E, 18 unordered pieces.//5.6e-47:335:83//AC005081  
 F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems H  
 uman BAC library) complete sequence.//1.2e-06:133:74//AC003684  
 F-NT2RP2003691//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL02380  
 7  
 F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, c  
 omplete cds.//1.3e-65:458:82//U44803  
 F-NT2RP2003704//H.sapiens CpG island DNA genomic MseI fragment, cl  
 one 2a9, reverse read cpg2a9.rtl.//3.8e-17:170:84//Z60615  
 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cd  
 s.//2.6e-108:518:98//AB011097  
 F-NT2RP2003713//HS\_2016\_B1\_B05\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=0, geno  
 mic survey sequence.//1.3e-11:102:90//AQ226895  
 F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, co  
 mplete sequence.//1.4e-27:249:78//AC003973  
 F-NT2RP2003727//RPC111-77119.TV RPC111 Homo sapiens genomic clone  
 R-77119, genomic survey sequence.//3.4e-26:294:74//AQ268303  
 F-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENC  
 E, 14 unordered pieces.//2.6e-74:194:91//AC004951  
 F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-91  
 1E12, complete sequence.//1.7e-92:165:96//AC003964  
 F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop.//4.  
 5e-76:696:73//X92987  
 F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequ  
 ence.//1.0:109:69//AB013275  
 F-NT2RP2003769  
 F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, c  
 omplete sequence.//3.0e-96:467:98//AC004771  
 F-NT2RP2003777  
 F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial,  
 2986 nt].//7.2e-107:731:82//S70011  
 F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic cl  
 one 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761  
 F-NT2RP2003825//Homo sapiens BAC clone R3139P11 from 7q11-q21, com  
 plete sequence.//8.9e-06:151:74//AC004491  
 F-NT2RP2003840//Arabidopsis thaliana chromosome 11 BAC F12A24 geno  
 mic sequence, complete sequence.//0.018:145:69//AC005167  
 F-NT2RP2003857//HS\_3227\_A2\_G04\_T7 CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=W, geno  
 mic survey sequence.//0.96:257:61//AQ303467  
 F-NT2RP2003859  
 F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park C  
 ancer Institute Human PAC library) complete sequence.//2.0e-12:36  
 9:65//AC002375  
 F-NT2RP2003885//CITBI-EI-251406.TF CITBI-EI Homo sapiens genomic c  
 lone 251406, genomic survey sequence.//0.13:167:64//AQ265722  
 F-NT2RP2003912//nak=serine/threonine- and tyrosine-specific prote  
 in kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:  
 838:86//S45828  
 F-NT2RP2003952  
 F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific prot  
 ease, complete cds.//2.1e-28:165:96//AB014458  
 F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome  
 1p36.21-36.33. Contains the alternatively spliced gene for Matrix  
 Metalloproteinase in the Female Reproductive tract MFR1, -2, MMP2  
 1/2ZA, -8 and -C, a novel gene, the alternatively spliced CDC2L2 g  
 ene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyl  
 transferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2  
 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the  
 KIAA0447 gene, a novel alternatively spliced gene similar to many  
 (archae)bacterial, worm and yeast hypothetical genes, and the GNB1  
 gene for Guanine Nucleotide Binding Protein (G protein), Beta pol  
 ypeptide 1 (Transducin Beta chain 1). Contains putative CpG island s.  
 ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL0312  
 82  
 F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cd  
 s.//9.9e-160:783:96//AB018347  
 F-NT2RP2003984  
 F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT S  
 EQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382  
 F-NT2RP2003988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL03168  
 1  
 F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome  
 6q24 Contains EST, STS, GSS and CpG island, complete sequence.//3.  
 0e-123:693:91//AL023580  
 F-NT2RP2004014  
 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complet  
 e sequence.//5.8e-83:427:87//AC004780  
 F-NT2RP2004042  
 F-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 134019, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034  
 555  
 F-NT2RP2004081  
 F-NT2RP2004098//HS\_2216\_A1\_B12\_MF CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, gen  
 omic survey sequence.//1.0e-07:86:84//AQ145694  
 F-NT2RP2004124//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, geno  
 mic survey sequence.//3.0e-25:155:94//AQ136993  
 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TA  
 C clone: K8K14, complete sequence.//1.0:220:62//AB007645  
 F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252  
 (D97)), complete sequence.//0.93:480:56//AC002493  
 F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42  
 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//  
 0.051:265:61//AC005140  
 F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) g  
 ene, complete cds.//1.0:162:66//AF028235  
 F-NT2RP2004172//S.pombe chromosome 11 cosmid c24E9.//1.7e-06:466:5  
 9//AL021816  
 F-NT2RP2004187//Homo sapiens full length insert cDNA YQ86E07.//3.5  
 e-17:354:64//AF075093  
 F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete  
 cds.//9.4e-53:397:82//AF003998  
 F-NT2RP2004196  
 F-NT2RP2004207//Human von Willebrand factor pseudogene correspondi  
 ng to exons 23 through 34.//0.0023:386:61//M60676  
 F-NT2RP2004226//HS\_2186\_A1\_D03\_MF CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, geno  
 mic survey sequence.//7.8e-58:370:87//AQ063813  
 F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34 4  
 48:67//X75756  
 F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete  
 cds.//5.2e-108:510:99//AB015718  
 F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-148  
 5000 nt, position (6/7).//1.1e-12:489:61//AP000006  
 F-NT2RP2004245  
 F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:6  
 2//AL034446  
 F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complet  
 e sequence.//3.5e-11:299:64//AC005781  
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, com  
 plete cds.//4.5e-150:735:97//AF000416  
 F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110  
 (D147)), complete sequence.//0.98:267:59//AC004423  
 F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, co  
 mplete sequence.//1.6e-40:419:75//AC002519  
 F-NT2RP2004347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*

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from clone 1018D12. WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650  
 F-NT2RP2004364  
 F-NT2RP2004365  
 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3. Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//0.92:427:57//AL031864  
 F-NT2RP2004373//Homo sapiens cosmid Qc15C1 and 9486 from Xq28, complete sequence.//2.6e-26:493:65//AF035397  
 F-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969  
 F-NT2RP2004392  
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164  
 F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799  
 F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441  
 F-NT2RP2004412//H.sapiens CpG island DNA genomic MseI fragment, clone 3464, reverse read cpg3464.rta.//5.0e-27:154:98//Z65369  
 F-NT2RP2004425  
 F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530  
 F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388  
 F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591  
 F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556  
 F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890  
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163  
 F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555  
 F-NT2RP2004568//H.vulgaris GAA-satellite DNA.//2.0e-07:292:62//Z50100  
 F-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22. WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755  
 F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908  
 F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020  
 F-NT2RP2004600  
 F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176  
 F-NT2RP2004614  
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291  
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929  
 F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE. 33 unordered pieces.//0.092:239:61//AC005805  
 F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome 12q26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:23:61//AL031312  
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525  
 F-NT2RP2004709//HS\_2033\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714  
 F-NT2RP2004710//HS\_3185\_B2\_D07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885  
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947  
 F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022  
 F-NT2RP2004767//H.sapiens CpG island DNA genomic MseI fragment, clone 65c11, reverse read cpg65c11.rta.//1.3e-24:217:81//Z62210  
 F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:541:71//AF024636  
 F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398  
 F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-53:353:84//J56252  
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953  
 F-NT2RP2004802  
 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179  
 F-NT2RP2004841//Human DNA sequence from cosmid J138017, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519  
 F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040017bA3, genomic survey sequence.//0.96:183:64//AL025645  
 F-NT2RP2004897//Human Chromosome X clone bWDX187, complete sequence.//4.8e-142:710:96//AC004383  
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144  
 F-NT2RP2004936  
 F-NT2RP2004959//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183  
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-59:339:79//U56732  
 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ro Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-19:187:72//U91328  
 F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551  
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029  
 F-NT2RP2004982//F2604-Sp6 IGF Arabidopsis thaliana genomic clone F2604, genomic survey sequence.//0.13:273:61//B12642  
 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478  
 F-NT2RP2004999  
 F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375  
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515  
 F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200  
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141  
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//AC004849  
 F-NT2RP2005020  
 F-NT2RP2005022//Human Chromosome 3 pac pDJ70111, WORKING DRAFT SEQUENCE. 2 unordered pieces.//3.0e-43:98:93//AC000380  
 F-NT2RP2005031//HS\_2052\_B2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464  
 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454  
 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//0.20:519:57//AC005696  
 F-NT2RP2005108  
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564  
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//X98743  
 F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547:59//AJ223012  
 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//0.95:191:62//AC004527  
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583  
 F-NT2RP2005147//HS\_3184\_A1\_E01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226  
 F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read cpg132g6.rta.//1.1e-13:93:97//Z59162  
 F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070  
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein 1.//1.4e-125:633:96//AJ007509  
 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808  
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//AC005189  
 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536  
 F-NT2RP2005254  
 F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3: clone NL197R).//0.58:132:65//X87513

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F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666  
 F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335  
 F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//AF060219  
 F-NT2RP2005289//Homo sapiens mRNA for IXP2 protein.//4.0e-140:670:98//AJ007590  
 F-NT2RP2005293//HS\_3245\_B1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454  
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576  
 F-NT2RP2005325//Human LIM-homeobox domain protein (LH-2) mRNA, complete cds.//8.2e-122:166:90//U11701  
 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAIP90) mRNA, complete cds.//0.39:353:62//AF032387  
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138  
 F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92844  
 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MB03 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247  
 F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358  
 F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184  
 F-NT2RP2005407  
 F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LAN L), complete sequence.//0.014:235:62//AC005346  
 F-NT2RP2005441//CIT-HSP-2338P5, TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532:97//AQ055548  
 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865  
 F-NT2RP2005457//B. taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647  
 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679  
 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//6.5e-18:152:75//AC006116  
 F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo) gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBP11, TNF-R2, CD120B, TNFR2). Contains ESTs, STSs, GSSs, genomic marker D15434 and a ca repeat polymorphism, complete sequence.//4.4e-12:89:97//AL031276  
 F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//AC004130  
 F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228:99//AC006030  
 F-NT2RP2005491//HS\_2253\_A2\_G10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=W, genomic survey sequence.//4.6e-23:234:80//AQ116847  
 F-NT2RP2005495  
 F-NT2RP2005496//HS\_3064\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097  
 F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931  
 F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//0.86:183:63//AC005880  
 F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695  
 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444:92//AF092563  
 F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307  
 F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993  
 F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449  
 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963  
 F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734  
 F-NT2RP2005555//HS\_2188\_A2\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723  
 F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//2.5e-44:473:71//AF062529  
 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//0.99:213:65//AC005016  
 F-NT2RP2005600//H. sapiens CpG island DNA genomic MseI fragment, clone 172d12, reverse read cpg172d12.rta.//0.32:134:63//Z57359  
 F-NT2RP2005605  
 F-NT2RP2005620//Homo sapiens epsilon 2a mRNA, complete cds.//9.8e-91:447:97//AF062085  
 F-NT2RP2005622  
 F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556  
 F-NT2RP2005637//NAT1 (NAT10)=acetyltransferase 1 (3' region, polyadenylation polymorphism) [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829  
 F-NT2RP2005640//Mouse US RNA gene.//5.5e-19:249:76//X06980  
 F-NT2RP2005645//HS\_2201\_B2\_D07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763  
 F-NT2RP2005651//H. sapiens DNA sequence.//0.00037:150:66//Z22493  
 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626  
 F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605  
 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814  
 F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405  
 F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836  
 F-NT2RP2005694  
 F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPC111-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183  
 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342  
 F-NT2RP2005719//R. norvegicus mRNA for metallothionein-III.//0.86:17:64//X89603  
 F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367  
 F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528  
 F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627  
 F-NT2RP2005732//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017  
 F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270  
 F-NT2RP2005748//Human Koz11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342  
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF088868  
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516  
 F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853  
 F-NT2RP2005767//G. gallus PB1 gene.//2.1e-73:544:80//X90849  
 F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836  
 F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336  
 F-NT2RP2005781//Pseudomonas aeruginosa gene for MexI and MexY, complete cds.//0.96:184:60//AB015853  
 F-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423  
 F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579  
 F-NT2RP2005812  
 F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103  
 F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086  
 F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873  
 F-NT2RP2005853//RPC111-24D4, TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490

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F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564  
 F-NT2RP2005859//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553  
 F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103124aF4, genomic survey sequence.//7.8e-06:92:79//AL027276  
 F-NT2RP2005886//HS\_3187\_A2\_008\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885  
 F-NT2RP2005890//Mouse oncogene (cct2) mRNA, complete cds.//2.7e-32:660:66//L11316  
 F-NT2RP2005901//H. sapiens CpG island DNA genomic MseI fragment, clone 15b5, reverse read cpg15b5.rta.//0.0026:66:84//Z54729  
 F-NT2RP2005908//Homo sapiens l2q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241  
 F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840  
 F-NT2RP2005942//H. sapiens PAP mRNA.//1.6e-46:618:67//X76770  
 F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//1.0e-48:533:71//AC005207  
 F-NT2RP2006023//HS\_3048\_A1\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553  
 F-NT2RP2006038//CIT-HSP-384K4, TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912  
 F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495  
 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861  
 F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047  
 F-NT2RP2006071  
 F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207  
 F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073  
 F-NT2RP2006103//HS\_2254\_A2\_002\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602  
 F-NT2RP2006106//Human Chromosome 11 pac pD1173a5, complete sequence.//1.2e-62:655:71//AC000378  
 F-NT2RP2006141//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405  
 F-NT2RP2006166//Homo sapiens chromosome 4 clone 83218, complete sequence.//3.1e-45:387:81//AC004063  
 F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lcc4A cell line point mutant mRNA, complete cds.//0.99:111:73//U62587  
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554  
 F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232  
 F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057  
 F-NT2RP2006219//H. sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484  
 F-NT2RP2006237//CIT-HSP-2300P9, TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480  
 F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein RAB mRNA, complete cds.//7.6e-102:635:86//U49055  
 F-NT2RP2006258//RPC111-9N9, TP RPC111 Homo sapiens genomic clone RPC111-9N9, genomic survey sequence.//8.6e-05:181:63//B71615  
 F-NT2RP2006261//H. sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630  
 F-NT2RP2006275//Pseudorabies virus UL5.6, 7, 8, 5, 9, 10, 11, 12, 13 genes.//2.0e-05:501:59//X97257  
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262  
 F-NT2RP2006320//P. falciparum pfmdrl gene.//0.00013:425:60//X56851  
 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973  
 F-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532  
 F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893  
 F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514  
 F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590  
 F-NT2RP2006393//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727  
 F-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808  
 F-NT2RP2006441  
 F-NT2RP2006454//Sequence 8 from Patent W09517522.//2.9e-06:180:66//A45338  
 F-NT2RP2006456  
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266  
 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding chl-ch4 and secretion domains, partial cds.//0.061:201:66//U50149  
 F-NT2RP2006472  
 F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MOW2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//8.8e-10:273:66//Z93929  
 F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174:59//U40965  
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966  
 F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone 82-1.//6.0e-26:503:63//M20855  
 F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315  
 F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537  
 F-NT2RP3000002//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571  
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//AJ011972  
 F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320  
 F-NT2RP3000047  
 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.0e-67:626:74//M27877  
 F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227  
 F-NT2RP3000068  
 F-NT2RP3000072//Homo sapiens BAC clone RC290G13 from 7q21, complete sequence.//1.0:301:61//AC004746  
 F-NT2RP3000080//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391  
 F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536  
 F-NT2RP3000092//RPC111-22M5, TV RPC111 Homo sapiens genomic clone RPC111-22M5, genomic survey sequence.//3.3e-27:157:97//B84237  
 F-NT2RP3000109//Arabidopsis thaliana l-amino-l-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185:64//L29260  
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189  
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164  
 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPC.264\_B\_14, complete sequence.//4.2e-24:155:94//AC005884  
 F-NT2RP3000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583  
 F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063  
 F-NT2RP3000207//Drosophila melanogaster DNA sequence (PI D500164 (D269)), complete sequence.//0.96:608:55//AC004716  
 F-NT2RP3000220  
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569  
 F-NT2RP3000235//Mouse Cosmid wa53a016 from 14D1-D2, complete sequence.//3.5e-05:224:65//AC004101  
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972  
 F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119:68//ZT0213

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F-NT2RP3000252//Homo sapiens cosmid IF1, complete sequence.//9.8e-78:174:88//AF065393  
 F-NT2RP3000255  
 F-NT2RP3000267  
 F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374:82//U48853  
 F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds.//4.9e-22:583:63//J02932  
 F-NT2RP3000320//RPC111-36J1.TP RPC1-11 Homo sapiens genomic clone RPC1-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107  
 F-NT2RP3000324//Rattus norvegicus potassium channel regulator-1 mRNA, complete cds.//5.5e-26:283:79//U78090  
 F-NT2RP3000333//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 973W2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533  
 F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181  
 F-NT2RP3000348  
 F-NT2RP3000350//Homo sapiens cosmid IF1, complete sequence.//3.4e-79:174:88//AF065393  
 F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757  
 F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743  
 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//U49666  
 F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318  
 F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642  
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185  
 F-NT2RP3000418//Homo sapiens chromosome 17, clone HRPK.1053\_B\_8, complete sequence.//7.9e-53:817:68//AC006083  
 F-NT2RP3000433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681  
 F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22a810, genomic survey sequence.//4.0e-19:169:81//AL026471  
 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1s-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488  
 F-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650  
 F-NT2RP3000451//HS\_2024\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=1, genomic survey sequence.//0.011:367:57//AQ229420  
 F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548  
 F-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353  
 F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ftla.//1.7e-11:96:92//Z64440  
 F-NT2RP3000512//Human HMX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667  
 F-NT2RP3000526//Homo sapiens full length insert cDNA clone Y238E04.//4.1e-30:283:76//AF086071  
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966  
 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260  
 F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pJ404m15, complete sequence.//0.00019:361:60//AC002554  
 F-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//9.0e-171:827:98//AC005012  
 F-NT2RP3000562  
 F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271  
 F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//BT3597  
 F-NT2RP3000584  
 F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 17047, forward read cpg170d7.ftla.//3.0e-22:128:100//Z59723  
 F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868  
 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305  
 F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043  
 F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320  
 F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128  
 F-NT2RP3000622//HS\_3213\_A2\_D02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104  
 F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890  
 F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313  
 F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363  
 F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE. 5 unordered pieces.//5.2e-46:421:77//AC005089  
 F-NT2RP3000661  
 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237  
 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//Z99961  
 F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872  
 F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930  
 F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264  
 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655  
 F-NT2RP3000753  
 F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281  
 F-NT2RP3000815//HS\_2237\_A2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252  
 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387  
 F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513  
 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009  
 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:566:68//Z86062  
 F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581  
 F-NT2RP3000847//Human HepG2 3' region cDNA: clone hmd5d02.//3.4e-32:261:81//D16938  
 F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE. 7 unordered pieces.//5.1e-44:358:81//AC005082  
 F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LMHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SEL gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940  
 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831  
 F-NT2RP3000865  
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445  
 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367  
 F-NT2RP3000875//HS\_2236\_B1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=M, genomic survey sequence.//0.98:153:68//AQ154007  
 F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL2

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7) gene, complete cds.//0.44:213:65//AF021340  
 F-NT2RP3000904//Rat Nat channel mRNA, 3' end.//3.6e-106:505:99//M27223  
 F-NT2RP3000917//Mouse mRNA for Dhal protein, complete cds.//3.1e-132:691:93//D38517  
 F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264  
 F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326  
 F-NT2RP3000980//R. norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335  
 F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529  
 F-NT2RP3001004//H. sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.r1la.//5.9e-27:150:99//Z60925  
 F-NT2RP3001007//Homo sapiens clone MH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039  
 F-NT2RP3001055//Drosophila melanogaster: Chromosome 2R: Region 47F 1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653  
 F-NT2RP3001057//H. sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219  
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325  
 F-NT2RP3001096//CIT-HSP-2305P8, TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey sequence.//3.4e-37:222:93//AQ021278  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969  
 F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//AC005317  
 F-NT2RP3001111  
 F-NT2RP3001113//Human DNA sequence from cosmid U15704, between markers DXS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871  
 F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//AC005189  
 F-NT2RP3001116//HS\_3075\_A1\_F01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581  
 F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//1.4e-121:598:97//AL031864  
 F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367  
 F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:64//Z49078  
 F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//AF027735  
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305  
 F-NT2RP3001147//RPC111-3M16, TP RPC1-11 Homo sapiens genomic clone RPC1-11-3M16, genomic survey sequence.//2.1e-15:106:96//B48859  
 F-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:89:1:98//AJ006266  
 F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351  
 F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507  
 F-NT2RP3001216//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845  
 F-NT2RP3001221  
 F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619  
 F-NT2RP3001236  
 F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396  
 F-NT2RP3001245//CITB1-E1-2505C1, TF.1 CITB1-E1 Homo sapiens genomic clone 2505C1, genomic survey sequence.//8.5e-70:337:100//AQ242007  
 F-NT2RP3001253//CITB1-E1-2505N14, TR CITB1-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430  
 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete c

ds.//3.8e-47:761:64//AB018269  
 F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513  
 F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101  
 F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative a M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561  
 F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence.//5.9e-39:304:70//AC005837  
 F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457  
 F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465  
 F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709  
 F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790  
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966  
 F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935  
 F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105  
 F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 in CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052  
 F-NT2RP3001356  
 F-NT2RP3001374  
 F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628  
 F-NT2RP3001384//Homo sapiens HRHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332  
 F-NT2RP3001392//Human DNA sequence from PAC 30Z09 on chromosome 22 q11.2-pter. Contains STS, complete sequence.//0.045:359:61//Z82198  
 F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296  
 F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046  
 F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3.3, complete sequence.//5.4e-20:245:73//AC005521  
 F-NT2RP3001407//RPC111-41A20, TP RPC1-11 Homo sapiens genomic clone RPC1-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031  
 F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q 21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327  
 F-NT2RP3001426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447  
 F-NT2RP3001427//CIT-HSP-2302H24, TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997  
 F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U69668  
 F-NT2RP3001432//HS\_3032\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619  
 F-NT2RP3001447  
 F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP2 1/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyl transferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archaeo)bacterial, worm and yeast hypothetical genes, and the GMB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG island s, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282  
 F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065  
 F-NT2RP3001457  
 F-NT2RP3001459  
 F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836



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F-NT2RP3001490	F-NT2RP3001799//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469022, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284
F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395	F-NT2RP3001819//S. glaucescens genes strU, strX, strY and strW for 5'-hydroxystreptomycin production and transport polypeptides.//0.084:526:58//X89010
F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T RC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801	F-NT2RP3001844//HS_3110_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-40:232:82//AQ140433
F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds.//8.9e-140:743:91//U36499	F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505
F-NT2RP3001529//Streptomyces griseus DNA for ribosomal protein L21, ribosomal protein L27. Dbg. complete cds.//2.1e-14:517:59//D87916	F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknol1) mRNA, complete cds.//2.7e-39:575:67//AF061270
F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:63//AF078176	F-NT2RP3001857//M. musculus tex292 mRNA (5' region).//8.7e-07:106:81//X80434
F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1 A MAP1A (Map-1) mRNA, complete cds.//4.3e-17:332:67//M83196	F-NT2RP3001896
F-NT2RP3001580//RPC111-91E9.TV RPC111 Homo sapiens genomic clone R-91E9, genomic survey sequence.//4.2e-15:110:91//AQ281332	F-NT2RP3001898//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733
F-NT2RP3001587//S. pombe chromosome 11 cosmid c16H5.//6.6e-28:491:64//AL022104	F-NT2RP3001915//Caenorhabditis elegans cosmid C1208, complete sequence.//0.58:482:56//Z73969
F-NT2RP3001589//RPC111-68M15.TK RPC111 Homo sapiens genomic clone R-68M15, genomic survey sequence.//8.7e-108:517:98//AQ237629	F-NT2RP3001926//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557
F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600GB (Genome Systems Human BAC library) complete sequence.//1.0e-09:257:65//AC004674	F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LA NL), complete sequence.//3.1e-28:263:77//AC004651
F-NT2RP3001608//Methylococcus capsulatus methano monooxygenase component A alpha chain, methano monooxygenase A beta chain and methanone monooxygenase component C genes, complete cds.//0.59:450:57//M90050	F-NT2RP3001931
F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.8e-42:278:79//AL021808	F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475
F-NT2RP3001629	F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575
F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978	F-NT2RP3001944
F-NT2RP3001642//Caenorhabditis elegans cosmid F4SE6, complete sequence.//0.018:127:66//Z68117	F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844
F-NT2RP3001646	F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cqr2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694
F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449	F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822
F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793	F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386
F-NT2RP3001676//HS_3090_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250	F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137
F-NT2RP3001678//Drosophila melanogaster: Chromosome 3L: Region 63C 5-63D3: P1 clone DSO1859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358	F-NT2RP3002014//Drosophila melanogaster DNA sequence (Pis DSO7528 (D169) and DSO6665 (D220)), complete sequence.//1.3e-32:334:68//AC004640
F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.8e-130:355:96//AB020860	F-NT2RP3002033//H. sapiens DNA sequence.//0.012:214:63//Z22493
F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//2.1e-37:512:70//AF059273	F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773
F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.8e-19:123:95//AQ012480	F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome: segment 143/162.//1.6e-12:613:60//AL021841
F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9.4e-11:167:74//D31962	F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249
F-NT2RP3001708//H. sapiens CpG island DNA genomic MseI fragment, clone 4g7, reverse read cpg4g7.rtd.//1.3e-17:113:97//Z61312	F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682
F-NT2RP3001712//M. musculus mRNA for HPI-BP74 protein.//2.2e-95:601:88//X99642	F-NT2RP3002062
F-NT2RP3001716	F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome: segment 3/4.//0.24:508:58//AJ235272
F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:565:97//AF054177	F-NT2RP3002081//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494
F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//1.7e-132:786:88//AF008554	F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//9.6e-56:562:77//AC006210
F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918	F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040
F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence.//6.5e-07:178:69//AC009097	F-NT2RP3002108
F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//5.2e-31:311:77//AL031311	F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020
F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//162381	F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (plkB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370
F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888	F-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710
F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644	F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742
F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:98//AB007928	
F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.2e-26:213:85//U13262	

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F-NT2RP3002163	sequence. //1.3e-22:407:57//AC006129
F-NT2RP3002165//M.musculus HCNGP mRNA. //1.4e-142:867:87//X68061	F-NT2RP3002671//S.pombe chromosome III cosmid c553. //1.0e-12:336:66//AL023704
F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200.L_4, complete sequence. //0.090:394:59//AC006121	F-NT2RP3002682//Caenorhabditis elegans cosmid F17C11, complete sequence. //1.3e-21:448:64//Z72507
F-NT2RP3002173//HS_3062_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=M, genomic survey sequence. //3.3e-101:509:96//AQ193219	F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence. //2.5e-25:173:91//BS1656
F-NT2RP3002181//Human DNA sequence from clone 24e18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VND-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence. //4.5e-106:432:84//AL021808	F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds. //1.2e-73:728:74//D17577
F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence. //0.63:353:60//AC005321	F-NT2RP3002701//CITB1-E1-2507L14.TF CITB1-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence. //0.0012:55:92//AQ263530
F-NT2RP3002248//HS_3029_A1_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence. //3.5e-10:125:79//AQ094880	F-NT2RP3002713
F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end. //5.6e-09:629:59//L14321	F-NT2RP3002763//Caenorhabditis elegans cosmid T20F10, complete sequence. //0.98:209:63//Z81594
F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence. //4.9e-35:366:74//B03004	F-NT2RP3002770
F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex. //0.023:326:60//X64898	F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds. //0.78:515:57//AF029325
F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome. //3.8e-12:643:57//AE000810	F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence. //1.9e-21:167:79//AL022718
F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.6e-09:490:60//AC005504	F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPM.215_E_13, complete sequence. //0.32:187:66//AC005549
F-NT2RP3002330//Human DNA sequence from cosmid LS8b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches. //1.9e-93:572:88//Z49862	F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds. //6.9e-54:615:70//AF004715
F-NT2RP3002343//HS_3010_A2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence. //9.0e-75:373:97//AQ119068	F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4. //4.2e-05:226:65//U64601
F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15). //4.9e-64:588:75//X16396	F-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds. //2.0e-93:638:83//AF030430
F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (7-7A) gene, alternatively spliced form. //1.3e-164:770:98//Y16355	F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds. //8.5e-89:557:88//AB001895
F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds. //1.4e-190:911:98//AB018331	F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPC111-433J 6, WORKING DRAFT SEQUENCE, 100 unordered pieces. //7.9e-12:160:78//AC006087
F-NT2RP3002399	F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds. //5.7e-180:853:98//AB018314
F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase II, complete cds. //7.2e-25:249:79//D89340	F-NT2RP3002911//RPC111-24N15.TPC RPC111-Homo sapiens genomic clone RPC111-24N15, genomic survey sequence. //2.3e-13:442:61//B88815
F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds. //1.2e-138:649:99//AB014578	F-NT2RP3002948//, complete sequence. //2.2e-110:637:91//AC005500
F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence. //5.0e-18:115:96//B78927	F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBWL H169), complete sequence. //1.7e-166:793:98//AC005754
F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence. //0.00020:170:65//Z49068	F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5. //0.0001:61:95//D17024
F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence. //1.6e-59:308:97//AF091088	F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds. //1.2e-128:808:85//D30666
F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds. //1.4e-144:763:93//U35246	F-NT2RP3002972//H.sapiens (xsl168) mRNA, 381bp. //1.5e-43:312:85//Z36820
F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds. //1.8e-178:833:98//AB018272	F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.00044:527:57//AC005505
F-NT2RP3002549//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces. //4.7e-26:123:72//AC004821	F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence. //0.92:341:60//AC001644
F-NT2RP3002566//Streptomyces viridificans sigma factor (hrdD) gene, complete cds. //0.76:459:59//U60418	F-NT2RP3002988//HS_3015_A1_B07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence. //4.4e-05:379:58//AQ091708
F-NT2RP3002587//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //4.6e-13:199:76//AC004617	F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes. //1.4e-72:197:79//AF109905
F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome. //0.88:284:60//U38804	F-NT2RP3003032//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence. //1.6e-08:809:58//AL010153
F-NT2RP3002602//CIT978SK-A-441H11-2.TP8 CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence. //2.0e-22:140:95//B68331	F-NT2RP3003059//Rattus norvegicus potassium channel regulator I mRNA, complete cds. //4.1e-111:804:81//U78090
F-NT2RP3002603	F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1). //1.4e-12:633:59//X16609
F-NT2RP3002628//C.acetobutylicum dnaJ and orfB genes. //2.0e-05:333:60//X69050	F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence. //0.034:282:60//AC002410
F-NT2RP3002631	F-NT2RP3003071//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpgl13d12.rtlc. //6.8e-15:95:100//Z64565
F-NT2RP3002650//Mus musculus mRNA for cartilage-associated protein (CASP). //1.5e-20:641:62//AJ006469	F-NT2RP3003078
F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes. //5.2e-05:621:59//Z78205	F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds. //8.1e-72:732:71//D88315
F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from Tq31.2-q31, complete sequence. //0.98:453:57//AC004946	F-NT2RP3003121
F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete	F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence. //3.5e-12:168:76//AC004510

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n KIF4, complete cds.//4.0e-148:908:87//D12646  
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//U17995  
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639  
 F-NT2RP3003150  
 F-NT2RP3003157//HS\_3055\_B1\_G05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489  
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds.//8.6e-06:228:65//AF064868  
 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933  
 F-NT2RP3003197  
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//4.1e-48:640:67//AF015264  
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U101059  
 F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799  
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAPIC) mRNA, complete cds.//6.3e-75:776:74//U20286  
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064  
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460  
 F-NT2RP3003251//H.sapiens Stat50 mRNA.//3.5e-67:651:76//X82200  
 F-NT2RP3003264//Plasmodium falciparum 307 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153  
 F-NT2RP3003278//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ftla.//4.0e-27:174:93//Z60555  
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983  
 F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Ca p43) mRNA, complete cds.//1.7e-64:662:71//AF004162  
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//D85610  
 F-NT2RP3003302//Homo sapiens, clone hRPK.15\_A.1, complete sequence.//4.6e-95:680:82//AC006213  
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//1.0:191:62//AC004527  
 F-NT2RP3003313//Streptomyces coelicolor cosmid SA7.//0.0084:403:61//AL031107  
 F-NT2RP3003327//H.sapiens Stat50 mRNA.//2.5e-29:253:67//X82200  
 F-NT2RP3003330  
 F-NT2RP3003344  
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795\_F\_17, complete sequence.//9.0e-41:296:84//AC005284  
 F-NT2RP3003353//Human DNA sequence from PAC 97001 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).//0.047:404:60//AL021069  
 F-NT2RP3003377//Homo sapiens clone DJ091922, WORKING DRAFT SEQUENCE, 34 unordered pieces.//8.3e-122:632:96//AC005519  
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//0.0036:127:74//AC000360  
 F-NT2RP3003385//Mus musculus SK03 mRNA, complete cds.//2.0e-110:843:79//U09874  
 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:63//U90653  
 F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317  
 F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173  
 F-NT2RP3003433//HS\_2219\_B2\_A11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866  
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828  
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268  
 F-NT2RP3003491//CIT-HSP-234401.TR CIT-HSP Homo sapiens genomic clone 234401, genomic survey sequence.//1.2e-39:213:97//AQ057124  
 F-NT2RP3003500//HS\_3000\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347  
 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (L ANL), complete sequence.//0.95:279:60//AC004234  
 F-NT2RP3003552//Homo sapiens clone UMGc:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049  
 F-NT2RP3003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985  
 F-NT2RP3003564//HS\_3141\_B1\_G10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798  
 F-NT2RP3003572  
 F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632  
 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387  
 F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LA NL), complete sequence.//6.0e-88:463:84//AC004235  
 F-NT2RP3003625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600  
 F-NT2RP3003656  
 F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271  
 F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096  
 F-NT2RP3003672  
 F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B 1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811  
 F-NT2RP3003686//HS\_3064\_B2\_A04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993  
 F-NT2RP3003701  
 F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel K v4.3 mRNA, complete cds.//4.6e-107:788:82//U42975  
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300  
 F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785  
 F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGRIA, SYNGR1B, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326  
 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R3115 B, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458  
 F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031  
 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321  
 F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801  
 F-NT2RP3003819  
 F-NT2RP3003825  
 F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626  
 F-NT2RP3003831//RPC111-S0N15.TJ RPC111 Homo sapiens genomic clone R-S0N15, genomic survey sequence.//1.1e-21:174:85//AQ082633  
 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070811  
 F-NT2RP3003842//RPC111-44E5.TJ RPC111 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884  
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268  
 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343  
 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181  
 F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein g lucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554  
 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds.//2.6e-47:404:77//AF057358  
 F-NT2RP3003932//Plasmodium falciparum 307 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504  
 F-NT2RP3003989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661  
 F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG 2) mRNA, complete cds.//0.021:433:58//U58837

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- F-NT2RP3004013//M. musculus Spnr mRNA for RNA binding protein.//1.4 e-164:838:94//X84692
- F-NT2RP3004016//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9. WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726
- F-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 809F4. WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400
- F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317
- F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939
- F-NT2RP3004078//M. musculus (BALB/c) MRF2 mRNA.//1.9e-102:684:83//X76089
- F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433
- F-NT2RP3004095//Homo sapiens clone NHD486122. WORKING DRAFT SEQUENCE. 5 unordered pieces.//3.5e-25:272:77//AC005038
- F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973
- F-NT2RP3004125//Homo sapiens TTF-1 interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560
- F-NT2RP3004145
- F-NT2RP3004148
- F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900
- F-NT2RP3004189//M. musculus tez292 mRNA (5' region).//1.1e-06:102:82//X80434
- F-NT2RP3004206//D. melanogaster crn mRNA.//7.3e-69:715:71//X58374
- F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009
- F-NT2RP3004209//Human cosmid Q7A10 (D215246) insert DNA, complete sequence.//8.4e-55:184:84//D42052
- F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNI H127), complete sequence.//0.22:458:60//AC006084
- F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181
- F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385
- F-NT2RP3004253//H. sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353
- F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967
- F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982
- F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871
- F-NT2RP3004332
- F-NT2RP3004334//L. esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908
- F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020
- F-NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
- F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
- F-NT2RP3004378//Drosophila melanogaster: Chromosome 2R: Region 47F1-47F7: P1 clone DS02304. WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653
- F-NT2RP3004399//H. sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249
- F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
- F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
- F-NT2RP3004451//RPC111-51J15.TK RPC111 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326
- F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917
- F-NT2RP3004466//HS\_3038\_B2\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
- F-NT2RP3004470//H. sapiens CpG island DNA genomic MseI fragment, clone B1a11, reverse read cpgB1a11.r1a.//7.0e-25:148:96//Z56029
- F-NT2RP3004472//RPC111-42M5.TJ RPC111 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792
- F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925
- F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024
- F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851
- F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE. 25 unordered pieces.//4.0e-67:265:84//AC006023
- F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673
- F-NT2RP3004504//M. musculus mRNA for CPBE protein.//2.0e-110:618:91//X08260
- F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//AC005328
- F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574
- F-NT2RP3004534//Mouse oncogene (cct2) mRNA, complete cds.//2.0e-93:442:84//L11316
- F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532
- F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126
- F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emz1) mRNA, complete cds.//6.9e-18:433:64//AF031955
- F-NT2RP3004569//CITB1-E1-2522H6.TF CITB1-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780
- F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15D) mRNA, complete cds.//1.0e-179:860:97//AF026445
- F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946
- F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266
- F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE. 1 unordered pieces.//9.3e-14:360:65//AC004977
- F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor rIF2C mRNA, complete cds.//2.9e-52:539:73//AF005355
- F-NT2RP3004669//Brn-3a-class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350
- F-NT2RP3004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 35688. WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882
- F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200.L4, complete sequence.//1.5e-155:844:92//AC006121
- F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TA clone: K24G6, complete sequence.//0.012:417:59//AB012242
- F-NT2RP4000035//Homo sapiens BAC clone NHD353P23 from 2, complete sequence.//8.0e-18:242:74//AC005035
- F-NT2RP4000049//Homo sapiens decay receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761
- F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469
- F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449
- F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558
- F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538
- F-NT2RP4000111//B. taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931
- F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952
- F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776
- F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681
- F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088
- F-NT2RP4000159//RPC111-75N16.TJ RPC111 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551
- F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210
- F-NT2RP4000185//Homo sapiens clone DT1PIE11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989
- F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600
- F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300
- F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete

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to sequence.//1.8e-161:751:99//AC005261  
 F-NT2RP4000218//RPC111-6987.TJ RPC111 Homo sapiens genomic clone R-6987, genomic survey sequence.//1.7e-84:413:98//AQ268504  
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470  
 F-NT2RP4000246//Mus musculus neural variant menat+ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523  
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092  
 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515  
 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408  
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481  
 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322  
 F-NT2RP4000323  
 F-NT2RP4000355  
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//ABD18281  
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195  
 F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome: segment 3/4.//2.0e-23:524:62//AJ235272  
 F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//130536  
 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.//4.3e-05:450:58//D63850  
 F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//9.2e-37:336:69//AC006116  
 F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966  
 F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086  
 F-NT2RP4000424//Homo sapiens chromosome 17, clone HRP41C23, complete sequence.//1.6e-42:265:81//AC003101  
 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194  
 F-NT2RP4000449//CIT-HSP-2366N18.TF CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183  
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12Q, complete sequence.//0.17:158:67//AC003982  
 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499  
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483  
 F-NT2RP4000481  
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125  
 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904  
 F-NT2RP4000515  
 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPC.474\_N\_24, complete sequence.//1.6e-179:851:98//AC006238  
 F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840  
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720  
 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498  
 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386  
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (DS3)), complete sequence.//1.3e-05:498:58//AC002443  
 F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//105465  
 F-NT2RP4000560//Murine genomic DNA: partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580  
 F-NT2RP4000588//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 41407, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730  
 F-NT2RP4000638//HS\_3042\_B2\_005\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333  
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335  
 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904  
 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852  
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149  
 F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272  
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0506 protein, partial cds.//3.1e-41:350:71//ABD11178  
 F-NT2RP4000737//Mycobacterium xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//L19301  
 F-NT2RP4000739//CIT-HSP-2010022.TR CIT-HSP Homo sapiens genomic clone 2010022, genomic survey sequence.//1.1e-24:161:93//B57903  
 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//ACD04917  
 F-NT2RP4000787//Cricetus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818  
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189  
 F-NT2RP4000837//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420  
 F-NT2RP4000839//RPC111-608.TP RPC111 Homo sapiens genomic clone R-PC111-608, genomic survey sequence.//1.5e-44:281:91//B48216  
 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515  
 F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367  
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616  
 F-NT2RP4000879//N.tabacum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804  
 F-NT2RP4000907//Mouse MLR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//D45913  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901  
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290  
 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975  
 F-NT2RP4000927//H.sapiens genomic DNA (Chromosome 3: clone NRL062R).//0.75:175:62//X87547  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532  
 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE. 4 unordered pieces.//0.94:763:56//AC004688  
 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519  
 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657  
 F-NT2RP4000975//CIT-HSP-230716.TF CIT-HSP Homo sapiens genomic clone 230716, genomic survey sequence.//6.5e-31:317:79//AQ015742  
 F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942  
 F-NT2RP4000984//Rhodospirillum rubrum sphaeroides mRNA.//0.76:214:64//M83823  
 F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911  
 F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358  
 F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424  
 F-NT2RP4001004  
 F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176  
 F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140  
 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086  
 F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170  
 F-NT2RP4001057  
 F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469

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## 【表451】

F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124  
 F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018  
 F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372  
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164  
 F-NT2RP4001095  
 F-NT2RP4001100//CITBI-EI-2503J7.TR CITBI-EI Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402  
 F-NT2RP4001117//Canis familiaris sec6l homologue mRNA, complete cds.//1.0e-143:760:87//M96629  
 F-NT2RP4001122  
 F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668  
 F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969  
 F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079  
 F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095  
 F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067  
 F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952  
 F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476  
 F-NT2RP4001174//FMR1 (CCG repeats) [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494  
 F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds.//0.032:453:58//U82511  
 F-NT2RP4001207//HS\_2248\_A1\_C03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358  
 F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019018 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877  
 F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251  
 F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657  
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059559  
 F-NT2RP4001235//RPC111-18E11.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081  
 F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061  
 F-NT2RP4001260//Sequence 2 from Patent W09601901.//0.0018:246:63//A48324  
 F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854  
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138:92//AQ040728  
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250  
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795:91//AJ001119  
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870  
 F-NT2RP4001339//HS\_3205\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-24:305:73//AQ183725  
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106:91//AC004918  
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:66//X91011  
 F-NT2RP4001351//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428  
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107  
 F-NT2RP4001372//RPC111-49L11.TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129:100//AQ051701  
 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609  
 F-NT2RP4001375  
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311\_F\_12, complete sequence.//7.3e-28:153:88//AC005722  
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518:73//AC004691  
 F-NT2RP4001407//P.falciapum glutamic acid-rich protein gnan, complete cds.//0.00079:686:57//J03998  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818:71//D86957  
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839:73//X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:63//AB018326  
 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884  
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523  
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612  
 F-NT2RP4001502//H.sapiens (DBS135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693  
 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//M32513  
 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394:58//AC005308  
 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086  
 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNRO4Bw.//2.2e-05:319:61//Z71663  
 F-NT2RP4001551//S.pombe chromosome II pl p8B7.//0.64:335:60//AL032684  
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309:58//AC004806  
 F-NT2RP4001567//HS\_2166\_B1\_C07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188:59//AQ086290  
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566:72//D79989  
 F-NT2RP4001571//RPC111-21F20.TP RPC1-11 Homo sapiens genomic clone RPC1-11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885  
 F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129:813:85//X92987  
 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795:86//AJ223830  
 F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3e-14:663:59//X74219  
 F-NT2RP4001610//Homo sapiens Xp22 Cosmid U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:135:73//AC002364  
 F-NT2RP4001614//HS\_3042\_B2\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-06:78:89//AQ099333  
 F-NT2RP4001634  
 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-161F1, genomic survey sequence.//4.9e-12:144:76//B02870  
 F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092  
 F-NT2RP4001656//HS\_2013\_A1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793  
 F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362  
 F-NT2RP4001679//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462023, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431  
 F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//U96629  
 F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 D508860 (D181)), complete sequence.//1.1e-13:402:63//AC004296  
 F-NT2RP4001730//RPC111-37M21.TK RPC1-11 Homo sapiens genomic clone RPC1-11-37M21, genomic survey sequence.//0.88:177:67//AQ029840  
 F-NT2RP4001739  
 F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTEL00023.seq.//4.9e-36:192:98//Z96232  
 F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316  
 F-NT2RP4001790//Homo sapiens clone NH0569124, complete sequence.//1.4e-29:327:74//AC005678  
 F-NT2RP4001803  
 F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//AF054841

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## 【表452】

F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAP12 Leucine Rich Acidic Nuclear Protein in pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence.//2.1e-08:601:59//Z98743

F-NT2RP4001828

F-NT2RP4001830//Human mRNA for KIAA0071 gene, partial cds.//2.2e-5 3:555:73//D31888

F-NT2RP4001841

F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572

F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691

F-NT2RP4001889//HS\_2052\_B1\_H06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//AC005014

F-NT2RP4001896//T384TFC TAMU Arabidopsis thaliana genomic clone T3 B4, genomic survey sequence.//0.99:354:61//B26193

F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//0.031:409:60//AB011413

F-NT2RP4001927//HS\_2216\_B1\_D03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677

F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046

F-NT2RP4001946//HS\_3021\_B2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185

F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577

F-NT2RP4001953//CIT-HSP-2294D14. TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey sequence.//0.030:358:61//AQ005028

F-NT2RP4001966//Mus musculus DDC4 (Dcc4) mRNA, complete cds.//2.5e-68:812:68//AF059485

F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91\_J\_4, complete sequence.//1.9e-57:555:75//AC003976

F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950

F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 800 3.//1.6e-29:520:64//U17243

F-NT2RP4002052//CIT-HSP-2045A15. TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//2.8e-22:137:96//B80243

F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9. TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223

F-NT2RP4002075//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

F-NT2RP4002078//RPC111-73M20. TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//F.rubripes GSS sequence, clone 190022b89, genomic survey sequence.//0.0024:350:60//Z92062

F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437

F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LE T-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (CA PDH) mRNA, complete cds.//2.9e-37:193:99//M33197

F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901

F-NT2RP5003477//Human Chromosome 3 pac pD17011, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380

F-NT2RP5003492

F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365

F-NT2RP5003506//H.sapiens CpG island DNA genomic MseI fragment, clone 71h2, reverse read cpg71h2.r11a.//1.4e-49:283:93//Z62703

F-NT2RP5003512//HS\_3084\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RP5003522//Homo sapiens clone NHD479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236

F-NT2RP5003524//Homo sapiens beta-spectrin (HSPB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178

F-NT2RP5003534//H.sapiens CpG island DNA genomic MseI fragment, clone 14c10, forward read cpg14c10.f11b.//0.00013:70:91//Z54631

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934

F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510

F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933

F-OVARC1000013

F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922

F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674

F-OVARC1000035//Homo sapiens GAI7 protein mRNA, complete cds.//6.8e-36:238:89//AF064603

F-OVARC1000058

F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625

F-OVARC1000068//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

F-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HCS, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259

F-OVARC1000087//HS\_2004\_B2\_E11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489

F-OVARC1000092//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//1.1e-10:720:58//AC004617

F-OVARC1000106//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (O448-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

F-OVARC1000114//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

F-OVARC1000133//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

F-OVARC1000139//Caenorhabditis elegans cosmid F0SD1.//2.5e-18:314:64//AF040640

F-OVARC1000145//HS\_2257\_B2\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=N, genomic survey sequence.//5.8e-30:203:90//AQ304854

F-OVARC1000148//CIT-HSP-2345A22. TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//164695

F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764

F-OVARC1000191//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

F-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07: HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604

F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332

F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910

F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//181226

F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194

F-OVARC1000288

2.2e-22:181:83//J00345

F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-1

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【表453】

92A9, genomic survey sequence.//4.8e-18:110:99//B18003  
 F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574  
 F-OVARC1000309  
 F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE. 12 unordered pieces.//3.1e-122:325:95//AC005236  
 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide IC (LAPIC) mRNA, complete cds.//4.0e-46:339:84//U19614  
 F-OVARC1000335//Caenorhabditis elegans cosmid F15810.//0.020:545:57//AF036696  
 F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007  
 F-OVARC1000384//Homo sapiens expanded SCAT CAG repeat.//2.2e-09:276:64//AF020275  
 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693  
 F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201  
 F-OVARC1000414//Homo sapiens PAC clone DJ905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166  
 F-OVARC1000420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718  
 F-OVARC1000427//Homo sapiens clone UWCC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826  
 F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558  
 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165  
 F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284  
 F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678  
 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583  
 F-OVARC1000461  
 F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEPI) mRNA, complete cds.//4.7e-124:650:93//AF023451  
 F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221  
 F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence.//2.5e-06:272:62//AJ227191  
 F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829  
 F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neurexectin, Myotendinous antigen)-LIKE gene and a mitochondrial/c chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297  
 F-OVARC1000496//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031713  
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850  
 F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE. 17 unordered pieces.//8.0e-149:716:98//AC005024  
 F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510  
 F-OVARC1000543//HS\_3055\_A2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820  
 F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, ES T1, GSS, STS, CpG island, complete sequence.//4.4e-136:670:97//AL020669  
 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R2709D, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985  
 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733  
 F-OVARC1000573//HS\_3241\_B1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942  
 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE. 2 unordered pieces.//9.7e-97:445:90//AC002414  
 F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1e-27:354:72//AC003973

F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775  
 F-OVARC1000605  
 F-OVARC1000622//Homo sapiens (subclone 2\_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648  
 F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069  
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772  
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162  
 F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244  
 F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713  
 F-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424  
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds.//1.5e-151:549:99//AF027156  
 F-OVARC1000689//nbxb0003aC01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003  
 F-OVARC1000700  
 F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-4) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925  
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661  
 F-OVARC1000730  
 F-OVARC1000746  
 F-OVARC1000769//HS\_2056\_B2\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905  
 F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403  
 F-OVARC1000781//Sequence 5 from Patent W09722695.//1.9e-89:705:78//A63552  
 F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542  
 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691  
 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE. 99 unordered pieces.//3.2e-55:356:88//AC004469  
 F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CA LC.//9.5e-27:163:94//Y17711  
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543  
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584  
 F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963  
 F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125  
 F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086  
 F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to kata).//0.25:231:61//Z82044  
 F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721  
 F-OVARC1000890  
 F-OVARC1000891  
 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494  
 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320  
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172  
 F-OVARC1000924//HS\_2022\_A1\_C01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493  
 F-OVARC1000936//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.2e-113:476:91//AC003983  
 F-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031814

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【表454】

8	F-0VARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549	plate genome.//1.0:265:59//AE001141
	F-0VARC1000948//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276	F-0VARC1001170//H.sapiens (xsi70) mRNA, 350bp.//4.6e-58:355:90//Z36823
	F-0VARC1000959//CIT-HSP-2348016. TR CIT-HSP Homo sapiens genomic clone 2348016, genomic survey sequence.//0.99:270:59//AQ062850	F-0VARC1001171//CIT-HSP-2285E22. TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152:83//AQ002315
	F-0VARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CoQ island, CA repeat.//3.9e-41:577:72//AL009181	F-0VARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94:80//AL022323
	F-0VARC1000964//P. falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270	F-0VARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//AF063001
	F-0VARC1000971//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841	F-0VARC1001180//G.gallus DNA for polyubiquitin gene Ub 11.//0.0062:275:60//X58195
	F-0VARC1000984//Leishmania major chromosome I, complete sequence.//0.80:345:58//AE001274	F-0VARC1001188//Homo sapiens full length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486
	F-0VARC1000996//M205 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858	F-0VARC1001200
	F-0VARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785	F-0VARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128:67//Z48334
	F-0VARC1001000//HS_2247_AI_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=0, genomic survey sequence.//3.1e-60:315:96//AQ153910	F-0VARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811:87//AC001235
	F-0VARC1001004//Homo sapiens from UMGCC:yl8c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190	F-0VARC1001243//Human BAC clone GS117010 from Tq21-q22, complete sequence.//0.044:457:59//AC003078
	F-0VARC1001010//CIT-HSP-2034M3. TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290	F-0VARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613
	F-0VARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021	F-0VARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95:649:84//AF027505
	F-0VARC1001032//Yeast (S. cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451	F-0VARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776
	F-0VARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:73:76//AF001533	F-0VARC1001270
	F-0VARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149	F-0VARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543
	F-0VARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081	F-0VARC1001282//RPC111-60K8.TK RPC111 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857
	F-0VARC1001044//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING DRAFT SEQUENCE.//0.0017:387:61//AL031319	F-0VARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018
	F-0VARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768	F-0VARC1001306//nxb0002M13r CUGI Rice BAC Library Oryza sativa genomic clone nxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061
	F-0VARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//J30292	F-0VARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986
	F-0VARC1001062//nxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878	F-0VARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504
	F-0VARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525	F-0VARC1001339//Homo sapiens chromosome 17, clone hCIT.124.H.2, complete sequence.//0.76:89:74//AC006071
	F-0VARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657	F-0VARC1001341//CITB1-E1-2503J7. TR CITB1-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402
	F-0VARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529	F-0VARC1001342
	F-0VARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153	F-0VARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=0, genomic survey sequence.//1.5e-07:254:67//B44456
	F-0VARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333	F-0VARC1001357//Homo sapiens Xp22-149 BAC RPC111-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297
	F-0VARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897	F-0VARC1001360
	F-0VARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913	F-0VARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811
	F-0VARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782	F-0VARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801
	F-0VARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (BLN1 HS3), complete sequence.//0.99:148:67//AC005178	F-0VARC1001376//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680
	F-0VARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382	F-0VARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819
	F-0VARC1001129//CIT-HSP-647P20. TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106:66//B79052	F-0VARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287
	F-0VARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//Z62322	F-0VARC1001399//CIT-HSP-229118. TR CIT-HSP Homo sapiens genomic clone 229118, genomic survey sequence.//1.7e-11:104:87//AQ007611
	F-0VARC1001161//Homo sapiens chromosome 4 clone 871M12 map 4q25, complete sequence.//2.9e-90:496:84//AC004069	F-0VARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651
	F-0VARC1001162	F-0VARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426
	F-0VARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219:64//AC004961	F-0VARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudogene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714
	F-0VARC1001169//Borrelia burgdorferi (section 27 of 70) of the com	F-0VARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387
		F-0VARC1001442//Human DNA sequence *** SEQUENCING IN PROGRESS ***

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from clone 998H5, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687  
 F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482  
 F-OVARC1001476//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277  
 F-OVARC1001480  
 F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140  
 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507  
 F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13 F4 complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039  
 F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411  
 F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219  
 F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140  
 F-OVARC1001555//Homo sapiens clone MH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037  
 F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retro pseudogene.//2.4e-115:540:99//AF031165  
 F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945  
 F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409  
 F-OVARC1001611  
 F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682  
 F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543  
 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867  
 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85:69//B92840  
 F-OVARC1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651  
 F-OVARC1001713//Rattus norvegicus neuroigin 2 mRNA, complete cds.//1.0:262:59//U41662  
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752  
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650  
 F-OVARC1001745//HS\_3007\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522  
 F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:708:98//U97670  
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575  
 F-OVARC1001768  
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from Bq21, complete sequence.//5.7e-64:477:78//AC005066  
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704  
 F-OVARC1001802//CITBI-EI-2502A17. TR CITBI-EI Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481  
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat at polymorphism, complete sequence.//9.5e-151:712:99//AL023694  
 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748  
 F-OVARC1001812//Homo sapiens chromosome 17, clone HC1T04N19, complete sequence.//1.7e-63:526:81//AC003662  
 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224  
 F-OVARC1001820//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779  
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBML H155), complete sequence.//2.8e-17:509:62//AC005609  
 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403:58//Z73361  
 F-OVARC1001861//CIT-HSP-2165M3. TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611  
 F-OVARC1001879//HS\_3026\_B1\_F09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748  
 F-OVARC1001880//Human interferon regulatory factor 5 (Hmif15) mRNA, complete cds.//3.5e-05:489:60//U51127  
 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020  
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749  
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904  
 F-OVARC1001911//HS\_2196\_B2\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069  
 F-OVARC1001916//HS\_3054\_B1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979  
 F-OVARC1001928  
 F-OVARC1001942//H.sapiens CpG island DNA genomic MseI fragment, clone 21d7, forward read cpq21d7.ftla.//7.2e-12:83:98//Z60390  
 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179  
 F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263  
 F-OVARC1001950//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//1.5e-20:261:68//AJ011929  
 F-OVARC1001987//D.melanogaster CGPD gene, exons 2-4.//0.99:447:57//Z19021  
 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//2.9e-19:178:83//AC005995  
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934  
 F-OVARC1002056//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011  
 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-136:683:96//AC006015  
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from Tq22-q31.1, complete sequence.//1.0:220:61//AC004668  
 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483  
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK\_202\_H\_3, complete sequence.//0.013:461:57//AC006241  
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AFD16427  
 F-OVARC1002143//CIT-HSP-2343H20. TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey sequence.//2.3e-11:258:67//AQ055576  
 F-OVARC1002156  
 F-OVARC1002158//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence.//1.8e-16:383:66//B11616  
 F-OVARC1002165//H.sapiens BDPI mRNA for protein-tyrosine-phosphatase.//0.0041:300:64//X79568  
 F-OVARC1002182//F.rubripes GSS sequence, clone 123123aA7, genomic survey sequence.//1.4e-10:240:66//AL017241  
 F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey sequence.//8.2e-10:158:75//AQ003859  
 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585  
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789  
 F-PLACE1000014  
 F-PLACE1000031//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:333:61//AC004821  
 F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023  
 F-PLACE1000048//Homo sapiens chromosome 17, clone HC1T462L7, complete sequence.//3.6e-63:488:82//AC005177  
 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508  
 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-

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30:190:94//L22154  
F-PLACE1000065//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521  
F-PLACE1000078//Homo sapiens chromosome 11 clone C1T987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848  
F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R2846 1, genomic sequence, complete sequence.//0.52:390:60//AC002389  
F-PLACE1000094  
F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG island, complete sequence.//4.4e-129:731:92//AL023580  
F-PLACE1000142//H. sapiens ALH mRNA.//6.4e-09:328:62//X79888  
F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291  
F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//176211  
F-PLACE1000213  
F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504  
F-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695020, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818  
F-PLACE1000246//HS\_2008\_A2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813  
F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584  
F-PLACE1000308//D. teissieri mitochondrial DNA for tRNA-met, tRNA-Ile, tRNA-Gln & tRNA-Val.//0.00013:369:59//X54011  
F-PLACE1000332//HS\_2016\_B2\_D08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106  
F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350  
F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891  
F-PLACE1000380//F. rubripes GSS sequence, clone 047P21a10, genomic survey sequence.//0.43:198:62//Z88163  
F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//U58032  
F-PLACE1000401//Pinctada lucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074  
F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867  
F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK\_227\_G\_15, complete sequence.//1.6e-85:421:87//AC005899  
F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16' and 17.//0.88:145:68//U61515  
F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189  
F-PLACE1000435//HS\_3217\_A2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698  
F-PLACE1000444//Homo sapiens chromosome 16 BAC clone C1T987SK-A-15 2ES, complete sequence.//6.9e-61:616:71//AC004382  
F-PLACE1000453//Murine genomic DNA: partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580  
F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a 1 n DGCR Region, complete sequence.//1.1e-33:349:76//AC002491  
F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245  
F-PLACE1000540//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276  
F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484  
F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409  
F-PLACE1000564  
F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877  
F-PLACE1000588//Human guanylate binding protein isoform 1 (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542  
F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449  
F-PLACE1000599//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276  
F-PLACE1000610//HS\_2056\_A1\_D10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967  
F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201  
F-PLACE1000636  
F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265  
F-PLACE1000656//Homo sapiens mRNA for JMA protein, complete CDS (clone IMAGE 546750 and LMLC10F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896  
F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219  
F-PLACE1000712  
F-PLACE1000716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026  
F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey sequence.//0.023:157:68//AQ113109  
F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:664:57//AL034559  
F-PLACE1000755//H. sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589  
F-PLACE1000769//RPC111-3J18.TPB RPC111 Homo sapiens genomic clone RPC111-3J18, genomic survey sequence.//6.5e-08:93:89//B63806  
F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548  
F-PLACE1000786//Drosophila melanogaster cosmid 80MT.//1.4e-43:589:68//AL031027  
F-PLACE1000793//H. sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpq13d12.rtlc.//4.6e-09:71:100//Z64565  
F-PLACE1000798//Human Chromosome 16 BAC clone C1T987SK-A-635H12, complete sequence.//5.0e-14:235:72//AC002310  
F-PLACE1000841//Homo sapiens clone NHD441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.013:404:60//AC006158  
F-PLACE1000849//H. sapiens CpG island DNA genomic MseI fragment, clone 72a10, reverse read cpq72a10.rtlc.//3.3e-09:82:92//Z62712  
F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935  
F-PLACE1000863//H. sapiens CpG island DNA genomic MseI fragment, clone 53d2, forward read cpq53d2.ftlb.//7.3e-37:199:98//Z55621  
F-PLACE1000909//H. sapiens CpG island DNA genomic MseI fragment, clone 173f8, reverse read cpq173f8.rtlc.//1.5e-17:128:92//Z57391  
F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181  
F-PLACE1000948  
F-PLACE1000972//RPC111-61B1.TJ RPC111 Homo sapiens genomic clone R-61B1, genomic survey sequence.//1.0e-26:148:99//AQ194348  
F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572  
F-PLACE1000979//H. sapiens CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpq76e8.rtlc.//2.7e-10:84:94//Z55963  
F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267  
F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011  
F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey sequence.//0.99:277:58//B58681  
F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357  
F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//AC004741  
F-PLACE1001024  
F-PLACE1001036//CIT-HSP-2373110.TF CIT-HSP Homo sapiens genomic clone 2373110, genomic survey sequence.//1.1e-80:393:98//AQ108662  
F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K919, complete sequence.//8.8e-40:483:66//AB013390  
F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761  
F-PLACE1001076//HS\_2195\_B1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066559  
F-PLACE1001088  
F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485  
F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:62//U01400  
F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:71//AF022158  
F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambd

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【表457】

a-ARH(6,12).//3.8e-25:174:93//M30702  
 F-PLACE1001168  
 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete s  
 equence.//7.6e-23:245:68//ACD05603  
 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome  
 Xq22.1-22.3. Contains part of the gene for a novel protein simila  
 r to X. laevis Cortical Thymocyte Marker CTX, the possibly alterna  
 tively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat  
 protein), a novel gene and exons 36 through 45 of the COL4A6 for  
 Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG  
 island, complete sequence.//0.010:102:70//AL031177  
 F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor  
 (PAF53), complete cds.//9.3e-82:684:77//D14336  
 F-PLACE1001241  
 F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:  
 60//AF067219  
 F-PLACE1001272//H. sapiens subunit of coatomer complex.//0.31:50:95  
 //X70476  
 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62  
 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//  
 0.054:352:60//ACD05507  
 F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate trans  
 cription control protein (BICP4) gene, complete cds.//1.0e-10:520:  
 61//L14320  
 F-PLACE1001294//M. musculus GEG-154 mRNA.//5.0e-107:826:80//X71642  
 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//  
 1.2e-67:510:77//X17617  
 F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUEN  
 CE, 4 unordered pieces.//1.6e-47:491:73//ACD05282  
 F-PLACE1001323//HS-1007-AZ-B10-MF.abi CIT Human Genomic Sperm Libr  
 ary C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genom  
 ic survey sequence.//9.6e-26:142:100//B31181  
 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cd  
 s.//8.6e-25:155:95//ABD18342  
 F-PLACE1001377//H. sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48  
 614  
 F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome  
 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein)  
 pseudogene, EST, CA repeats (D225414, D225925, D225926), STS, GSS  
 and CpG island, complete sequence.//1.5e-119:705:91//AL022324  
 F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//  
 5.7e-08:117:84//AJ001319  
 F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58  
 //157340  
 F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC g  
 enes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.  
 6).//7.2e-11:620:60//X52177  
 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22.W.12, W  
 ORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:709:98//ACD0541  
 2  
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequ  
 ence.//2.0e-69:365:96//AF091087  
 F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202.H.3, com  
 plete sequence.//8.2e-121:608:97//ACD06241  
 F-PLACE1001440//Human Chromosome 11 pac pDJ393015, WORKING DRAFT S  
 EQUENCE, 8 unordered pieces.//1.3e-06:437:61//ACD00384  
 F-PLACE1001456//Homo sapiens Xp22 GS-52411 (Genome Systems Human B  
 AC library), complete sequence.//0.98:348:60//ACD03106  
 F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromo  
 some Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148  
 F-PLACE1001484//Homo sapiens DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL0316  
 60  
 F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3)  
 gene, exon 1.//0.00015:333:59//L78720  
 F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273  
 (DSB)), complete sequence.//0.00016:161:66//ACD04373  
 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome X  
 q21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudog  
 ene and ESTs.//3.7e-22:260:76//AL021786  
 F-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031  
 667  
 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165.I.16, co  
 mplete sequence.//2.7e-139:482:96//ACD05669  
 F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, comple  
 te sequence.//6.9e-116:681:89//ACD05261  
 F-PLACE1001570//HS\_3105\_A1\_F06\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, gen  
 omic survey sequence.//1.2e-10:137:79//AQ139817  
 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge  
 ne of hepatocellular colorectal and non-small cell lung cancer, s  
 egment 3/11.//1.8e-102:217:99//AB020860  
 F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alte  
 rnatively spliced product, complete cds.//3.7e-104:501:98//AF06998  
 4  
 F-PLACE1001608//HS\_2189\_A1\_G07\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, gen  
 omic survey sequence.//2.9e-60:429:84//AQ221959  
 F-PLACE1001610//Homo sapiens clone NHD469M07, WORKING DRAFT SEQUEN  
 CE, 7 unordered pieces.//4.4e-114:552:98//ACD05037  
 F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome  
 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding p  
 rotein, gene similar to monocarboxylate transporter (MCT3), ESTs,  
 STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL0315  
 87  
 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete c  
 ds.//1.1e-74:702:75//AB018341  
 F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-1  
 8:114:100//U17032  
 F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651.L.9, co  
 mplete sequence.//7.7e-159:788:97//ACD05971  
 F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome  
 Xp11. Contains a probable Zinc Finger protein (pseudogene), an unk  
 nown putative gene, a pseudogene with high similarity to part of a  
 ntigen Ki-67, a putative Chondroitin 6-Sulfotransferase LIKE gene  
 and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Co  
 ntains a predicted CpG island, ESTs, STSs and GSSs and genomic mar  
 kers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL02  
 2165  
 F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294.J.22, c  
 omplete sequence.//9.1e-149:760:96//ACD05921  
 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio  
 ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200  
 F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958.E.11, W  
 ORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//ACD05883  
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-6  
 8:369:73//D83776  
 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3  
 In IGLC Region, complete sequence.//1.0:274:59//ACD00051  
 F-PLACE1001729//Streptomyces coelicolor cosmid IC2.//0.22:433:57//  
 AL031124  
 F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61  
 //AF067607  
 F-PLACE1001740//Homo sapiens chromosome 5, PI clone 1108H7 (LBNL H  
 81), complete sequence.//4.8e-26:372:68//ACD05221  
 F-PLACE1001745  
 F-PLACE1001746//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE  
 SS \*\*\* from MAL1PI, WORKING DRAFT SEQUENCE.//0.018:472:57//AL03174  
 4  
 F-PLACE1001748//Homo sapiens metalloprotease 1 (MPI) mRNA, complet  
 e cds.//8.8e-159:773:97//AF061243  
 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPC111-303E  
 5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//A  
 CD05842  
 F-PLACE1001761//HS\_3027\_A1\_D02\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, geno  
 mic survey sequence.//0.095:49:93//AQ130972  
 F-PLACE1001771//Homo sapiens transient receptor potential protein  
 6 mRNA, complete cds.//1.0e-146:709:97//AF080394  
 F-PLACE1001781  
 1.3e-08:238:65//ACD05637  
 F-PLACE1001799//HS\_3075\_B1\_H03\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, geno  
 mic survey sequence.//1.7e-09:166:69//AQ138474  
 F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, PI  
 clone: MRC8, complete sequence.//0.00035:196:66//AB020749  
 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase  
 beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953  
 F-PLACE1001821//RPC111-35D17.TK RPC1-11 Homo sapiens genomic clone  
 RPC1-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286  
 F-PLACE1001844//Homo sapiens chromosome 17, clone HCT1462L7, compl  
 ete sequence.//2.8e-67:443:86//ACD05177  
 F-PLACE1001845//Arabidopsis thaliana chromosome 1 BAC T25B24 genom  
 ic sequence, complete sequence.//0.34:219:64//ACD05850  
 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ri  
 bitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF0  
 45244  
 F-PLACE1001897//RPC111-46D15.TJ RPC111 Homo sapiens genomic clone

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【表458】

R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408  
 F-PLACE1001912  
 F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935  
 F-PLACE1001928//HS\_2220\_B2\_G04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361  
 F-PLACE1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596  
 F-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755  
 F-PLACE1002004//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996  
 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337  
 F-PLACE1002052//HS\_2178\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=M, genomic survey sequence.//4.8e-22:140:95//AQ307908  
 F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284  
 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195  
 F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178  
 F-PLACE1002090//Homo sapiens full length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131  
 F-PLACE1002115//nxb0038A2Or CUGI Rice BAC Library Oryza sativa genomic clone nxb0038A2Or, genomic survey sequence.//0.039:210:69//AQ291086  
 F-PLACE1002119//Mus musculus IER5 (ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527  
 F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162  
 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556  
 F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539  
 F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662  
 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC: GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805  
 F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244  
 F-PLACE1002205//Drosophila melanogaster: Chromosome 3L: Region 79F-1-80A2: BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720  
 F-PLACE1002213//HS\_3238\_B1\_G03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965  
 F-PLACE1002227//HS-1056-B1-C01-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800  
 F-PLACE1002256//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-72, complete sequence.//0.022:458:59//AL010142  
 F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D225414, D225925, D225926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324  
 F-PLACE1002319  
 F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956  
 F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623  
 F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235\_1\_10, complete sequence.//5.6e-05:474:59//AC005922  
 F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928  
 F-PLACE1002437//M. musculus abcl mRNA.//5.5e-62:452:85//X75926  
 F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801  
 F-PLACE1002450//HS\_3233\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=N, genomic survey sequence.//3.1e-07:449:59//AQ204769  
 F-PLACE1002465  
 F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262  
 F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926  
 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPC14-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060  
 F-PLACE1002499  
 F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927  
 F-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930  
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256  
 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from Tq21-q31.1, complete sequence.//0.00019:193:65//AC004774  
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575  
 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA A, complete cds.//2.0e-13:400:60//L25314  
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523  
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443  
 F-PLACE1002591//H. sapiens mRNA for coronin.//7.2e-26:279:74//X89109  
 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE. 6 unordered pieces.//0.0013:375:64//AC005537  
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785  
 F-PLACE1002625  
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from Tq31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281  
 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765  
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180  
 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726  
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723  
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273  
 F-PLACE1002772//HS\_3058\_A1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567  
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259  
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927  
 F-PLACE1002794//CIT-HSP-2368A17, TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879  
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994  
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295  
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691  
 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//9.3e-41:240:93//M27877  
 F-PLACE1002839//Human BAC clone RG205C13 from Tq31, complete sequence.//0.00087:213:63//AC003045  
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140  
 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126  
 F-PLACE1002881//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111822, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200  
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKI

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【表459】

1) mRNA, complete cds.//0.00012:200:64//U19889	(hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401
F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120	F-PLACE1003493
F-PLACE1002962	F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994
F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558	F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23 a.//6.2e-21:247:76//AF064859
F-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755	F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs. STSs and a GSS.//4.4e-68:502:79//AL008729
F-PLACE1002993//CIT-HSP-2338116, TF CIT-HSP Homo sapiens genomic clone 2338116, genomic survey sequence.//1.9e-13:100:95//AQ054760	F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336
F-PLACE1002996//House U6 RNA gene.//2.0e-13:113:90//X06980	F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831
F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551	F-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297
F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088	F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547
F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829	F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688
F-PLACE1003045//H. sapiens CpG island DNA genomic MseI fragment, clone 4766, forward read cpg47g6.ftla.//0.0064:52:96//Z61200	F-PLACE1003583//Human DNA sequence from clone 245H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324
F-PLACE1003092//CIT-HSP-387P22, TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158	F-PLACE1003584//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-56, complete sequence.//0.0038:465:57//AL010230
F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875	F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557
F-PLACE1003108	F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476
F-PLACE1003136//Homo sapiens chromosome 5, PI clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219	F-PLACE1003596//Mus musculus integral membrane protein 1 (Itim) mRNA, complete cds.//1.4e-54:685:68//L34260
F-PLACE1003145	F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200
F-PLACE1003153//RPC111-13P16, TP RPC1-11 Homo sapiens genomic clone RPC1-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206	F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RTB1 (LAN U), complete sequence.//0.0074:265:63//AC005356
F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495	F-PLACE1003611//HS_2198_B1_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475
F-PLACE1003176//HS_2255_A2_B01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934	F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226
F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:90//AC005095	F-PLACE1003625//HS_2238_B2_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=2 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662
F-PLACE1003200//P. falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276	F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MKD10, complete sequence.//0.043:264:63//AB011478
F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466	F-PLACE1003669
F-PLACE1003238//HS_3239_A2_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954	F-PLACE1003704//RPC111-23H21, TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830
F-PLACE1003249	F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bubl1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305
F-PLACE1003256	F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F1551A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920
F-PLACE1003258//HS_3223_A1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317	F-PLACE1003723//HS_2231_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672
F-PLACE1003296//CIT-HSP-2337F11, TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429	F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297
F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//2.3e-92:485:95//M27877	F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840
F-PLACE1003334	F-PLACE1003762
F-PLACE1003342	F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014
F-PLACE1003343//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951	F-PLACE1003771//Homo sapiens BAC clone GS164805 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715	F-PLACE1003783//HS_2190_A2_C02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757
F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095	F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210
F-PLACE1003366	
F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558	
F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247	
F-PLACE1003375	
F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//2.3e-157:779:96//AB020878	
F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680	
F-PLACE1003401//RPC111-71J5, TJ RPC111 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588	
F-PLACE1003420//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone YIE3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388	
F-PLACE1003454//Plasmodium falciparum microsatellite pa63 sequence.//0.0084:219:61//AF015470	
F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1	

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F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RBP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds. and Xq28lu2 gene.//0.015:296:60//US2112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N7583 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

F-PLACE1003850//P. falciparum histidine-rich protein genes.//0.39:330:60//N17028

F-PLACE1003858//Human DNA sequence from PAC 332011 on chromosome 1 q24-q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 307 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.02:6:538:56//AC005139

F-PLACE1003870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54820, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//US8134

F-PLACE1003886//Homo sapiens clone NH0091P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//U42108

F-PLACE1003892//RPC111-24P17.TV RPC1-11 Homo sapiens genomic clone RPC1-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPSH) mRNA, complete cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

F-PLACE1003932//Plasmodium falciparum 307 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954

F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666

F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651

F-PLACE1004128//Mus musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658

F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099

F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-148:731:96//AJ010071

F-PLACE1004197

F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493

F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

F-PLACE1004256//HS\_2010\_B2\_G04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434

F-PLACE1004257//Homo sapiens BAC clone RH0342X06 from 2, complete sequence.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121

F-PLACE1004274//H. sapiens CpG island DNA genomic MseI fragment, clone 18g6, forward read cpg18g6.ft1b.//8.5e-37:196:98//Z57691

F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:97//AF084830

F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MP17, complete sequence.//0.0060:635:57//AB011480

F-PLACE1004289//HS\_3023\_B1\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411

F-PLACE1004316//H. sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588

F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 D507968 (D117)), complete sequence.//0.87:206:59//AC004267

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631

F-PLACE1004384//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653

F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:61:5:62//U70855

F-PLACE1004405//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027

F-PLACE1004425//Homo sapiens PAC clone DJ0733809 from Tpi4-p13, complete sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//R. norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188

F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//Homo sapiens PAC clone DJ1064822 from Tq21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS\_2058\_B1\_C09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//Plasmodium falciparum 307 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//Homo sapiens TATA binding protein associated factor 9 (TAF1150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//Dictyostelium discoideum Miga (miga) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//B. taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001858

F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome: segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H. sapiens CpG island DNA genomic MseI fragment, clone 55h1, forward read cpg55h1.ft1a.//2.4e-34:188:98//Z61632

F-PLACE1004664//Caenorhabditis elegans cosmid W10C6, complete sequence.//1.0:148:65//Z81140

F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:18:2:95//U07561

F-PLACE1004674//Homo sapiens calcium binding protein (ALC-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.9e-152:759:96//AB020860

F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and

【表461】

two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152  
 F-PLACE1004691//HS\_3044\_A1\_G01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323  
 F-PLACE1004693//Human DNA sequence from clone 353HG on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577  
 F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551  
 F-PLACE1004722//HS\_3052\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959  
 F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498  
 F-PLACE1004740//RPC111-58A7.TJ RPC111 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766  
 F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555  
 F-PLACE1004751  
 F-PLACE1004773//Homo sapiens invasin protein mRNA, complete cds.//5.4e-171:828:97//AF084367  
 F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713  
 F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34)), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157  
 F-PLACE1004804  
 F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710  
 F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294\_J\_22, complete sequence.//9.8e-39:207:99//AC005921  
 F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613  
 F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849  
 F-PLACE1004827//HS\_2230\_A2\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313  
 F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825  
 F-PLACE1004838//HS\_3241\_A2\_A04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740  
 F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//192819  
 F-PLACE1004868  
 F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA1 contig fragment No. 9.//0.14:465:59//Z97344  
 F-PLACE1004900  
 F-PLACE1004902//CITBI-E1-2510J4.TJ CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184  
 F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058  
 F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571  
 F-PLACE1004930//Homo sapiens TNF-induced protein CG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671  
 F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmodin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989  
 F-PLACE1004937  
 F-PLACE1004969  
 F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843  
 F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073  
 F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833  
 F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373  
 F-PLACE1005026  
 F-PLACE1005027  
 F-PLACE1005046  
 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867  
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148  
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569  
 F-PLACE1005077  
 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253:77//AC004673  
 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316  
 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225  
 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476  
 F-PLACE1005108//Human BAC clone RGD09H02 from 7q31, complete sequence.//0.46:179:64//AC003081  
 F-PLACE1005111  
 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287:63//U14320  
 F-PLACE1005146//HS\_3071\_A1\_E03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=1, genomic survey sequence.//7.4e-38:299:82//AQ103361  
 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//AC002451  
 F-PLACE1005176  
 F-PLACE1005181//CIT-HSP-234005.TR CIT-HSP Homo sapiens genomic clone 234005, genomic survey sequence.//0.99:211:63//AQ054651  
 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence.//2.7e-07:80:90//AQ074445  
 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061  
 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.70:245:63//AC004965  
 F-PLACE1005243  
 F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812  
 F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4\_2g).//9.6e-33:177:98//Z70695  
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182  
 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M59183  
 F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//M25757  
 F-PLACE1005308//Clostridium glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621  
 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167  
 F-PLACE1005327//HS\_3080\_B2\_A12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116  
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794  
 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380  
 F-PLACE1005373  
 F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104  
 F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991  
 F-PLACE1005453//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854  
 F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859  
 F-PLACE1005471//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581  
 F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191  
 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257120 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878  
 F-PLACE1005481//RPC111-74L17.TJ RPC111 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885  
 F-PLACE1005494//Homo sapiens transient receptor potential protein



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6 mRNA, complete cds. //2.1e-67:325:99//AF080394  
 F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence. //0.015:403:61//AC005589  
 F-PLACE1005526//H. sapiens CpG island DNA genomic MseI fragment, clone 9f1, reverse read cpg9f1.r1la. //3.6e-27:159:96//Z66485  
 F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE. //2.6e-28:449:67//AP000038  
 F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence. //5.5e-18:234:72//AC004860  
 F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence. //1.2e-14:123:75//AL025925  
 F-PLACE1005554//Leishmania tarantolae mitochondrial 12S ribosomal RNA gene. //0.43:209:66//X02354  
 F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B.12, complete sequence. //9.3e-113:536:97//AC004707  
 F-PLACE1005574//Plasmodium falciparum 307 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.1e-10:514:58//AC005504  
 F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds. //0.00056:289:63//AB014517  
 F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence. //1.2e-111:262:89//AC004126  
 F-PLACE1005603  
 F-PLACE1005611//F1605TFC IGF Arabidopsis thaliana genomic clone F1605, genomic survey sequence. //2.0e-10:209:66//B98589  
 F-PLACE1005623  
 F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces. //1.2e-93:230:98//AC005840  
 F-PLACE1005639//HS\_3095\_B1\_A03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3095 Col=5 Row=B, genomic survey sequence. //1.2e-05:220:63//AQ123022  
 F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds. //6.4e-150:721:98//AF083255  
 F-PLACE1005656//H. sapiens RR2 mRNA for small subunit ribonucleotide reductase. //1.3e-51:480:74//X59618  
 F-PLACE1005666//RPC111-78015.TV RPC111 Homo sapiens genomic clone R-78015, genomic survey sequence. //7.8e-05:243:62//AQ284667  
 F-PLACE1005698//Human membrane-associated lectin type-C mRNA. //1.9e-63:374:85//M98457  
 F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence. //0.69:633:57//AE001422  
 F-PLACE1005730//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2026 Col=21 Row=P, genomic survey sequence. //2.0e-24:286:74//AQ231147  
 F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds. //2.8e-55:621:71//U15635  
 F-PLACE1005755//HS\_2213\_A2\_H11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2213 Col=22 Row=O, genomic survey sequence. //1.4e-25:290:75//AQ136844  
 F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thioester hydrolase (MCH), complete cds. //4.5e-40:297:70//M16200  
 F-PLACE1005799//R. norvegicus mRNA for mitochondrial isoform of cytochrome b5. //0.91:287:63//Y12517  
 F-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence. //5.0e-109:530:98//AC004827  
 F-PLACE1005803//HS\_3092\_B1\_A10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3092 Col=19 Row=B, genomic survey sequence. //2.4e-08:76:96//AQ103695  
 F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds. //1.4e-126:636:96//AF027156  
 F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. //2.6e-154:739:98//AF065482  
 F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WORKING DRAFT SEQUENCE, 1 ordered pieces. //2.2e-37:355:77//AC004150  
 F-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-105, complete sequence. //0.00080:663:58//AL010283  
 F-PLACE1005845//Plasmodium falciparum 307 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.0015:340:58//AC004153  
 F-PLACE1005850//Human DNA sequence from clone 46SN24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG island s, complete sequence. //1.8e-46:278:85//AL031432  
 F-PLACE1005851  
 F-PLACE1005876//B. taurus mRNA for cleavage and polyadenylation specificity factor. //5.0e-120:701:89//X75931  
 F-PLACE1005884//CIT-HSP-2333012.TR CIT-HSP Homo sapiens genomic clone 2333012, genomic survey sequence. //4.6e-78:385:98//AQ039226  
 F-PLACE1005890//Schizosaccharomyces pombe bemi/bud5 suppressor (Be  
 m46+) mRNA, partial cds. //9.3e-16:638:57//U29892  
 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds. //1.0:178:65//U87136  
 F-PLACE1005921//M. musculus mRNA for immunity associated protein 3.8. //6.6e-17:614:59//Y08026  
 F-PLACE1005923//RPC111-33G19.TJ RPC111 Homo sapiens genomic clone RPC111-33G19, genomic survey sequence. //4.0e-10:535:57//AQ046151  
 F-PLACE1005925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE. //0.17:159:65//AL034405  
 F-PLACE1005932  
 F-PLACE1005934//H. sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cpg165g2.f1la. //8.3e-43:247:93//Z57153  
 F-PLACE1005936//F. rubripes GSS sequence, clone 069X22aG2, genomic survey sequence. //0.91:116:68//AL014719  
 F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds. //0.0022:495:59//AF016236  
 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence. //2.9e-05:442:61//AC004081  
 F-PLACE1005955//Caenorhabditis elegans cosmid F01F1. //4.3e-20:409:64//U13070  
 F-PLACE1005966//P. falciparum aarp3 gene, exon. //0.0083:270:64//Y08925  
 F-PLACE1005968  
 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC111-407G, WORKING DRAFT SEQUENCE, 51 ordered pieces. //1.0e-100:513:96//AC005866  
 F-PLACE1006002//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE. //2.5e-54:444:77//Z66090  
 F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate-CT 781 Col=2 Row=W, genomic survey sequence. //3.4e-05:214:64//B44442  
 F-PLACE1006011//Mus musculus poly-(ADP-ribose)-transferase homolog PARP mRNA, complete cds. //4.3e-71:580:79//AF072521  
 F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-11JAG6 complete genomic sequence, complete sequence. //8.6e-32:177:83//AC002299  
 F-PLACE1006037//Mus musculus B6D2F1 clone 2C118 mRNA. //1.8e-34:269:83//U01139  
 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine. //3.4e-147:719:97//X99906  
 F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence. //0.37:332:62//Z97200  
 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds. //1.3e-145:679:99//AF039023  
 F-PLACE1006129  
 F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965. //4.8e-27:693:60//D44597  
 F-PLACE1006143//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING DRAFT SEQUENCE. //4.7e-46:435:77//Z93015  
 F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:82. //0.048:290:60//D85750  
 F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-105402 map 10q25, complete sequence. //3.2e-129:466:96//AC005661  
 F-PLACE1006164//HS\_3003\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3003 Col=15 Row=K, genomic survey sequence. //1.4e-70:388:93//AQ118200  
 F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence. //4.3e-78:385:86//AC005239  
 F-PLACE1006170//Mouse mRNA for alpha-adaptin (C). //3.5e-91:630:84//X14972  
 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds. //3.9e-149:694:99//AF091433  
 F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence. //2.5e-16:283:70//AC003658  
 F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds. //2.2e-94:648:84//L25125  
 F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence. //0.15:533:58//U75931  
 F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence. //0.0068:175:64//B19803  
 F-PLACE1006225//CIT-HSP-2335123.TF CIT-HSP Homo sapiens genomic clone 2335123, genomic survey sequence. //2.1e-19:149:90//AQ039880  
 F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-9908 complete sequence. //0.51:290:58//U91327

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F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//1.4e-158:452:96//AC004142  
 F-PLACE1006246//RPC111-36123.TK RPC1-11 Homo sapiens genomic clone RPC1-11-36123, genomic survey sequence.//2.6e-31:176:97//AQ045400  
 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548  
 F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447  
 F-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20R2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320  
 F-PLACE1006318  
 F-PLACE1006325//Homo sapiens PAC clone DJ088L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454  
 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721  
 F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504  
 F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559  
 F-PLACE1006368//X.laavis mRNA for KLP2 protein.//3.0e-25:376:68//X94082  
 F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LA NL), complete sequence.//2.0e-146:711:97//AC004232  
 F-PLACE1006382  
 F-PLACE1006385//Homo sapiens epsilon 2a mRNA, complete cds.//5.1e-110:539:97//AF062085  
 F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029  
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735  
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129  
 F-PLACE1006445//HS\_3071\_A1\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ103347  
 F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496  
 F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA A.//0.99:250:59//Z15118  
 F-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977  
 F-PLACE1006488//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744  
 F-PLACE1006492  
 F-PLACE1006506  
 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083  
 F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355  
 F-PLACE1006534//Caenorhabditis elegans cosmid Y40HTA, complete sequence.//0.00031:671:58//AL033510  
 F-PLACE1006540  
 F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998  
 F-PLACE1006598//Homo sapiens BAC clone NH0539824 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044  
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670  
 F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470  
 F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589  
 F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015  
 F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276  
 F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688  
 F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyl transferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790  
 F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916  
 F-PLACE1006731//Human DNA sequence from PAC 40B23 on chromosome 2 2q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN). ESTs and STS.//1.5e-78:520:86//Z98048  
 F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.9e-135:378:99//AC005626  
 F-PLACE1006760//CIT-HSP-2336013.TR CIT-HSP Homo sapiens genomic clone 2336013, genomic survey sequence.//0.018:147:66//AQ039246  
 F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426  
 F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487  
 F-PLACE1006792//HS\_3165\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559  
 F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513  
 F-PLACE1006800//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272  
 F-PLACE1006805//paramecium species 1,168 nt dna dimer: replication init. region.//9.1e-09:369:62//K00915  
 F-PLACE1006815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033  
 F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230  
 F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350  
 F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559  
 F-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378  
 F-PLACE1006878  
 F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome: segment 138/162.//1.0:236:62//Z95120  
 F-PLACE1006901//Mus musculus t complex testis-specific protein (Tc tex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672  
 F-PLACE1006904  
 F-PLACE1006917//H.sapiens CpG island DNA genomic MseI fragment, clone 79g10, forward read cpg79g10.f11a.//1.3e-21:131:98//Z63175  
 F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063  
 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308  
 F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447  
 F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//U23921  
 F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.6e-06:651:58//AJ223323  
 F-PLACE1006962//H.sapiens iriB mRNA.//7.1e-15:202:71//X63417  
 F-PLACE1006966//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y10SE8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594  
 F-PLACE1006989//cSRL-172A-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A, genomic survey sequence.//1.0:97:67//B03188  
 F-PLACE1007014//Rattus norvegicus equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305  
 F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//5.1e-17:285:70//AC005777  
 F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeats.//6.2e-131:775:89//Z82899  
 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895  
 F-PLACE1007068//Homo sapiens chromosome 17, clone hRPC.214\_0\_1, complete sequence.//1.3e-131:652:97//AC005224  
 F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368  
 F-PLACE1007105//Mus musculus muskellin mRNA, complete cds.//4.1e-124:687:91//U72194  
 F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC136 g

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【表465】

F-PLACE1007990//H. sapiens genomic DNA fragment (clone J31A212R) // 6.6e-35:198:96//294758  
 F-PLACE1008000//Mus musculus vcl 3 mRNA, complete cds. //1.5e-118:706:88//AF087695  
 F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENC E, 4 unordered pieces. //6.4e-163:786:98//AC005628  
 F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP 107 mRNA, complete cds. //1.2e-95:625:84//L31840  
 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequ ence. //0.016:165:65//Z35719  
 F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington 's Disease Region, chromosome 4p16.3. //4.0e-07:251:64//Z68883  
 F-PLACE1008095//RPC111-21F19, TP RPC1-11 Homo sapiens genomic clone RPC1-11-21F19, genomic survey sequence. //1.5e-30:166:99//B85883  
 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitoch ondril gene encoding mitochondrial protein, partial cds. //7.5e-0 6:414:60//AF069163  
 F-PLACE1008122//S. cerevisiae chromosome XIV reading frame ORF YOL12 Sw. //0.046:477:59//Z74867  
 F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 conta ining fur, fes, and alpha sannosidase 1lx genes, WORKING DRAFT SEQ UENCE, 9 unordered pieces. //0.0068:446:57//AC004586  
 F-PLACE1008132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 31605, WORKING DRAFT SEQUENCE. //3.6e-20:111:93//Z82199  
 F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds. //2.5e-88:866:73//D14849  
 F-PLACE1008181//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE. //0.0033:727:56//AL034397  
 F-PLACE1008198//HS\_3073\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, gen omic survey sequence. //2.3e-12:94:92//AQ171450  
 F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENC E, 1 unordered pieces. //2.5e-162:791:97//AC005069  
 F-PLACE1008209  
 F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds. / /0.65:174:66//W26332  
 F-PLACE1008244//CIT-HSP-233784, TR CIT-HSP Homo sapiens genomic clo ne 233784, genomic survey sequence. //6.7e-28:165:95//AQ039317  
 F-PLACE1008273//B. primigenius mRNA for coat protein gamma-cop. //2. 8e-71:709:71//X92987  
 F-PLACE1008275//D. discoideum actin A-13 gene, 5' flank. //0.12:131: 64//W29123  
 F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence. //0.011:96:73//AC0059 13  
 F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds. //8.2e-86:672:77//AF078779  
 F-PLACE1008329//HS\_2027\_A1\_C06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, gen omic survey sequence. //8.7e-09:116:81//AQ244432  
 F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complet e sequence. //2.2e-141:670:98//AC005176  
 F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENC E, 7 unordered pieces. //2.1e-27:157:78//AC005000  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cd s. //1.1e-137:659:98//AB014579  
 F-PLACE1008368//CIT-HSP-2311C9, TR CIT-HSP Homo sapiens genomic clo ne 2311C9, genomic survey sequence. //7.1e-08:398:60//AQ016352  
 F-PLACE1008369//HS\_2251\_B1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, geno mic survey sequence. //2.1e-35:217:93//AQ066512  
 F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136\_H\_19, c omplete sequence. //1.4e-11:403:64//AC005856  
 F-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE. //3.7e-144:681:99//AL034 417  
 F-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromo some 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces. //2.8e-45:257:96//AC004604  
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds. //4.3e-14 8:711:98//D86326  
 F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 ge nomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.08 9:672:56//AC004688  
 F-PLACE1008424  
 F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge ne of hepatocellular colorectal and non-small cell lung cancer, s egment 7/11. //1.0e-88:331:84//AB020864  
 F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence. //0.55:530:58//U62317  
 F-PLACE1008437//CIT-HSP-2376H4, TR CIT-HSP Homo sapiens genomic clo ne 2376H4, genomic survey sequence. //3.3e-78:349:94//AQ112479  
 F-PLACE1008455//HS\_2064\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, gen omic survey sequence. //4.7e-59:471:81//AQ246589  
 F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence. //8.9e-43:307:73//AC004526  
 F-PLACE1008465//CIT-HSP-2163F24, TR CIT-HSP Homo sapiens genomic cl one 2163F24, genomic survey sequence. //8.9e-41:210:99//B90014  
 F-PLACE1008488//Mus musculus mRNA for testis-specific protein kina se 1, complete cds. //0.00013:516:58//AB003494  
 F-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34821, WORKING DRAFT SEQUENCE. //1.3e-161:778:98//AL0317 78  
 F-PLACE1008531//Homo sapiens wbscr1 (WBSR1) and replication facto r C subunit 2 (RFC2) genes, complete cds. //1.1e-78:191:100//AF0455 55  
 F-PLACE1008532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE. //3.8e-24:257:70//Z93097  
 F-PLACE1008533//Homo sapiens PAC clone DJ130M16 from 22q12.1-qter, complete sequence. //1.0e-13:215:71//AC004997  
 F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome X q21.1. //0.66:263:64//Z99571  
 F-PLACE1008584//Homo sapiens cosmid clone U3983 from Xp22.1-22.2, complete sequence. //1.1e-19:315:68//U73023  
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete c ds. //1.2e-173:812:98//AB018334  
 F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENC E, 2 unordered pieces. //3.9e-09:198:71//AC005077  
 F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBML H 91), complete sequence. //0.58:568:59//AC005373  
 F-PLACE1008626//HS\_3221\_A2\_F03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=M, geno mic survey sequence. //1.7e-13:147:82//AQ180967  
 F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor. //9.7 e-98:586:88//Y12836  
 F-PLACE1008629//CIT-HSP-201214, TR CIT-HSP Homo sapiens genomic clo ne 201214, genomic survey sequence. //0.00085:203:66//B53732  
 F-PLACE1008630//Sequence 26 from Patent W09517522. //9.7e-05:97:80/ /A45356  
 F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor famil y heavy chain-related protein (IHRP), complete cds. //1.4e-23:299:6 4//D38595  
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds. //1.1e-133:622:99//AF044333  
 F-PLACE1008693//CIT-HSP-2346F2, TF CIT-HSP Homo sapiens genomic clo ne 2346F2, genomic survey sequence. //0.24:89:76//AQ060732  
 F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S pr otein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitoch ondril protein, complete cds. //1.4e-94:420:97//AF038406  
 F-PLACE1008715//CIT-HSP-2294K20, TR CIT-HSP Homo sapiens genomic c one 2294K20, genomic survey sequence. //2.1e-70:349:98//AQ007199  
 F-PLACE1008748//Arabidopsis thaliana chromosome 1 BAC T14N5 genom ic sequence, complete sequence. //0.14:347:59//AC004260  
 F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence. //7.9e-25:244:71//AC003037  
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, comple te cds. //4.5e-120:503:97//AF060543  
 F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, co mplete sequence. //0.00026:370:61//AF001549  
 F-PLACE1008807//CIT-HSP-2334B19, TF CIT-HSP Homo sapiens genomic c one 2334B19, genomic survey sequence. //3.3e-08:220:65//AQ036643  
 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds. //1.7e-120:470:97//AF030933  
 F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds. //2.8 e-87:504:89//AF032668  
 F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromo some 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1 F1551A pseudogene, ESTs, STS, GSS, complete sequence. //4.0e-21:21 2:74//AL021920  
 F-PLACE1008854  
 F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DR AFT SEQUENCE. //4.7e-77:477:84//Z82209  
 F-PLACE1008887//Homo sapiens BAC clone RH0335J18 from 2, complete sequence. //3.4e-53:699:70//AC005539  
 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds. //2.1 e-06:164:68//W63660  
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cd s. //6.4e-158:753:98//AB018308  
 F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987S

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【表466】

K-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:40  
0:63//AC002042  
F-PLACE1008934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022  
312  
F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete  
cds.//4.3e-41:282:87//L15309  
F-PLACE1008947//Pseudorabies virus with upstream and downstream seq  
uences.//5.9e-15:710:60//M34651  
F-PLACE1009020//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, geno  
mic survey sequence.//1.9e-21:167:86//AQ253727  
F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome  
Xq23 Contains calpain-like protease gene, DCX (doublecortin) EST  
s, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117  
F-PLACE1009039//HS\_2034\_A2\_F08\_T7 CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, gen  
omic survey sequence.//0.17:252:59//AQ230137  
F-PLACE1009045//HS\_3185\_B2\_B03\_T7 CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, geno  
mic survey sequence.//1.9e-34:260:86//AQ172861  
F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit g  
ene, 5' flank and exon 1.//4.7e-70:463:80//D00766  
F-PLACE1009050//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Par  
k Cancer Institute Human PAC library) complete sequence.//0.63:28  
0:61//AC004241  
F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting prot  
ein X), complete CDS.//5.9e-113:725:85//AJ005073  
F-PLACE1009090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021  
919  
F-PLACE1009091//Homo sapiens clone DJ0968116, complete sequence.//  
0.027:630:58//AC006016  
F-PLACE1009094  
F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cd  
s.//2.1e-85:726:76//M36515  
F-PLACE1009110  
F-PLACE1009111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 13887, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752  
F-PLACE1009113//Homo sapiens X-ray repair cross-complementing prot  
ein 3 (XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586  
F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-  
23:718:59//D25215  
F-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKI  
NG DRAFT SEQUENCE.//6.1e-142:684:98//AJ011929  
F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segm  
ent 2/28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031  
F-PLACE1009158//H. sapiens genomic sequence for ERCC2 gene 3' region  
involved in DNA excision repair.//1.0:173:60//XS2222  
F-PLACE1009166  
F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//  
4.0e-35:257:85//AC002070  
F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Geno  
me Systems Human BAC Library) complete sequence.//2.9e-19:288:72//  
AC004805  
F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, Pl  
clone: MHJ24, complete sequence.//0.053:388:60//AB008266  
F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, c  
omplete cds.//1.8e-50:317:89//AF061242  
F-PLACE1009190//RPC111-B1N5.TJ RPC111 Homo sapiens genomic clone  
R-B1N5, genomic survey sequence.//0.91:114:67//AQ281881  
F-PLACE1009200//CITB1-E1-2509J16.TF CITB1-E1 Homo sapiens genomic  
clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198  
F-PLACE1009230//H. sapiens gene for pregnancy specific beta-1 glyco  
protein.//1.1e-106:495:88//X63203  
F-PLACE1009246//HS\_3058\_B1\_A06\_MF CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, gen  
omic survey sequence.//0.10:175:68//AQ185945  
F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, com  
plete cds.//1.8e-94:575:89//U47024  
F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.  
//0.0017:350:62//U23862  
F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD  
95) mRNA, complete cds.//3.0e-06:411:59//U83192  
F-PLACE1009328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034  
399  
F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//  
0.071:253:62//D87015  
F-PLACE1009338//RPC111-74N24.TV RPC111 Homo sapiens genomic clone  
R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811  
F-PLACE1009368  
F-PLACE1009375  
F-PLACE1009388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022  
311  
F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cd  
s.//4.3e-78:730:74//M27878  
F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt.].//  
0.16:95:71//S71494  
F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, c  
omplete sequence.//1.6e-150:701:99//AC005919  
F-PLACE1009434//Mus musculus clone OST431, genomic survey sequenc  
e.//2.9e-73:442:88//AF046700  
F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome:  
segment 148/162.//0.012:582:56//AL022022  
F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi  
4K230) mRNA, complete cds.//4.6e-21:146:93//AF012872  
F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequenc  
e.//2.9e-31:264:81//AF046660  
F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84  
//I30536  
F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67  
A1, complete sequence.//1.9e-142:704:97//AC004531  
F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequen  
ce.//2.2e-09:235:68//AC004601  
F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, co  
mplete sequence.//2.9e-83:171:92//U91321  
F-PLACE1009524//Homo sapiens DNA sequence from PAC 63GS on chromos  
ome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog  
B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an un  
known gene and a gene coding for a Leucine rich protein. Contains  
ESTs, STSs and GSSs, complete sequence.//3.8e-69:175:92//Z94160  
F-PLACE1009539//Mus musculus synaptotagmin 2 isoform alpha mRNA, co  
mplete cds.//7.0e-26:237:78//AF041862  
F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome  
22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding p  
rotein, gene similar to monocarboxylate transporter (MCT3), ESTs,  
STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//ALD  
31587  
F-PLACE1009571//RPC111-60K12.TK RPC111 Homo sapiens genomic clone  
R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869  
F-PLACE1009581  
F-PLACE1009595//Homo sapiens chromosome 5, Pl clone 1029A7 (LBNI H  
15), complete sequence.//6.6e-19:309:70//AC003959  
F-PLACE1009596//Rattus norvegicus platelet-activating factor acety  
lhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-0  
9:485:59//AF016049  
F-PLACE1009607//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824  
F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 g  
enomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.01  
7:655:57//AC004157  
F-PLACE1009621  
F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Libr  
ary C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genom  
ic survey sequence.//2.7e-15:100:98//B33248  
F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 g  
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.6  
3:130:67//AC005308  
F-PLACE1009639//S.pombe chromosome 11 cosmid c24E9.//0.86:509:58//  
AL021816  
F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete c  
ds.//1.4e-171:816:98//AB011159  
F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, compl  
ete sequence.//3.4e-67:437:87//AC005177  
F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5  
e-147:701:98//AF062534  
F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//  
1.5e-98:228:100//AC006011  
F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete seque  
nce.//2.2e-130:736:91//AC000109  
F-PLACE1009731//M. musculus mRNA for immunity associated protein 3  
8.//1.1e-13:311:64//Y08026  
F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2  
e-125:602:98//AF046024  
F-PLACE1009794  
F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosom  
e Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit  
(EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogen

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## 【表467】

e Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996

F-PLACE1009845

F-PLACE1009861//B. tauris cathepsin B mRNA, 3' end.//0.00023:147:65//N64620

F-PLACE1009879//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397

F-PLACE1009886//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427

F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431

F-PLACE1009908//S. pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369

F-PLACE1009921//Homo sapiens cosmid clone HDAB (15149) insert DNA, complete cosmid.//5.9e-48:304:87//N63005

F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT9875 K-201104, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066

F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//J25655

F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS\_3178\_B1\_F04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311

F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029

F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP220 mRNA, complete cds.//7.9e-87:552:80//U48288

F-PLACE1010023

F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6 p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and arc haea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775

F-PLACE1010053//M. musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692

F-PLACE1010069//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925

F-PLACE1010089//HS\_3111\_A1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=L, genomic survey sequence.//4.8e-07:124:78//AQ101268

F-PLACE1010096//R. norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411

F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-25:728:60//AF059569

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome X q22.//6.5e-25:488:63//Z93928

F-PLACE1010134//S. pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164

F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83:409:98//AJ222636

F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757

F-PLACE1010181//Homo sapiens PAC clone DJ1139101 from Xq23, complete sequence.//2.4e-15:197:72//AC004973

F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967

F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829

F-PLACE1010231//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033

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F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917

F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710

F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029

F-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464

F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-10:185:67//AL031005

F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468

F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837

F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178

F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252

F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome: segment 155/162.//0.94:398:57//AL022121

F-PLACE1010364//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985

F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//0.066:88:76//AC004675

F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825

F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081

F-PLACE1010492

F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695

F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR016417

F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677

F-PLACE1010562//RPC111-65116.TX RPC111 Homo sapiens genomic clone R-65116, genomic survey sequence.//0.017:216:67//AQ200831

F-PLACE1010579//Homo sapiens full length insert cDNA Y123D12.//3.9e-19:147:89//AF075014

F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HSPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186

F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308

F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558

F-PLACE1010624//Streptomyces coelicolor cosmid SA7.//1.4e-05:518:61//AL031107

F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846

F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-25 SH10, complete sequence.//2.5e-17:187:80//AC004682

F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K21P3, complete sequence.//0.21:159:64//AB016872

F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069

F-PLACE1010661

F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F737 (ESSA project).//0.90:257:61//AL021960

F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376

F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583

F-PLACE1010720//Mouse TPA-induced T1S11 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS\_2013\_B2\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864

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F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609  
 F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294\_J.22, complete sequence.//4.7e-45:235:99//AC005921  
 F-PLACE1010771//M.musculus HCNBP mRNA.//1.6e-135:801:88//X68061  
 F-PLACE1010786//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-15, complete sequence.//0.35:334:60//AL010221  
 F-PLACE1010800//RPC111-79H17.TV RPC111 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252  
 F-PLACE1010802//Human Chromosome X clone BWX0531, complete sequence.//1.6e-30:693:63//AC004384  
 F-PLACE1010811//RPC111-51N5.TK RPC111 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380  
 F-PLACE1010833//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467X16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283  
 F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229  
 F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868  
 F-PLACE1010870//M.musculus mRNA for ZF3 zinc finger factor.//1.3e-93:530:90//Z67747  
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182  
 F-PLACE1010891  
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-02 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-26:394:68//AC003997  
 F-PLACE1010900  
 F-PLACE1010916//HS\_2242\_A1\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687  
 F-PLACE1010917  
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688  
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126  
 F-PLACE1010942//Homo sapiens interseitin short form mRNA, complete cds.//5.6e-90:437:98//AF064243  
 F-PLACE1010944//Homo sapiens full length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247  
 F-PLACE1010947  
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence.//2.1e-29:190:91//B98965  
 F-PLACE1010960//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//0.00074:421:60//AL010226  
 F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence.//1.8e-84:412:99//AQ240696  
 F-PLACE1011026//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.00037:257:64//AL008972  
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBML H176), complete sequence.//3.8e-06:315:65//AC005348  
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669  
 F-PLACE1011045//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20536  
 F-PLACE1011054//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 981L23, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686  
 F-PLACE1011058//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049  
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:100//S75548  
 F-PLACE1011090//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687  
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//2.3e-24:192:84//L14684  
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249  
 F-PLACE1011133//T7E9-17.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//0.010:345:60//B19698  
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00013:95:76//AQ109305  
 F-PLACE1011160//Homo sapiens PAC clone D0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:87//AC004893  
 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443  
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 9B10, complete sequence.//3.1e-43:447:72//AC002288  
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyl transferase mRNA, complete cds.//3.3e-124:584:99//AF038664  
 F-PLACE1011214//HS\_2046\_A2\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305865  
 F-PLACE1011219  
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801  
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101  
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from Tp21, complete sequence.//1.7e-42:212:84//AC005014  
 F-PLACE1011273//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y370B, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819  
 F-PLACE1011291//RPC111-16P9.TP RPC111 Homo sapiens genomic clone RPC111-16P9, genomic survey sequence.//8.0e-08:66:98//B81770  
 F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LA ML), complete sequence.//0.027:135:67//AC004647  
 F-PLACE1011310//H.sapiens CpG island DNA genomic MseI fragment, clone 53c10, reverse read cpg53c10.rtlb.//1.4e-05:57:100//Z61496  
 F-PLACE1011325//Human immunodeficiency virus type 1 (HIV) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290  
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265  
 F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388\_F.14, complete sequence.//2.4e-38:186:83//AC005375  
 F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919  
 F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310  
 F-PLACE1011399//parametium species 7, 325 mt dna dimer: replication init. region.//0.00011:255:63//K00919  
 F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996  
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102  
 F-PLACE1011452//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929  
 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 8F7, complete sequence.//3.5e-71:498:80//AC004605  
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255  
 F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482  
 F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964  
 F-PLACE1011503  
 F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968  
 F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546  
 F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from Tp21-p22, complete sequence.//1.1e-38:315:82//AC004984  
 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180  
 F-PLACE1011586//Homo sapiens chromosome 17, clone HRPK890E16, complete sequence.//2.0e-82:188:96//AC004477  
 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214\_0\_1, complete sequence.//1.8e-153:752:97//AC005224  
 F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660  
 F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729  
 F-PLACE1011646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383  
 F-PLACE1011649  
 F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062  
 F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374  
 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507  
 F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome

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## 【表469】

22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:1  
27:71//AL008719  
F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487  
F-PLACE1011725  
F-PLACE1011729//Human Chromosome 15q11-q13 clone pD276c12 from the Prader-Willi/Angelman syndrome region. WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737  
F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157  
F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003  
F-PLACE1011778//RPC111-22D17.TYB RPC111 Homo sapiens genomic clone RPC111-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944  
F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330  
F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147  
F-PLACE1011874//Homo Sapiens Chromosome X clone BXD312, complete sequence.//2.5e-141:678:98//AC004478  
F-PLACE1011875//Homo sapiens mRNA for KIA0580 protein, partial cds.//1.6e-108:526:98//AB011152  
F-PLACE1011891//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392  
F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969  
F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400  
F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617  
F-PLACE1011962//HS\_3212\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3212 Col=24 Row=M, genomic survey sequence.//2.4e-07:154:74//AQ175369  
F-PLACE1011964//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799  
F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate-CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529  
F-PLACE1011995//Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054  
F-PLACE1012031//Homo sapiens mRNA for KIA0713 protein, partial cds.//1.2e-146:690:98//AB018256  
F-PLACE2000003//Homo sapiens chromosome 17, clone HRPX.318\_A\_15, complete sequence.//1.7e-62:293:88//AC005837  
F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057  
F-PLACE2000007  
F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578  
F-PLACE2000014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574  
F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069  
F-PLACE2000017//HS\_3042\_A1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074  
F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556  
F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638  
F-PLACE2000033//C. capitata mRNA for chorion protein s18.//0.0019:342:63//Y08913  
F-PLACE2000034//Rattus norvegicus transmembrane receptor Robol mRNA, complete cds.//2.8e-13:335:63//AF041082  
F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505  
F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626  
F-PLACE2000050//Homo sapiens chromosome 17, clone HRPX41C23, complete sequence.//1.1e-32:527:68//AC003101  
F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010  
F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457  
F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219  
F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-119:93//AC005910  
F-PLACE2000100//HS\_3184\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004  
F-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848  
F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491  
F-PLACE2000115  
F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67 A1, complete sequence.//6.2e-43:362:80//AC004531  
F-PLACE2000132//RPC111-79F15.TV RPC111 Homo sapiens genomic clone R-79F15, genomic survey sequence.//5.4e-35:206:94//AQ284166  
F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070  
F-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995  
F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701  
F-PLACE2000170  
F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//AC006005  
F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 in BCRL2-CGT Region, complete sequence.//0.98:201:64//AC004032  
F-PLACE2000187  
F-PLACE2000216  
F-PLACE2000223//RPC111-12L17.TP RPC111 Homo sapiens genomic clone RPC111-12L17, genomic survey sequence.//0.00039:325:58//B75888  
F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//AC003003  
F-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236:94//AC005902  
F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577  
F-PLACE2000274//Anthracidaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308  
F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF7 3 homolog gene, complete cds.//8.3e-08:662:58//U52064  
F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95:81//AC006021  
F-PLACE2000317//HS\_3183\_B2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747  
F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402:65//AC004952  
F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555:82//AF026554  
F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//1.8e-14:259:71//U66829  
F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmid R32543, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376:74//AC003006  
F-PLACE2000359//RPC111-23J20.TKBR RPC111 Homo sapiens genomic clone RPC111-23J20, genomic survey sequence.//8.4e-21:288:69//AQ013849  
F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692:80//U49973  
F-PLACE2000371//Homo sapiens 12p13.3 PAC RPC111-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182  
F-PLACE2000373//RPC111-49C18.TJ RPC111 Homo sapiens genomic clone R-49C18, genomic survey sequence.//0.064:132:68//AQ051776  
F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.6e-130:776:88//AC003658  
F-PLACE2000394//Homo sapiens chromosome 18 BAC RPC111-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:83//AC005909  
F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:286:63//X06967  
F-PLACE2000399

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F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532:68//Z36238  
 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//0.44:553:56//U89984  
 F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:86//M13792  
 F-PLACE2000425//HS\_3047\_A1\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=0, genomic survey sequence.//2.8e-42:224:97//AQ126949  
 F-PLACE2000427  
 F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156\_L14, complete sequence.//1.1e-19:363:67//AC005821  
 F-PLACE2000435//HS\_3036\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999  
 F-PLACE2000438//Caenorhabditis elegans cosmid Y45F100, complete sequence.//4.6e-23:550:62//AL021492  
 F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from Tq11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025  
 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279810, complete sequence.//8.2e-05:330:63//AC002300  
 F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBML H154), complete sequence.//5.7e-168:816:97//AC005740  
 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037  
 F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057  
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602  
 F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187  
 F-PLACE3000020//R. norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075  
 F-PLACE3000029  
 F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267  
 F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBML H158), complete sequence.//1.8e-17:250:74//AC005368  
 F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006  
 F-PLACE3000119//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0180L06: HTGS phase I, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670  
 F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668  
 F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//1.8e-48:330:79//AC005695  
 F-PLACE3000136  
 F-PLACE3000142//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520  
 F-PLACE3000145//Callus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662  
 F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053  
 F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474  
 F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//7.4e-173:822:98//AC005277  
 F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682  
 F-PLACE3000157  
 F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500  
 F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878  
 F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-8-191n6, complete sequence.//9.8e-158:749:98//AC006130  
 F-PLACE3000194  
 F-PLACE3000197//F. rubripes GSS sequence, clone 075N04b87, genomic survey sequence.//1.4e-08:164:68//AL003352  
 F-PLACE3000199//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207  
 F-PLACE3000207//Homo sapiens BAC clone GS165L15 from Tpl5, complete sequence.//6.6e-21:312:67//AC005013  
 F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982  
 F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086  
 F-PLACE3000220//RPC111-5484.TV RPC111 Homo sapiens genomic clone R-5484, genomic survey sequence.//2.4e-36:381:76//AQ082056  
 F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-135:721:91//AC005231  
 F-PLACE3000226  
 F-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626  
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain 1 LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046  
 F-PLACE3000244//M. musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169  
 F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424  
 F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-B15A9, complete sequence.//1.8e-21:350:68//AF001548  
 F-PLACE3000276//HS\_2026\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147  
 F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328  
 F-PLACE3000310  
 F-PLACE3000320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379  
 F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//3.3e-35:419:68//AC005822  
 F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543  
 F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunit Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642  
 F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswe II Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055  
 F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TA01 mRNA, complete cds.//2.3e-107:592:92//AF084205  
 F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 2, complete sequence.//2.1e-37:480:70//Z83732  
 F-PLACE3000353  
 F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, complete sequence.//0.00011:373:60//AC005969  
 F-PLACE3000363  
 F-PLACE3000365//Human DNA sequence from PAC 227P17, between marker s:DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007  
 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545  
 F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from Tpl4-p15, complete sequence.//2.2e-25:288:71//AC005154  
 F-PLACE3000399//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630  
 F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239  
 F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023  
 F-PLACE3000402//RPC111-2006.TVB RPC111 Homo sapiens genomic clone RPC111-2006, genomic survey sequence.//1.1e-10:154:74//AQ008761  
 F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//2.9e-41:515:72//AC005701  
 F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443  
 F-PLACE3000413  
 F-PLACE3000416//F19L8-Sp6 IQF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//0.0018:664:55//B11305  
 F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719  
 F-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469022, WORKING DRAFT SEQUENCE.//3.6e-145:732:96//AL031284  
 F-PLACE3000475//HS\_2164\_A2\_H10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=0, gen

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omic survey sequence.//1.5e-07:159:71//AQ132983  
 F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//2.9e-11:213:70//Z83843  
 F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08:692:60//139845  
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.1e-116:331:100//AB018352  
 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69 G12, complete sequence.//5.0e-05:244:63//AC004131  
 F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926  
 F-PLACE4000052//M. musculus abcl mRNA.//1.5e-110:671:88//X75926  
 F-PLACE4000063  
 F-PLACE4000089//M. musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311  
 F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence.//0.11:245:60//AQ108342  
 F-PLACE4000100//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848  
 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931  
 F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234  
 F-PLACE4000129  
 F-PLACE4000131//HS\_3139\_B2\_F12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207  
 F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5 (IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622  
 F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367  
 F-PLACE4000192  
 F-PLACE4000211  
 F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158  
 F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:89//AF030430  
 F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973  
 F-PLACE4000247  
 F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673  
 F-PLACE4000252  
 F-PLACE4000259//H. sapiens gene for US snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200  
 F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259  
 F-PLACE4000269//Rattus norvegicus rozo70 mRNA, complete cds.//5.5e-122:734:88//AF032667  
 F-PLACE4000270  
 F-PLACE4000300  
 F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075  
 F-PLACE4000323//HS\_2165\_B1\_B02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036  
 F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296  
 F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401  
 F-PLACE4000367  
 F-PLACE4000369  
 F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661  
 F-PLACE4000387//CIT-HSP-2382F11.TA CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649  
 F-PLACE4000392//Rattus norvegicus polymorphic marker D20U1A1 sequence.//1.2e-05:222:58//AF054088  
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540  
 F-PLACE4000411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984  
 F-PLACE4000431//H. sapiens gene for US snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200  
 F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=M, genomic survey sequence.//0.070:47:100//B41346  
 F-PLACE4000450  
 F-PLACE4000465//Homo sapiens BAC clone RG114B19 from Tq31.1, complete sequence.//2.3e-07:273:65//AC005065  
 F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156\_L14, complete sequence.//4.1e-34:351:70//AC005821  
 F-PLACE4000489//HS\_3012\_B1\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=M, genomic survey sequence.//2.0e-36:220:92//AQ095537  
 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865  
 F-PLACE4000521//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\*, WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929  
 F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645  
 F-PLACE4000548  
 F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747  
 F-PLACE4000581  
 F-PLACE4000590//Homo sapiens chromosome Y, clone 47511, complete sequence.//3.6e-20:747:59//AC004474  
 F-PLACE4000593//Caenorhabditis elegans cosmid F2507, complete sequence.//5.6e-16:326:65//Z78418  
 F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from Tq31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281  
 F-PLACE4000638//Homo sapiens clone MH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039  
 F-PLACE4000650  
 F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267  
 F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816  
 F-SKMC1000011//Callus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577  
 F-SKMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312  
 F-SKMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554  
 F-SKMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616  
 F-SKMC1000091//Human NK homeobox protein (Hx6.1) gene, exon 1.//0.0018:375:60//U66797  
 F-THYR1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561  
 F-THYR1000026//Human DNA sequence from clone 83387 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637  
 F-THYR1000034//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353  
 F-THYR1000035//Human Chromosome X clone BWXD187, complete sequence.//1.2e-39:303:83//AC004383  
 F-THYR1000040  
 F-THYR1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383  
 F-THYR1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557  
 F-THYR1000085  
 F-THYR1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606  
 F-THYR1000107  
 F-THYR1000111//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403  
 F-THYR1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055  
 F-THYR1000124//H. sapiens CpG island DNA genomic MseI fragment, clone 72a7, forward read cpg72a7.f11a.//9.5e-26:169:94//Z62724  
 F-THYR1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142  
 F-THYR1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096  
 F-THYR1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574

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F-THYR01000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331  
 F-THYR01000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419  
 F-THYR01000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207  
 F-THYR01000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214  
 F-THYR01000190//Homo sapiens chromosome 17, clone hRPK.332\_H18, complete sequence.//0.38:184:64//AC005746  
 F-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698  
 F-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552  
 F-THYR01000206//HS\_3047\_A1\_A05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134  
 F-THYR01000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157  
 F-THYR01000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186  
 F-THYR01000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156  
 F-THYR01000253//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055  
 F-THYR01000270  
 F-THYR01000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664  
 F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068  
 F-THYR01000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894  
 F-THYR01000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233  
 F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333  
 F-THYR01000358//Human selenin-binding protein (HSBP) mRNA, complete cds.//2.2e-32:177:84//U29091  
 F-THYR01000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080  
 F-THYR01000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668  
 F-THYR01000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019  
 F-THYR01000394//HS\_2061\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672  
 F-THYR01000395//Drosophila melanogaster ring canal protein and ORF 2 mRNA, complete cds.//4.3e-15:512:59//L08483  
 F-THYR01000401  
 3.2e-116:504:80//AF051908  
 F-THYR01000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308  
 F-THYR01000452//RPC111-1C19.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-1C19, genomic survey sequence.//0.27:132:64//B49573  
 F-THYR01000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229  
 F-THYR01000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196  
 F-THYR01000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBML H154), complete sequence.//6.3e-130:327:97//AC005740  
 F-THYR01000501//H. sapiens Staf50 mRNA.//9.8e-74:615:77//X82200  
 F-THYR01000502//Human DNA sequence from PAC 436M11 on chromosome X p22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the R51 gene for retinoblastoma (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056  
 F-THYR01000505  
 F-THYR01000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563  
 F-THYR01000569//HS\_2178\_B2\_E03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499  
 F-THYR01000570  
 F-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587  
 F-THYR01000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323  
 F-THYR01000602//HS\_3037\_B2\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057  
 F-THYR01000605//Homo sapiens map 2p11.2: 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777  
 F-THYR01000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546  
 F-THYR01000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474  
 F-THYR01000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559  
 F-THYR01000658//Homo sapiens chromosome 17, clone hRPK.74\_E22, complete sequence.//1.1e-68:468:84//AC005696  
 F-THYR01000662//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K23L20, complete sequence.//0.0072:141:70//AB016874  
 F-THYR01000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437  
 F-THYR01000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778  
 F-THYR01000684//Fugu rubripes cosmid 16SK09 DNA for GRM7, TRIP, Sand, PRGR3 genes.//6.6e-13:236:69//AJ010317  
 F-THYR01000699//RPC111-50D4.TK RPC111 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641  
 F-THYR01000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053  
 F-THYR01000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320  
 F-THYR01000734//HS\_3233\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143  
 F-THYR01000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871  
 F-THYR01000756//M. musculus mRNA for Gal beta1, 3GalNAc alpha2, 3-sialyltransferase.//0.00034:349:60//X73523  
 F-THYR01000777//S. griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763  
 F-THYR01000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373  
 F-THYR01000787//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986  
 F-THYR01000793  
 F-THYR01000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422  
 F-THYR01000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468  
 F-THYR01000815//Homo sapiens chromosome 5, BAC clone 189 (LBML H135), complete sequence.//5.5e-43:405:77//AC005914  
 F-THYR01000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053  
 F-THYR01000843  
 F-THYR01000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782  
 F-THYR01000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:64//AF008573  
 F-THYR01000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.1e-30:286:74//AC005477  
 F-THYR01000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720  
 F-THYR01000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015  
 F-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529  
 F-THYR01000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836  
 F-THYR01000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229  
 F-THYR01000952  
 F-THYR01000974//HS\_3238\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//2.4e-26:154:96//AQ219846  
 F-THYR01000975//Plasmodium falciparum Topol1 gene.//0.32:491:58//X79345  
 F-THYR01000983//Mv9A3 exon amplification products from BACs in M

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【表473】

vwf region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457

F-THYR0100984//CIT-HSP-2167017, TR CIT-HSP Homo sapiens genomic clone 2167017, genomic survey sequence.//0.00015:186:66//B91313

F-THYR0100988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588

F-THYR01001003

F-THYR01001031//Homo sapiens chromosome 17, clone hRPC.859\_0\_20, complete sequence.//1.1e-55:543:72//AC003695

F-THYR01001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799

F-THYR01001062//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320

F-THYR01001093//Homo sapiens chromosome 9, clone hRPC.202\_M\_3, complete sequence.//4.9e-34:353:76//AC006241

F-THYR01001100//Human DNA-binding protein mRNA, 3' end.//1.1e-72:742:74//L14787

F-THYR01001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522

F-THYR01001121//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 671014, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595

F-THYR01001133//Homo sapiens PAC clone DJ1200123 from 7p15, complete sequence.//4.0e-35:349:76//AC004996

F-THYR01001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486

F-THYR01001142//Human DNA sequence from clone B7984 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178

F-THYR01001173

F-THYR01001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953

F-THYR01001189//HS\_3171\_B2\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330

F-THYR01001204//Drosophila melanogaster DNA repair protein (mei-4) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925

F-THYR01001213//, complete sequence.//1.7e-45:257:84//AC005300

F-THYR01001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036

F-THYR01001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496

F-THYR01001287//Drosophila melanogaster cosmid clone 86E4.//9.6e-49:586:69//AL021086

F-THYR01001290//HS\_2045\_B1\_H09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237

F-THYR01001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693

F-THYR01001320//Homo sapiens Chromosome 22q11.2 PAC Clone p\_n5 in BCRL2-CGT Region, complete sequence.//1.1e-88:672:82//AC002472

F-THYR01001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114

F-THYR01001322//HS\_3205\_B2\_C12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025

F-THYR01001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288

F-THYR01001363//Homo sapiens PAC clone DJ0845121 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905

F-THYR01001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//7.6e-168:821:97//AC005660

F-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607

F-THYR01001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239

F-THYR01001403//Homo sapiens chromosome 12p13.3 clone RPC13-454823, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845

F-THYR01001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852

F-THYR01001406//Mus musculus putative steroid dehydrogenase (KIK-1) mRNA, complete cds.//1.0e-91:631:82//AF064635

F-THYR01001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126

F-THYR01001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 1118122) from chromosome 11: HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553

F-THYR01001434//Human Chromosome 11 pac pDJ393015, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384

F-THYR01001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265

F-THYR01001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001

F-THYR01001487//H. sapiens DNA sequence.//0.92:160:64//Z22449

F-THYR01001534//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666

F-THYR01001537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687

F-THYR01001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074

F-THYR01001559//Rattus norvegicus simple sequence repeat D18Mc6.//1.6e-09:351:63//AF006056

F-THYR01001570//RPC111-49823.TJ RPC111 Homo sapiens genomic clone R-49823, genomic survey sequence.//1.4e-65:384:91//AQ052105

F-THYR01001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572

F-THYR01001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-THYR01001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808

F-THYR01001602//Homo sapiens chromosome 17, clone hRPK.786\_0\_4, complete sequence.//2.9e-26:393:68//AC005863

F-THYR01001605//Dictyostelium discoideum filopodin (tala) gene, complete cds.//0.0012:436:58//U14576

F-THYR01001617//Homo sapiens full length insert cDNA clone ZD69005.//8.6e-43:342:82//AF086381

F-THYR01001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950

F-THYR01001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827

F-THYR01001661

F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089

F-THYR01001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071

F-THYR01001703//S. coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857

F-THYR01001706//Homo sapiens BAC clone RG281809 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745

F-THYR01001721//, complete sequence.//9.9e-134:770:91//AC005500

F-THYR01001738//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327

F-THYR01001745

F-THYR01001746

F-THYR01001772//HS\_3069\_B1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021

F-THYR01001793//B. taurus mRNA for beta-subunit of rod photoreceptor CNB-channel.//0.028:446:58//X89626

F-THYR01001809

F-THYR01001828//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526

F-THYR01001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664

F-THYR01001895

4.4e-13:248:68//AB012576

F-THYR01001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058

F-VESEN1000122//HS\_3075\_B1\_C09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749

F-Y79AA1000013

F-Y79AA1000033//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027

F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689

F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521

F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:1

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## 【表474】

17:83//Z72005  
 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U82893  
 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNI1). ESTs, STS, GSS, CpG island, complete sequence.//1.4e-165:732:99//AL031864  
 F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 D506882 (D310)), complete sequence.//9.1e-20:339:65//AC005115  
 F-Y79AA1000214//Homo sapiens clone DJ0673W15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//3.7e-72:397:93//AC004854  
 F-Y79AA1000230  
 F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232  
 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SACP-1) gene, complete cds.//0.0099:547:58//U78522  
 F-Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.//4.0e-11:424:62//AF035207  
 F-Y79AA1000313  
 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//5.9e-07:173:69//B55085  
 F-Y79AA1000342//RPC111-H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.ttc.//0.00016:53:98//Z56610  
 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987  
 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692  
 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484  
 F-Y79AA1000368//H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.ttc.//0.00016:53:98//Z56610  
 F-Y79AA1000405//Pissomidium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MALIP4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747  
 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061  
 F-Y79AA1000420//H.sapiens CpG island DNA genomic MseI fragment, clone 82c3, forward read cpg82c3.tta.//2.0e-36:194:98//Z63378  
 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736  
 F-Y79AA1000480//HS\_2175\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=0, genomic survey sequence.//2.5e-26:178:89//AQ307693  
 F-Y79AA1000538//Homo sapiens clone DJ1158801, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.67:111:72//AC004980  
 F-Y79AA1000539//HS\_2237\_B2\_F10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence.//1.2e-14:168:77//AQ153503  
 F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.94:127:67//AC005193  
 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84//X14972  
 F-Y79AA1000574//M.musculus tex23 mRNA (5' region).//1.8e-23:291:75//X80424  
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//8.6e-153:755:97//AF091080  
 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//5.2e-135:644:98//AF060503  
 F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-148:902:86//X69942  
 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds.//4.8e-180:850:98//AB018080  
 F-Y79AA1000748//Caenorhabditis elegans cosmid F2585.//0.00019:308:60//U23172  
 F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//1.7e-40:513:68//AJ003023  
 F-Y79AA1000774  
 F-Y79AA1000782  
 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//3.5e-177:847:97//AF098799  
 F-Y79AA1000794//H.sapiens CpG island DNA genomic MseI fragment, clone 45a4, forward read cpg45a4.tta.//2.5e-13:104:92//Z61120  
 F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//0.98:244:60//AF056085  
 F-Y79AA1000802  
 F-Y79AA1000805//Human Chromosome 11 Cosmid cSL30h1, complete sequence.//9.3e-76:528:85//U73642  
 F-Y79AA1000824//RPC111-26B4.TP RPC1-11 Homo sapiens genomic clone RPC1-11-26B4, genomic survey sequence.//4.4e-14:99:95//B84538  
 F-Y79AA1000827//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//1.5e-08:249:69//AL022315  
 F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757  
 F-Y79AA1000850  
 F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203  
 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314  
 F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253  
 F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397  
 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:73//U88165  
 F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823  
 F-Y79AA1001023  
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3e-13:90:100//U63329  
 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682  
 F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence.//9.4e-36:292:82//AC004701  
 F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//S64314  
 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452  
 F-Y79AA1001078  
 F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173  
 F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-23:228:76//AC005015  
 F-Y79AA1001167  
 F-Y79AA1001177//M.musculus mRNA for Nfix1-protein.//4.0e-10:398:64//Y07688  
 F-Y79AA1001185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015  
 F-Y79AA1001211//HS\_3124\_B2\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//5.5e-12:87:96//AQ187492  
 F-Y79AA1001216  
 F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome: segment 143/162.//0.028:188:67//AL021841  
 F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds.//3.5e-24:731:60//W36263  
 F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110113307 (RZPD Berlin)).//1.2e-133:441:97//AJ005892  
 F-Y79AA1001281//HS\_2241\_B2\_F09\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence.//5.0e-27:169:94//AQ217497  
 F-Y79AA1001299//Human Inil mRNA, complete cds.//6.7e-115:323:93//U04847  
 F-Y79AA1001312  
 F-Y79AA1001323  
 F-Y79AA1001384  
 F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322  
 F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence.//7.8e-18:636:58//Z48583  
 F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005924  
 F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497  
 F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430  
 F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336  
 F-Y79AA1001541//HS\_3197\_A2\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183  
 F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151  
 F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59267  
 F-Y79AA1001581//FMR1 (CGG repeats) [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:65//S74494

【0774】

【表475】

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPT) gene, complete cds.//7.2e-33:375:76//M26434  
 F-Y79AA1001594  
 F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21 q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861  
 F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583  
 F-Y79AA1001647//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860  
 F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.99:273:63//Z84468  
 F-Y79AA1001679//O. cuniculus lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743  
 F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:425:59//S37712  
 F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyp protein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136  
 F-Y79AA1001705//M. musculus fkh-5 gene.//0.18:153:64//X71943  
 F-Y79AA1001711//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240  
 F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017  
 F-Y79AA1001805//H. sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12, rtic.//2.6e-13:88:100//Z64565  
 F-Y79AA1001827//Oryctolagus cuniculus P1US mRNA, complete cds.//3.7e-130:775:88//U74297  
 F-Y79AA1001846//CIT-HSP-2300M6, TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369  
 F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388  
 F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds.//6.9e-41:441:71//U41164  
 F-Y79AA1001874//Homo sapiens hJAG2, del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779  
 F-Y79AA1001875//CIT-HSP-2317G18, TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654  
 F-Y79AA1001923//H. sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12, rtic.//0.0031:108:75//Z60186  
 F-Y79AA1001963//CITBI-E1-2510J4, TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184  
 F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340  
 F-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 526114, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214  
 F-Y79AA1002089  
 F-Y79AA1002093//Mus musculus transcription factor like protein 4 T CFL4 mRNA, partial cds.//1.2e-112:678:88//U43548  
 F-Y79AA1002103//HS\_3052\_B1\_H08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014  
 F-Y79AA1002115  
 F-Y79AA1002125//H. sapiens (DBS135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693  
 F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog H1jlp (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358  
 F-Y79AA1002204//HS\_2235\_B2\_D12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=M, genomic survey sequence.//2.9e-13:89:98//AQ154260  
 F-Y79AA1002208//CIT-HSP-2006M21, TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397  
 F-Y79AA1002209//E. coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719  
 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615  
 F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043  
 F-Y79AA1002220//CIT-HSP-2374P23, TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738  
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045  
 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592  
 F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555  
 F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534  
 F-Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877  
 F-Y79AA1002351//S. clavuligerus pah and cas genes.//1.0:369:58//X84101  
 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208  
 F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPC.700\_H\_6, complete sequence.//1.0e-159:411:100//AC005920  
 F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//1.1e-118:609:84//AC004662  
 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//4.4e-90:529:88//U49385  
 F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA A, complete cds.//1.0:166:66//U36196  
 F-Y79AA1002433//CIT-HSP-384K8, TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917  
 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-8-393115 (BC301323), complete sequence.//1.9e-13:242:69//AC006116  
 F-Y79AA1002482//Homo sapiens full length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022  
 F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

【0775】

3'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ  
各データは、

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

【0776】

【表476】

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953  
 R-HEMBA1000030//F. rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864  
 R-HEMBA1000042//RPC111-77G23.TV RPC111 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-55:292:97//AQ268240  
 R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696  
 R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948  
 R-HEMBA1000076//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520  
 R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684  
 R-HEMBA1000129//Homo sapiens chromosome 17, clone HC1T48C15, complete sequence.//2.4e-93:503:93//AC003104  
 R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340  
 R-HEMBA1000150//Homo sapiens clone RC086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060  
 R-HEMBA1000156//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631  
 R-HEMBA1000158  
 R-HEMBA1000160  
 R-HEMBA1000180//Plasmodium falciparum encoding Pf27/25.//0.073:292:56//X84904  
 R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146  
 R-HEMBA1000193  
 R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126  
 R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655  
 R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548  
 R-HEMBA1000227  
 R-HEMBA1000231//Human DNA sequence from PAC 21ZP9 on chromosome 1p34.1-p35. Contains delta opiate receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181  
 R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526  
 R-HEMBA1000244  
 R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds: transfer RNA-His gene: 16S ribosomal RNA gene: ND3 gene, complete cds: cytochrome B (cytb) gene, 5' end of cds.//0.16:338:60//L76262  
 R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012  
 R-HEMBA1000280//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037  
 R-HEMBA1000282//Arabidopsis thaliana BAC 1C002P16.//0.71:344:60//AF007270  
 R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046  
 R-HEMBA1000290//Homo sapiens chromosome 17, clone HRP837J1, complete sequence.//2.2e-15:249:69//AC004223  
 R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105  
 R-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131  
 R-HEMBA1000304//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802  
 R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496  
 R-HEMBA1000333//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505  
 R-HEMBA1000338//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//2.0e-33:399:72//AL031667  
 R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147  
 R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829  
 R-HEMBA1000357//Homo sapiens (subclone 9\_h8 from P1 M16) DNA sequence.//8.7e-93:426:88//L42086  
 R-HEMBA1000366//Homo sapiens PAC clone DJ0942116 from Tq11, complete sequence.//1.7e-12:130:83//AC006012  
 R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587  
 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC3D1323), complete sequence.//3.7e-66:410:89//AC006116  
 R-HEMBA1000387//Homo sapiens chromosome 17, clone HC1T169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993  
 R-HEMBA1000390//Homo sapiens BAC clone RC041D11 from Tq21, complete sequence.//4.6e-23:417:69//AC005053  
 R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582  
 R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575  
 R-HEMBA1000411  
 R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465  
 R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233  
 R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//2.0e-93:526:90//Z95400  
 R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826  
 R-HEMBA1000442//E. caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733  
 R-HEMBA1000456//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226  
 R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein Gtp (ATG1), putative nuclear DNA-binding protein G2p (ATG2), Eml protein (ATEM1), putative chlorophyll synthetase (ATG4), putative transmembrane protein G5p (ATG5), putative acyl-coA dehydrogenase (ATG6), and calcium dependent protein kinase genes, complete cds: and unknown genes.//0.013:212:63//AF049236  
 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//AC004839  
 R-HEMBA1000464//Caenorhabditis elegans cosmid C3487, complete sequence.//0.086:334:61//Z83220  
 R-HEMBA1000469//Homo sapiens BAC clone RC442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104  
 R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500  
 R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278  
 R-HEMBA1000491  
 R-HEMBA1000504//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014  
 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858  
 R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280  
 R-HEMBA1000518//RPC111-6022.TV RPC111 Homo sapiens genomic clone RPC111-6022, genomic survey sequence.//0.0035:293:61//B49544  
 R-HEMBA1000519  
 R-HEMBA1000520//Arabidopsis thaliana chromosome 11 BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232  
 R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782  
 R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638  
 R-HEMBA1000540//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044  
 R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103  
 R-HEMBA1000555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555  
 R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381  
 R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762  
 R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368  
 R-HEMBA1000568//RPC111-49PB.TK.1 RPC111 Homo sapiens genomic clone R-49PB, genomic survey sequence.//1.7e-101:498:97//AQ116293  
 R-HEMBA1000569

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R-HEMBA1000575//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:94//AJ007509

R-HEMBA1000592//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

R-HEMBA1000594//Homo sapiens clone RG004M09, WORKING DRAFT SEQUENCE. 5 unordered pieces.//1.1e-15:421:66//AC005044

R-HEMBA1000604//HS\_2220\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991

R-HEMBA1000608

R-HEMBA1000622//H. sapiens CpG island DNA genomic MseI fragment, clone 155e4, reverse read cpg155e4.rtl.a.//4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008

R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590

R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome X q26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196

R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE. 4 unordered pieces.//1.2e-50:298:79//AC005377

R-HEMBA1000686//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513

R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE. 7 unordered pieces.//9.7e-54:317:88//AC005000

R-HEMBA1000705//Glossonotus univittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.08:0:138:65//U77850

R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864

R-HEMBA1000722

R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q35, complete sequence.//4.4e-26:284:77//AC005531

R-HEMBA1000727//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266

R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS\_3050\_A2\_B08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//\*\*\*ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA1000817//Sequence 1 from Patent WO 8904839.//0.86:148:67//U09339

R-HEMBA1000822//T. brucei kinetoplast maxicircle variable region DNA A.//0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. C contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome 1 BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE. 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT9875 K-A-180G2, WORKING DRAFT SEQUENCE. 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE. 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-237314.TR CIT-HSP Homo sapiens genomic clone 237314, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T. pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPC111-68E14.TX RPC111 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZB Pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE. 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640\_1\_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//TSM8TFB TAMU Arabidopsis thaliana genomic clone T5 N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE. 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPC111-54D1.TJ RPC111 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE. 1 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPC111-22017.TVB RPC111 Homo sapiens genomic clone RPC11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//O. sativa osr40g2 gene.//0.99:203:62//Y08987

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547

R-HEMBA1001020//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

R-HEMBA1001024//Homo sapiens BAC clone 393122 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

R-HEMBA1001043//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPC13-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751

R-HEMBA1001060//HS\_2056\_B1\_C01\_MR CIT Approved Human Genomic Sperm

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Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004  
 R-HEMBA1001071//Homo sapiens COL3A1 gene for collagen alpha-1.//6.9e-38:513:70//X52046  
 R-HEMBA1001077//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318  
 R-HEMBA1001080  
 R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIX genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586  
 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607  
 R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105  
 R-HEMBA1001099  
 R-HEMBA1001109//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527  
 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833  
 R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551  
 R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511  
 R-HEMBA1001133  
 R-HEMBA1001137//Homo sapiens full length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241  
 R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077  
 R-HEMBA1001172//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304  
 R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398  
 R-HEMBA1001197  
 R-HEMBA1001208//HS\_2233\_A1\_G10\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789  
 R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377  
 R-HEMBA1001235//RPC111-50E6.TJ RPC111 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666  
 R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761  
 R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905  
 R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from Tq11-q21, complete sequence.//9.9e-21:537:63//AC004491  
 R-HEMBA1001281//Homo sapiens chromosome 17, clone HC1775G16, complete sequence.//0.022:169:65//AC003042  
 R-HEMBA1001286  
 R-HEMBA1001289  
 R-HEMBA1001294//HS\_3219\_A2\_G01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882  
 R-HEMBA1001299//Homo sapiens, clone hRPK.12\_A\_1, complete sequence.//1.3e-38:381:76//AC006222  
 R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258  
 R-HEMBA1001303//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744  
 R-HEMBA1001310  
 R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504  
 R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240  
 R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (CAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368  
 R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509  
 R-HEMBA1001330//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216  
 R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474\_N\_24, complete sequence.//7.1e-45:252:94//AC006238  
 R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//1.4e-113:569:97//AC006241  
 R-HEMBA1001375//Homo sapiens full length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542  
 R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865  
 R-HEMBA1001383  
 R-HEMBA1001387  
 R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073  
 R-HEMBA1001391//Yeast mitochondrial aapl gene for ATPase subunit 8.//7.3e-08:500:59//X00960  
 R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050  
 R-HEMBA1001405//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35:464:68//AL034380  
 R-HEMBA1001407  
 R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981  
 R-HEMBA1001413  
 R-HEMBA1001415//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732  
 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.3e-37:302:81//AC006146  
 R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome X p11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054  
 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527  
 R-HEMBA1001442//Human DNA sequence from PAC 507115 on chromosome X q26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950  
 R-HEMBA1001446//HS\_3207\_A1\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385  
 R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from Tq31.1, complete sequence.//0.0043:266:63//AC005065  
 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from Tq31, complete sequence.//7.1e-25:210:82//AC004855  
 R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//2.7e-08:316:62//AC005324  
 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064\_E\_11, complete sequence.//0.57:219:60//AC005208  
 R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840  
 R-HEMBA1001478  
 R-HEMBA1001497  
 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337  
 R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6 q22. Contains EST and STS.//1.9e-79:529:86//Z98753  
 R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549  
 R-HEMBA1001522  
 R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning Zmb of 16p13.3. Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258  
 R-HEMBA1001533//Human DNA sequence from PAC 17SM20 on chromosome 2 q012-13.1. Contains adenosine deaminase (ADA), placental protein D1133, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053  
 R-HEMBA1001557  
 R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383  
 R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//177040  
 R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453  
 R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506

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【表479】

R-HEMBA1001581//P. falciparum complete gene map of plastid-like DNA (IR-B). //2.3e-07:491:58//X95276	t KIAA0500. //2.8e-112:548:98//AB007969
R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6. //0.68:224:62//U41012	R-HEMBA1001809
R-HEMBA1001589	R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC Library) complete sequence. //2.6e-48:363:84//AC004025
R-HEMBA1001595//CIT-HSP-2349G19. TF CIT-HSP Homo sapiens genomic clone 2349G19. genomic survey sequence. //8.0e-69:337:99//AQ060483	R-HEMBA1001819//Homo sapiens *** SEQUENCING IN PROGRESS *** from P AC 1577. WORKING DRAFT SEQUENCE. //1.1e-15:275:68//AJ009612
R-HEMBA1001608//Homo sapiens chromosome 17. clone HCIT462L7. complete sequence. //9.5e-59:514:78//AC005177	R-HEMBA1001820//HS_3022_B1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B. genomic survey sequence. //0.00054:335:59//AQ165107
R-HEMBA1001620//S. polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase. //4.5e-12:289:65//Z11693	R-HEMBA1001822//Xenopus laevis intersectin mRNA. complete cds. //1.4e-19:533:63//AF032118
R-HEMBA1001635//HS_2195_A1_E09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=1. genomic survey sequence. //5.8e-09:358:58//AQ292688	R-HEMBA1001824//S. clavuligerus linear plasmid pSCL (complete sequence). //0.62:189:65//X54107
R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA. complete cds. //0.77:225:59//U04270	R-HEMBA1001835//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18. WORKING DRAFT SEQUENCE. //1.0:450:60//AL024507
R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 5p 21. Contains ETS related protein TEL like and GS2 like genes. ESTs and an STS. //6.0e-49:404:79//Z84484	R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene. complete cds. //1.6e-07:170:68//U50871
R-HEMBA1001651	R-HEMBA1001847
R-HEMBA1001655//Homo sapiens chromosome 5. BAC clone 194j18 (LBNL H158). complete sequence. //1.1e-103:532:95//AC005368	R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein. complete cds. //3.3e-108:553:96//AB014517
R-HEMBA1001658//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4. WORKING DRAFT SEQUENCE. //1.0:197:64//AL023808	R-HEMBA1001864//Homo sapiens genomic DNA. 21q22.1 region. clone: Q 82F5A16. genomic survey sequence. //1.7e-14:245:67//AC002463
R-HEMBA1001661//Homo sapiens chromosome 5p. BAC clone 50g21 (LBNL H154). complete sequence. //1.5e-100:457:93//AC005740	R-HEMBA1001866//HS_2258_B2_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H. genomic survey sequence. //2.8e-39:397:75//AQ221138
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MB03 (MBD3) mRNA. complete cds. //1.2e-90:496:91//AF072247	R-HEMBA1001869//Homo sapiens BAC clone RG114819 from Tq31.1. complete sequence. //5.9e-56:303:94//AC005065
R-HEMBA1001675	R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence. //1.7e-43:281:88//AC006210
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA. complete cds. //1.3e-101:534:94//AF038962	R-HEMBA1001896
R-HEMBA1001681//CIT-HSP-2345M7. TF CIT-HSP Homo sapiens genomic clone 2345M7. genomic survey sequence. //0.21:124:68//AQ056593	R-HEMBA1001910
R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //8.3e-06:279:63//AC004801	R-HEMBA1001912//Homo sapiens chromosome 5. P1 clone 1308e5 (LBNL H13). complete sequence. //0.10:307:61//AC004775
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein. complete cds. //1.9e-96:483:96//AB014598	R-HEMBA1001913
R-HEMBA1001711//Human HepG2 3' region cDNA. clone hmd2b02. //2.3e-31:169:100//D16886	R-HEMBA1001915//HS_2037_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=1. genomic survey sequence. //0.071:206:64//AQ233106
R-HEMBA1001712//HS-1015-B1-E01-MR. abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J. genomic survey sequence. //0.0025:200:65//B32577	R-HEMBA1001918//Homo sapiens chromosome 5. P1 clone 1308e5 (LBNL H13). complete sequence. //0.97:449:59//AC004775
R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene. complete cds. //6.6e-27:316:75//U12250	R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA. complete cds. //2.0e-105:534:96//AF000145
R-HEMBA1001718//CIT-HSP-2171J2. TR CIT-HSP Homo sapiens genomic clone 2171J2. genomic survey sequence. //3.1e-41:167:87//B89781	R-HEMBA1001939//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508115. WORKING DRAFT SEQUENCE. //4.6e-13:120:82//AL021707
R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA. complete cds. //0.53:275:61//AF018261	R-HEMBA1001940//Homo sapiens clone DJ1093116. WORKING DRAFT SEQUENCE. 5 unordered pieces. //2.2e-36:301:81//AC005629
R-HEMBA1001731//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7. WORKING DRAFT SEQUENCE. //2.9e-48:292:84//AL023799	R-HEMBA1001942//Human PAC clone DJ0205E24 from Qx23. complete sequence. //1.9e-10:208:68//AC003013
R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3. WORKING DRAFT SEQUENCE. 2 ordered pieces. //3.2e-33:290:81//AC005959	R-HEMBA1001945//Plasmodium falciparum chromosome 2. section 70 of 73 of the complete sequence. //1.2e-06:393:60//AE001433
R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21. Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence. complete sequence. //0.98:203:62//AL022067	R-HEMBA1001950//R. prowazekii genomic DNA fragment (clone A43TR). //0.33:122:66//Z82646
R-HEMBA1001745//Homo sapiens BAC clone RG28G08 from 7p15-p21. complete sequence. //0.00019:312:59//AC005084	R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene. complete cds. //0.0086:427:59//U05329
R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYACB12 genomic sequence. WORKING DRAFT SEQUENCE. 8 unordered pieces. //0.045:457:61//AC004153	R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25. complete sequence. //4.5e-07:176:70//AC004069
R-HEMBA1001761//Homo sapiens chromosome X. clone hCIT.200_L_4. complete sequence. //3.8e-39:331:80//AC006121	R-HEMBA1001964//HS_2215_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P. genomic survey sequence. //7.3e-25:215:74//AQ151931
R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC Library) complete sequence. //0.0062:245:60//AC004554	R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isoform of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island. ESTs and GSSs. complete sequence. //1.7e-51:209:95//AL031178
R-HEMBA1001784//Homo sapiens chromosome 5p. BAC clone 50g21 (LBNL H154). complete sequence. //2.1e-22:370:63//AC005740	R-HEMBA1001979//CIT-HSP-2387I12. TF. CIT-HSP Homo sapiens genomic clone 2387I12. genomic survey sequence. //4.9e-06:153:71//AQ240461
R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs. GSSs and genomic marker DXS8098. complete sequence. //3.0e-50:408:80//AL023575	R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs. complete sequence. //3.1e-46:437:77//AL033521
R-HEMBA1001800//CIT-HFP-2049N5. TF CIT-HSP Homo sapiens genomic clone 2049N5. genomic survey sequence. //9.0e-37:335:71//AQ009222	R-HEMBA1001991//Human DNA sequence from PAC 42616 on chromosome 1p 34.1-p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1. ESTs, and a CA repeat. //1.1e-48:446:78//AL020997
R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence. WORKING DRAFT SEQUENCE. 7 unordered pieces. //0.86:536:56//AC005506	R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta). //5.1e-90:448:97//AJ005801
R-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA. 5' end. //2.9e-93:553:89//M21977	R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTC repeat polymorphisms. complete sequence. //3.2e-42:317:84//Z97181
R-HEMBA1001808//Homo sapiens mRNA. chromosome 1 specific transcript	R-HEMBA1002018//HS_3006_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H. genomic survey sequence. //1.1e-15:275:68//AJ009612

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omic survey sequence.//1.0:63:74//AQ089717  
 R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453\_M\_1, complete sequence.//0.93:339:59//AC006203  
 R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694  
 R-HEMBA1002039  
 R-HEMBA1002049//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315  
 R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078  
 R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703  
 R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357  
 R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800  
 R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924  
 R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378  
 R-HEMBA1002125  
 R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637  
 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC005728  
 R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide YB and (parts of) up to four novel genes, two with homology to Phorbolins and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence.//1.0:371:61//AL031846  
 R-HEMBA1002151  
 R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//2.4e-21:322:70//AC003971  
 R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//2.5e-38:216:84//Z97054  
 R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence.//3.1e-58:284:80//B89969  
 R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.//0.0079:286:57//Z80789  
 R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//5.9e-53:326:80//AC002980  
 R-HEMBA1002177  
 R-HEMBA1002185//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE.//9.5e-37:356:76//AL033532  
 R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.4e-43:244:77//AC003684  
 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE. 2 unordered pieces.//4.3e-37:323:78//AC005077  
 R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498  
 R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g in IGLC Region, complete sequence.//1.5e-31:313:71//AC000053  
 R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8.//0.0023:346:60//X57546  
 R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989  
 R-HEMBA1002226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//4.6e-46:375:77//AL033529  
 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//AF089814  
 R-HEMBA1002237//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.3e-26:469:67//AC004242  
 R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//5.1e-23:162:82//AC005016  
 R-HEMBA1002257  
 R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//AF038127  
 R-HEMBA1002270//Human BAC clone RG057M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//AC000057  
 R-HEMBA1002321  
 R-HEMBA1002328//HS\_3061\_A1\_D06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, gen

omic survey sequence.//1.0:151:65//AQ127617  
 R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds.//3.7e-07:328:63//U23811  
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314  
 R-HEMBA1002348//Human DNA sequence from clone 409010 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//3.7e-07:587:58//AL031256  
 R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438  
 R-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:661:93//AF092563  
 R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.1e-70:559:79//AB020868  
 R-HEMBA1002389//HS\_3218\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602  
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//AC005954  
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//AC004848  
 R-HEMBA1002430//P.falciiparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276  
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE. 3 unordered pieces.//3.4e-23:183:80//AC006026  
 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN, pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819  
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378  
 R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//I80068  
 R-HEMBA1002475  
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:80//AC004841  
 R-HEMBA1002486//ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573  
 R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey sequence.//1.0:122:68//AQ261762  
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE. 15 unordered pieces.//2.8e-22:210:78//AC004963  
 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPK1057M6, complete sequence.//2.7e-17:435:58//AC003043  
 R-HEMBA1002508//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.7e-09:408:61//AC006213  
 R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972  
 R-HEMBA1002515  
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923  
 R-HEMBA1002542//HS\_3197\_B2\_B10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792  
 R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658  
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378  
 R-HEMBA1002555//Homo sapiens full length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957  
 R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409  
 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634  
 R-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587  
 R-HEMBA1002583  
 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152  
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//AC004510  
 R-HEMBA1002621  
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351  
 R-HEMBA1002628//P.falciiparum complete gene map of plastid-like DNA

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## 【表481】

(IR-A). //8.8e-05:327:60//X95275  
R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence. //4.3e-06:205:66//AF046247  
R-HEMBA1002645//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence. //7.1e-39:281:84//U14567  
R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence. //1.1e-104:500:95//AC004839  
R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence. //1.2e-61:280:92//AL022323  
R-HEMBA1002661//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 225E12, WORKING DRAFT SEQUENCE. //3.2e-41:325:81//AL031772  
R-HEMBA1002665//Homo sapiens full length insert cDNA clone YY74A07. //0.00037:79:84//AF088008  
R-HEMBA1002678//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE. //2.3e-107:561:94//AL034421  
R-HEMBA1002679//CIT-HSP-2287E8, TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence. //5.4e-17:137:88//B99281  
R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 135A47 (LBNL H47), complete sequence. //0.033:146:70//AC004503  
R-HEMBA1002696  
R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence. //6.2e-44:302:87//AC003982  
R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds. //1.1e-31:332:76//AB004873  
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds. //1.2e-35:287:81//AB014521  
R-HEMBA1002730//D. discoideum actin M6 gene, 5' flank. //0.018:233:66//M29109  
R-HEMBA1002742//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1108H3, WORKING DRAFT SEQUENCE. //2.6e-13:419:62//AL033525  
R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence. //0.019:202:65//AC003694  
R-HEMBA1002748//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 404K8, WORKING DRAFT SEQUENCE. //0.046:263:60//AL023883  
R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium- and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs. //0.052:421:58//Z96810  
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds. //1.2e-104:545:95//AB011126  
R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //3.0e-07:523:59//AC005140  
R-HEMBA1002777  
R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmd1e03a3. //9.4e-25:158:93//D17139  
R-HEMBA1002780//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE. //1.6e-42:463:75//AL022344  
R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence. //2.2e-05:417:59//AL034560  
R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS. //0.00055:444:59//L76261  
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds. //4.4e-115:559:97//AF071185  
R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces. //4.3e-88:329:94//AC005043  
R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE. //1.9e-22:262:67//AP000041  
R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117\_B.12, complete sequence. //1.3e-79:396:97//AC004707  
R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces. //0.013:393:61//AC005506  
R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPC.271\_K.11, complete sequence. //4.1e-73:489:85//AC005562  
R-HEMBA1002876//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE. //0.21:549:55//AL034557  
R-HEMBA1002886//CIT-HSP-2013C4, TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence. //0.30:431:56//B53836  
R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds. //3.9e-106:541:95//AF037261  
R-HEMBA1002921  
R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10. //4.6e-19:139:78//AB020875  
R-HEMBA1002934//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE. //7.5e-45:282:89//AL031681  
R-HEMBA1002935//CIT-HSP-2282P14, TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence. //1.5e-102:514:97//AQ008584  
R-HEMBA1002937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 745114, WORKING DRAFT SEQUENCE. //3.3e-87:444:97//AL033532  
R-HEMBA1002939  
R-HEMBA1002944//HS\_3107\_A1\_C05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence. //6.3e-21:250:73//AQ103952  
R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene. //0.013:228:63//AJ008020  
R-HEMBA1002954//HS\_3246\_AZ\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence. //5.8e-42:258:91//AQ218005  
R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPC.112\_J.9, complete sequence. //4.2e-38:300:83//AC005553  
R-HEMBA1002970//Slime mold (D. discoideum) prestalk D11 gene, complete cds. //5.0e-05:541:57//M11012  
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds. //7.2e-29:162:99//AB014579  
R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence. //9.1e-36:520:69//AC006128  
R-HEMBA1002997//Homo Sapiens Chromosome X clone bWXD691, complete sequence. //0.00040:504:59//AC004386  
R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds. //3.7e-66:556:79//U19614  
R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces. //1.6e-44:530:70//AC000406  
R-HEMBA1003033//Homo sapiens full length insert cDNA clone ZC34B10. //4.6e-78:414:94//AF086194  
R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence. //9.0e-52:322:75//AC004026  
R-HEMBA1003035//HS\_2008\_A2\_G08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence. //4.0e-68:343:97//AQ269839  
R-HEMBA1003037//347G15, TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence. //0.57:188:58//B17694  
R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence. //6.3e-30:350:72//AC004983  
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds. //4.1e-118:578:97//AF054182  
R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13. //0.0018:271:60//U59962  
R-HEMBA1003067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 633019, WORKING DRAFT SEQUENCE. //5.3e-48:464:76//AL022302  
R-HEMBA1003071//CIT-HSP-2370D6, TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence. //0.19:48:87//AQ110136  
R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel K v4.3 mRNA, complete cds. //4.9e-69:494:84//U42975  
R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome X p11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S. cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS. //1.1e-11:331:64//Z97054  
R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence. //4.6e-116:576:98//AC004673  
R-HEMBA1003083//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0442P12: HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces. //3.1e-43:280:83//AC005798  
R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.2e-43:281:88//AC006039  
R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE. //0.00037:421:59//Z82213  
R-HEMBA1003098//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08: HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces. //1.4e-30:303:78//AC005598  
R-HEMBA1003117  
R-HEMBA1003129//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 407F11, WORKING DRAFT SEQUENCE. //7.9e-11:109:85//AL022329  
R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence. //3.9e-99:484:98//AC004472  
R-HEMBA1003136//CIT-HSP-2281L22, TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence. //2.0e-10:93:92//B99861  
R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence. //9.8e-40:

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270:87//AC004024  
R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-11  
6:586:96//AJ005670  
R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X  
contains ESTs.//6.4e-35:364:70//Z83822  
R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta recepto  
r.//1.9e-30:282:77//X60459  
R-HEMBA1003197  
R-HEMBA1003199//HS\_2166\_A1\_E12\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2166 Col=23 Row=1, gen  
omic survey sequence.//0.00026:271:61//AQ164162  
R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUEN  
CE, 3 unordered pieces.//5.4e-44:291:83//AC005480  
R-HEMBA1003204//Human BAC clone RG07ZE11 from 7q21-q22, complete  
sequence.//3.1e-10:293:62//AC000118  
R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUEN  
CE, 1 unordered pieces.//1.0:118:69//AC006148  
R-HEMBA1003220//HS\_3092\_B1\_F09\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3092 Col=17 Row=L, gen  
omic survey sequence.//0.00014:59:91//AQ128202  
R-HEMBA1003222//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGR  
ESS \*\*\* from clone Y43F8, WORKING DRAFT SEQUENCE.//0.84:214:62//Z9  
5393  
R-HEMBA1003229//RPC111-16F15.TPB RPC1-11 Homo sapiens genomic clon  
e RPC1-11-16F15, genomic survey sequence.//0.42:167:64//B83610  
R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic cl  
one 2320G19, genomic survey sequence.//3.6e-36:195:81//AQ037231  
R-HEMBA1003250//HS\_2168\_A2\_C09\_MF CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, gen  
omic survey sequence.//1.4e-22:158:89//AQ125356  
R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:26  
8:61//U53709  
R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Hu  
man BAC library) complete sequence.//1.0e-32:255:84//AC002549  
R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 g  
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00  
44:212:60//AC005308  
R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPC11-315L5 (Roswell Park  
Cancer Institute Human PAC library) complete sequence.//1.1e-34:2  
86:74//AC002395  
R-HEMBA1003281//High throughput sequencing of human chromosome 12,  
WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.8e-53:428:83//AC0058  
40  
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete c  
ds.//3.0e-115:551:99//AB011109  
R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic cl  
one 2196L16, genomic survey sequence.//2.9e-20:337:65//AQ003073  
R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:9  
7//125662  
R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TA  
C clone: K19E20, complete sequence.//0.00019:334:60//AB017061  
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinas  
e, complete cds.//2.8e-111:545:97//AB001872  
R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosom  
e Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.60:274:61/  
/AL022153  
R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, com  
plete sequence.//0.00028:172:65//AC005099  
R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENC  
E, 18 unordered pieces.//2.2e-44:268:90//AC005081  
R-HEMBA1003330//Homo sapiens poly(A) binding protein 11 (PABP2) ge  
ne, complete cds.//2.7e-61:312:97//AF026029  
R-HEMBA1003348//\*\*\*ALU WARNING: Human Alu-J subfamily consensus se  
quence.//7.2e-38:186:83//U14567  
R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequ  
ence.//0.00012:465:59//Z79600  
R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, comp  
lete sequence.//3.2e-42:301:87//AC002558  
R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome  
6p21.2-21.3. Contains the alternatively spliced gene for Transcri  
ptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A ge  
ne, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Prol  
iferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear  
Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative Cp  
G islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete  
sequence.//7.4e-34:375:74//AL022721  
R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LA  
NL), complete sequence.//1.6e-46:309:88//AC004651  
R-HEMBA1003380//HS\_3184\_B2\_E06\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, gen  
omic survey sequence.//1.0e-35:237:88//AQ189144  
R-HEMBA1003384//HS\_2193\_B2\_H08\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, gen  
omic survey sequence.//0.00029:96:76//AQ032212  
R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKI  
NG DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993  
R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic cl  
one 2166E19, genomic survey sequence.//0.99:144:61//B91549  
R-HEMBA1003408  
R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome  
6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:9  
8//AL031321  
R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, co  
mplete sequence.//0.082:352:59//AC004879  
R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NB  
S1) mRNA, complete cds.//9.9e-114:544:98//AF058696  
R-HEMBA1003461  
R-HEMBA1003463  
R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//  
9.1e-106:533:96//AC005041  
R-HEMBA1003528  
R-HEMBA1003531//Human BAC clone G5552A01 from 7q21-q22, complete s  
equence.//3.4e-08:333:64//AC002454  
R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:  
333:68//X04701  
R-HEMBA1003545//Zebrafish mRNA for zfish-2 (insulin gene enhancer  
binding protein homolog), complete cds.//0.030:144:68//D38453  
R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 g  
enomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00  
17:487:57//AC004153  
R-HEMBA1003555//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL03171  
8  
R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome  
Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC  
005913  
R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.  
24:116:67//AF034416  
R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUEN  
CE, 3 unordered pieces.//3.9e-05:422:63//AC006036  
R-HEMBA1003569//Homo sapiens full length insert cDNA clone ZD8200  
6.//8.7e-108:545:95//AF086450  
R-HEMBA1003571//Homo sapiens PAC clone DJ0886008 from 7q32-q35, co  
mplete sequence.//4.6e-51:570:71//AC004914  
R-HEMBA1003579//HS\_3237\_B2\_E05\_T7 CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, gen  
omic survey sequence.//8.5e-97:495:95//AQ209302  
R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123  
R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL),  
complete sequence.//2.9e-87:251:95//AC005774  
R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chro  
mosome 22q12. Contains a pseudogene with similarity to part of mou  
se Ninein and the KIAA0609 gene for a protein similar to C. elegans  
K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, com  
plete sequence.//4.5e-52:384:83//AL008715  
R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromo  
some 6q21. Contains the first (5') two exons of a CDK8 (Cell Divis  
ion Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogen  
e, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480  
R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12,  
complete sequence.//1.8e-23:177:88//AC005153  
R-HEMBA1003615  
R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 g  
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.03  
9:494:57//AC005139  
R-HEMBA1003621//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromo  
some 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE,  
4 unordered pieces.//2.3e-26:309:75//AC004599  
R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC l  
ibrary) complete sequence.//7.1e-56:545:75//AC002980  
R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete s  
equence.//2.8e-32:546:68//AF088219  
R-HEMBA1003637//Human BAC clone G5552A01 from 7q21-q22, complete s  
equence.//8.0e-25:457:68//AC002454  
R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete seq  
uence.//2.8e-40:280:86//AF031078  
R-HEMBA1003645//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693  
R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//  
0.44:319:59//AL034559

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R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-15 Z65, complete sequence.//6.9e-36:242:80//AC004382

R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332\_H18, complete sequence.//8.6e-117:588:96//AC005746

R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.6e-21:170:88//112222

R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065

R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313

R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (coxI) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872

R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466

R-HEMBA1003692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508115, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707

R-HEMBA1003711//Human Chromosome 11 overlapping pacs pD235k10 and pD239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC004046

R-HEMBA1003714

R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987S K-A-68508, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136

R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353

R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699

R-HEMBA1003729//RPC111-22D14, TV RPC1-11 Homo sapiens genomic clone RPC1-11-22D14, genomic survey sequence.//1.0:234:62//B86158

R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634

R-HEMBA1003742//HS\_3080\_B2\_H06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179

R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24, Contains ESTs, CA repeat, STS and CpG island.//4.5e-59:521:75//Z97876

R-HEMBA1003760

R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343

R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259

R-HEMBA1003784

R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1e-49:390:72//AC004455

R-HEMBA1003803

R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//9.4e-99:359:99//AC004596

R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27, Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse KKI-7 and KKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781

R-HEMBA1003807//Bovine dinucleotide microsatellite HJ1177.//5.4e-18:194:78//W96348

R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115

R-HEMBA1003838//CIT-HSP-2380F18, TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624

R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31, Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929

R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300

R-HEMBA1003866//HS\_3203\_B2\_CO1\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298

R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207

R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036

R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576

R-HEMBA1003893//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421

R-HEMBA1003902//HS\_3031\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549

R-HEMBA1003908//CIT-HSP-2367K7, TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795

R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368

R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718

R-HEMBA1003939

R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904

R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619

R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560

R-HEMBA1003958//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668

R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahyd4) gene, complete cds.//0.11:428:60//AF000132

R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414

R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060

R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPC15-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804

R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924

R-HEMBA1003989//RPC111-52K22, TJ RPC111 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484

R-HEMBA1004000

R-HEMBA1004011

R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//4.7e-38:284:85//AC005670

R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25, Contains STSs, GSSs and genomic marker DXS0898, complete sequence.//0.48:460:58//AL023575

R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081

R-HEMBA1004038//Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054

R-HEMBA1004042//Homo sapiens clone DJ0968116, complete sequence.//0.00071:263:68//AC006016

R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143

R-HEMBA1004048//CIT-HSP-2288N20, TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283

R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677

R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504

R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484

R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952

R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237

R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234

R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, complete sequence.//6.0e-49:491:76//AC003665

R-HEMBA1004133//HS\_3229\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003

R-HEMBA1004138//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498

R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970

R-HEMBA1004146//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820

R-HEMBA1004150//CITB1-E1-251712, TR CITB1-E1 Homo sapiens genomic

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## 【表484】

lone 251712, genomic survey sequence.//0.56:379:59//AQ277616  
 R-HEMBA1004164//Human BAC clone GS200K05 from Tq21-q22, complete s  
 equence.//4.6e-49:448:77//AC002429  
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-11  
 0:563:96//AF067855  
 R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z6  
 6569  
 R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems  
 Human BAC library) complete sequence.//6.3e-30:293:77//AC004552  
 R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell lin  
 e, mRNA, 993 nt].//3.0e-64:517:80//S72304  
 R-HEMBA1004203//Homo sapiens clone NHO313P13, WORKING DRAFT SEQUEN  
 CE, 15 unordered pieces.//1.0e-97:303:98//AC005488  
 R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA,  
 complete cds.//3.6e-116:573:97//U50748  
 R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12  
 tRNAs and 7 genes.//5.4e-11:493:60//M37275  
 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, com  
 plete cds.//6.1e-76:443:86//AF095927  
 R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complet  
 e sequence.//1.1e-42:330:83//AC005763  
 R-HEMBA1004241  
 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down  
 Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:  
 288:85//AP000011  
 R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from Tq11.23-q21.  
 1, complete sequence.//5.2e-09:516:61//AC004903  
 R-HEMBA1004264  
 R-HEMBA1004267//HS\_2255\_A2\_H12\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=0, gen  
 omic survey sequence.//8.6e-59:318:95//AQ068854  
 R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPC15-118D012 (Roswell Pa  
 rk Cancer Institute Human PAC Library) complete sequence.//1.1e-11  
 3:576:96//AC005831  
 R-HEMBA1004275//Homo sapiens clone 617 unknown mRNA, complete sequ  
 ence.//4.4e-110:553:96//AF091081  
 R-HEMBA1004276  
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-  
 1 mRNA, complete cds.//1.9e-106:538:97//AF022795  
 R-HEMBA1004289//RPC111-74010.TJ RPC111 Homo sapiens genomic clone  
 R-74010, genomic survey sequence.//2.3e-37:248:76//AQ266668  
 R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:2  
 73:64//L13174  
 R-HEMBA1004306//HS\_3175\_B2\_F01\_T7 CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, geno  
 mic survey sequence.//1.6e-28:190:77//AQ169206  
 R-HEMBA1004312//Human BAC clone RG119P24 from Tq31, complete seque  
 nce.//6.3e-36:267:82//AC003088  
 R-HEMBA1004321//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from P  
 AC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611  
 R-HEMBA1004323//CIT-HSP-237ACB.TR CIT-HSP Homo sapiens genomic cl  
 one 237ACB, genomic survey sequence.//2.7e-42:136:91//AQ114933  
 R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic cl  
 one 2303L24, genomic survey sequence.//1.0:78:67//AQ017600  
 R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUEN  
 CE, 5 unordered pieces.//2.3e-119:580:98//AC004987  
 R-HEMBA1004334//Pimpinella brachycarpa Phyl mRNA, complete cds.//  
 3.3e-14:238:69//AF082024  
 R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-11  
 6A10, complete sequence.//1.8e-21:291:71//AC004638  
 R-HEMBA1004341  
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, compl  
 ete cds.//4.1e-74:444:90//D89667  
 R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific  
 cosmids R29515 and R28253, genomic sequence, complete sequence.//  
 7.0e-38:287:82//AC003002  
 R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:9  
 2//158611  
 R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-  
 14:446:63//AC005949  
 R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic cl  
 one 2005C13, genomic survey sequence.//0.010:334:61//B55811  
 R-HEMBA1004389//Homo sapiens full length insert cDNA clone ZE09A1  
 1.//1.5e-19:170:83//AF086540  
 R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repe  
 at.//1.0:50:84//X58124  
 R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, c  
 omplete sequence.//8.2e-34:459:69//AC004057  
 R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, com  
 plete sequence.//2.8e-42:314:84//AC005030  
 R-HEMBA1004408  
 R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//  
 1.6e-66:449:82//Z54200  
 R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7.  
 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-3  
 2:460:68//AJ011930  
 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUEN  
 CE, 21 unordered pieces.//3.9e-113:581:96//AC004846  
 R-HEMBA1004461//HS\_3244\_A2\_F12\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, gen  
 omic survey sequence.//8.0e-83:397:99//AQ220876  
 R-HEMBA1004479//Homo sapiens PAC clone DJ0942116 from Tq11, comple  
 te sequence.//1.7e-40:485:70//AC006012  
 R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 7  
 3 of the complete sequence.//2.2e-11:513:59//AE001370  
 R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, c  
 omplete sequence.//2.0e-08:245:66//AC005951  
 R-HEMBA1004506//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487  
 R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequ  
 ence.//0.56:235:64//Z70266  
 R-HEMBA1004509  
 R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:8  
 3//176230  
 R-HEMBA1004538//HS\_3189\_B2\_C03\_T7 CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, geno  
 mic survey sequence.//6.1e-21:140:92//AQ170330  
 R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clon  
 e 712K9, genomic survey sequence.//1.7e-16:116:93//B73329  
 R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-  
 14:213:71//D87457  
 R-HEMBA1004573  
 R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's  
 Disease Region, chromosome 4p16.3 contains protein similar to Mo  
 use SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.  
 0:352:60//Z68279  
 R-HEMBA1004586  
 R-HEMBA1004596//Plasmodium falciparum MAL3P6, complete sequence.//  
 0.0012:359:60//Z98551  
 R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62/  
 AL022071  
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcrip  
 t KIAA0501.//1.4e-50:327:85//AB007970  
 R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Geno  
 me Systems Human BAC Library) complete sequence.//4.4e-13:527:63//  
 AC004805  
 R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//  
 U31866  
 R-HEMBA1004632  
 R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUEN  
 CE, 3 unordered pieces.//7.7e-117:573:98//AC005534  
 R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-119:118:99//X84076  
 R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genom  
 ic sequence, complete sequence.//0.00013:501:58//AC005171  
 R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome  
 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG island  
 s, complete sequence.//1.5e-120:571:98//AL031432  
 R-HEMBA1004670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241  
 R-HEMBA1004672//Human DNA sequence from PAC 308113 on chromosome 1  
 p35-1p36.3.//3.4e-38:324:81//Z99291  
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, PI  
 clone: MPO12, complete sequence.//0.86:309:57//AB006702  
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T  
 33B22, genomic survey sequence.//0.29:331:61//B97342  
 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//  
 0.051:424:58//AL034559  
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-11  
 6A10, complete sequence.//1.7e-49:497:76//AC004638  
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, c  
 omplete sequence.//1.6e-38:362:79//AC005562  
 R-HEMBA1004725  
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26,  
 complete sequence.//1.1e-58:489:79//AC002085  
 R-HEMBA1004733  
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome  
 6q16.1-16.3. Contains the gene for the N-Oct5a (N-Oct3, N-Oct5b)  
 POU domain proteins and an unknown gene. Contains a putative CpG i  
 sland, ESTs, STS, and GSSs, complete sequence.//0.0030:362:61//AL0  
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R-HEMBA1004736//Homo sapiens clone DJ0981007, complete sequence.//1.9e-58:282:87//AC005017

R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from Tq21-q31.1, complete sequence.//3.6e-34:287:81//AC004953

R-HEMBA1004751//Human DNA sequence from PAC 507115 on chromosome X q26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like genes, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950

R-HEMBA1004752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121

R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498

R-HEMBA1004758//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807

R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:72//AC004057

R-HEMBA1004763

R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 10q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kd) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310

R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:476:61//AE001371

R-HEMBA1004771//Homo sapiens Xp22 Cosmid U15207 (Lawrence Livermore human cosmid library) complete sequence.//5.0e-08:113:80//AC003047

R-HEMBA1004776

R-HEMBA1004778//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567

R-HEMBA1004795//HS\_3192\_B1\_F09\_T7 CIT Approved Human Genomic Spem Library D Homo sapiens genomic clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855

R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728

R-HEMBA1004806

R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE. 7 unordered pieces.//3.6e-20:333:69//AC005015

R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545

R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002

R-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//7.6e-80:297:85//X53744

R-HEMBA1004850

R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 2 q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201

R-HEMBA1004864

R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPC111-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297

R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE. 12 unordered pieces.//1.9e-49:551:73//AC004826

R-HEMBA1004889//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943

R-HEMBA1004909//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//6.6e-11:144:77//AC005972

R-HEMBA1004909//Human DNA sequence from clone 50S813 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052

R-HEMBA1004918//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554

R-HEMBA1004923//Homo sapiens 47kb DNA fragment from Xq28, proximal to NTM1 gene.//2.0e-07:182:69//Y15994

R-HEMBA1004929

R-HEMBA1004930//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE. 6 unordered pieces.//7.7e-66:547:79//AC005348

R-HEMBA1004933//H. sapiens Humig mRNA.//0.13:233:62//X72755

R-HEMBA1004934//CIT-HSP-2021116.TF CIT-HSP Homo sapiens genomic clone 2021116, genomic survey sequence.//0.66:268:62//B65345

R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849

R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146\_P\_2, WORKING DRAFT SEQUENCE. 4 unordered pieces.//0.00082:385:60//AC005341

R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408

R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249

R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982

R-HEMBA1004973//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECD region of chromosome 21, clones A68E8, B127P21, B173L3, B23M8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center. WORKING DRAFT SEQUENCE. 50 unordered pieces.//0.69:179:64//AC003656

R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495

R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HMRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509

R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614

R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389

R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LA ML), complete sequence.//1.6e-90:527:89//AC004224

R-HEMBA1005008//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663

R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548

R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA A-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179

R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175\_E\_5, complete sequence.//7.4e-101:537:94//AC004596

R-HEMBA1005039//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650

R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819

R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library: complete sequence.//4.0e-43:371:80//AC004040

R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186\_H\_2, complete sequence.//2.3e-15:269:66//AC004675

R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE. 1 unordered pieces.//4.0e-30:305:74//AC006030

R-HEMBA1005075

R-HEMBA1005079//Homo sapiens clone HS19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423

R-HEMBA1005101//Homo sapiens SYT interacting protein S1P mRNA, complete cds.//5.3e-110:545:96//AF080561

R-HEMBA1005113//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340

R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein

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## 【表486】

tein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence. //7.1e-55:306:82//AL022336

R-HEMBA1005133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE. //6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds. //3.2e-31:310:76//U81834

R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island. //1.4e-33:361:79//AL021407

R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence. //2.7e-22:440:66//AL031279

R-HEMBA1005185//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105E8, WORKING DRAFT SEQUENCE. //0.0017:381:58//AL022594

R-HEMBA1005201//P. falciparum complete gene map of plastid-like DNA (IR-B). //7.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA. //4.7e-38:236:91//X03205

R-HEMBA1005219

R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces. //1.0:209:65//AC004854

R-HEMBA1005232//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //0.0040:439:58//AC004617

R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence. //4.2e-111:568:96//AC005154

R-HEMBA1005244//HS\_3092\_B2\_C11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence. //4.9e-12:116:84//AQ127947

R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence. //3.2e-27:210:84//AC004548

R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318\_A\_15, complete sequence. //4.6e-105:437:97//AC005837

R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system. //0.011:339:59//D086630

R-HEMBA1005275//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence. //3.4e-17:269:71//AC004914

R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region on chromosome 13q12-13 contains xst mRNA, ESTs. //6.9e-20:193:73//Z75887

R-HEMBA1005296//HS\_3037\_B1\_D01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence. //0.26:184:64//AQ117120

R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces. //1.5e-58:445:78//AC006146

R-HEMBA1005311//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796E4, WORKING DRAFT SEQUENCE. //9.3e-42:383:78//AL022337

R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11. //0.80:179:65//AF003389

R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces. //2.4e-40:409:71//AC006030

R-HEMBA1005318//S.pombe chromosome I cosmid c2E11. //0.97:370:61//AL031181

R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence. //1.9e-112:577:95//AC005803

R-HEMBA1005353//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 429E7, WORKING DRAFT SEQUENCE. //8.9e-80:406:97//AL031722

R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces. //3.2e-50:320:84//AC005412

R-HEMBA1005367//RPC111-85E23, TV RPC111 Homo sapiens genomic clone R-85E23, genomic survey sequence. //0.39:148:67//AQ281915

R-HEMBA1005372//Homo sapiens full length insert cDNA YH93B03. //2.6e-108:557:95//AF074997

R-HEMBA1005374//Homo sapiens full length insert cDNA clone ZA9501. //1.9e-110:531:98//AF086142

R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN (CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence. //6.0e-41:432:75//Z92542

R-HEMBA1005394//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 681N20, WORKING DRAFT SEQUENCE. //4.9e-107:585:93//AL031670

R-HEMBA1005403//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423822, WORKING DRAFT SEQUENCE. //5.1e-118:586:97//AL034379

R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds. //1.6e-06:204:68//U95958

R-HEMBA1005410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE. //1.2e-23:452:66//AL008722

R-HEMBA1005411//RPC111-65N19, TX RPC111 Homo sapiens genomic clone R-65N19, genomic survey sequence. //2.2e-38:222:79//AQ237442

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds. //5.6e-117:453:99//AF041248

R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome X q26.1 contains ESTs and STS. //0.86:278:60//Z97196

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment. //5.4e-46:305:87//L40391

R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence. //3.3e-79:531:86//AL031054

R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence. //4.0e-27:469:66//AC004894

R-HEMBA1005469//Homo sapiens chromosome 16, Pl clone 96-48 (LANL), complete sequence. //7.2e-40:410:76//AC005212

R-HEMBA1005472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1090E8, WORKING DRAFT SEQUENCE. //3.1e-40:296:85//AL033524

R-HEMBA1005475//HS\_2266\_B2\_C04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence. //0.49:209:61//AQ069377

R-HEMBA1005497

R-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence. //4.5e-116:580:97//AC004957

R-HEMBA1005506//Arabidopsis thaliana BAC T26D22. //0.0050:442:59//AF058826

R-HEMBA1005508//Signalphus sp. 16S ribosomal RNA gene, partial sequence. //0.020:391:59//AF003509

R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21.1. Contains CA repeats, STS. //0.44:195:63//Z96811

R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds. //0.44:470:57//L14320

R-HEMBA1005518//M.musculus mRNA for paladin gene. //6.2e-29:183:81//X99384

R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces. //7.2e-40:281:86//AC004913

R-HEMBA1005526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE. //3.9e-40:482:73//Z97985

R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11. //3.8e-84:309:99//AB020860

R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence. //8.1e-25:154:94//U84091

R-HEMBA1005548//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 970A17, WORKING DRAFT SEQUENCE. //5.3e-105:534:96//AL034431

R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence. //2.8e-69:432:88//AC004743

R-HEMBA1005558

R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence. //5.9e-33:367:74//AC004087

R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ESTs and GSSs, complete sequence. //2.2e-67:399:91//AL020989

R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence. //1.0:156:63//AC005737

R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for NCF5, partial cds. //9.7e-27:561:64//AB011538

R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes. //2.3e-10:404:62//X02171

R-HEMBA1005583//HS\_3014\_B1\_D05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence. //3.0e-81:442:94//AQ154499

R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS802, complete sequence. //1.8e-54:490:77//Z98046

R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence. //2.2e-28:262:79//AC005746

R-HEMBA1005595//HS\_2224\_A2\_G03\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence. //3.6e-48:263:95//AQ033446

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R-HEMBA1005606//Human PAC clone DJ0093103 from Xq23, complete sequence.//2.5e-08:355:63//AC003983

R-HEMBA1005609//HS\_2182\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130

R-HEMBA1005616//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176

R-HEMBA1005621//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321

R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence.//1.4e-13:172:75//AL022069

R-HEMBA1005634//RPC111-13015.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-13015, genomic survey sequence.//1.0e-28:153:82//B73293

R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome X q21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786

R-HEMBA1005670//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3' end.//4.2e-49:322:88//M13450

R-HEMBA1005680//Homo sapiens Chr.14 PAC RPC14-79482 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924

R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eol8) mRNA, complete cds.//5.4e-46:376:84//U66406

R-HEMBA1005705//RPC111-13014.TP RPC1-11 Homo sapiens genomic clone RPC1-11-13014, genomic survey sequence.//0.071:182:59//B76186

R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATPSG2, ATPSG3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pD3363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

R-HEMBA1005737

R-HEMBA1005746//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

R-HEMBA1005755//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmid U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:368:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QK1-7 and QK1-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781

R-HEMBA1005852//F. rubripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730

R-HEMBA1005853//Human Chromosome 15 pac pD24a8, complete sequence.//1.1e-27:314:75//AC000379

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPC13-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC008207

R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072

R-HEMBA1005931//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304

R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261\_A\_13, complete sequence.//0.0052:179:71//AC005138

R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045

R-HEMBA1005963//HS\_3055\_A1\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=1, genomic survey sequence.//5.4e-79:403:97//AQ147357

R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516

R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1 q24.1-24.3. Contains STSs, GSSs, genomic marker DIS210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

R-HEMBA1005999//Homo sapiens clone DJ0891F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

R-HEMBA1006031//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

R-HEMBA1006042//HS\_2169\_A1\_B11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

R-HEMBA1006067

R-HEMBA1006081

R-HEMBA1006090//HS\_2262\_A2\_A01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ216324

R-HEMBA1006091

R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172

R-HEMBA1006108

R-HEMBA1006121

R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22 q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z95113

R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948

R-HEMBA1006138//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//AC005777

R-HEMBA1006142//, complete sequence.//1.0e-13:160:78//AC005500

R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688

R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:574:98//AF048693

R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86//U28217

R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//AC004491

R-HEMBA1006198//\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567

R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557

R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567

R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438:71//U91323

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384

R-HEMBA1006259//RPC111-44N14.TJ RPC111 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161

R-HEMBA1006268

R-HEMBA1006272//Human DNA sequence from clone 1158H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//

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【表488】

R-HEMBA1006273//AL023753  
R-HEMBA1006278//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770  
R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//A016240  
R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//0.97:447:59//AC004585  
R-HEMBA1006291//Homo sapiens full length insert cDNA clone ZB76B1.0.//2.9e-94:454:98//AF086161  
R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//189415  
R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22\_M\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412  
R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-29:132:81//AF076183  
R-HEMBA1006328//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429  
R-HEMBA1006334  
R-HEMBA1006344//Rattus norvegicus nitizin mRNA, partial cds.//8.7e-22:259:72//AF087945  
R-HEMBA1006347//Human prostaticin gene, complete cds.//1.8e-78:170:100//U33446  
R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682  
R-HEMBA1006359//CITBI-E1-2516C16. TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951  
R-HEMBA1006364//G.gallus gene for transforming growth factor-beta 2, exons 5-7.//2.5e-21:118:85//X59080  
R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//AC005239  
R-HEMBA1006380//Human BAC clone RC007J15 from Tq31, complete sequence.//6.1e-47:300:83//AC003989  
R-HEMBA1006381//Homo sapiens chromosome 5, BAC clone 189 (LBNL H135), complete sequence.//1.5e-47:336:86//AC005914  
R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.5e-67:501:83//AC005609  
R-HEMBA1006416//Homo sapiens chromosome 17, clone 347\_H\_5, complete sequence.//4.4e-37:319:76//AC002119  
R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence.//2.9e-50:502:75//AC004253  
R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds: a and unknown genes.//4.1e-116:572:97//AF107885  
R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse KKI-7 and KKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//9.4e-117:578:97//AL031781  
R-HEMBA1006426//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 291J10, WORKING DRAFT SEQUENCE.//2.2e-08:353:63//Z93017  
R-HEMBA1006438//HS\_2008\_A1\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence.//1.2e-29:194:91//AQ245162  
R-HEMBA1006445//Homo sapiens clone RC219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:330:60//AC005075  
R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.032:256:61//AE001398  
R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//5.6e-35:229:77//AC002364  
R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence.//1.1e-14:354:63//AC002052  
R-HEMBA1006471  
R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502  
R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551C9 complete sequence.//3.7e-37:290:82//U95742  
R-HEMBA1006485//H.sapiens mRNA for aminopeptidase.//7.6e-91:517:91//Y07701  
R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-33:289:81//AC005089  
R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ESTs and GSSs, complete sequence.//6.0e-07:485:60//AL020989  
R-HEMBA1006492//Homo sapiens chromosome 17 clone hRPK.269\_G\_24, complete sequence.//4.3e-112:572:95//AC005828  
R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPK987K16, complete sequence.//2.3e-10:186:67//AC002994

R-HEMBA1006497//RPC111-16L10.TPB RPC1-11 Homo sapiens genomic clone RPC1-11-16L10, genomic survey sequence.//1.5e-10:75:100//B88015  
R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.3e-36:516:70//Z93929  
R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//1.2e-115:570:96//AB014566  
R-HEMBA1006521//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54820, WORKING DRAFT SEQUENCE.//2.2e-20:266:71//Z98304  
R-HEMBA1006530//RPC111-52M1.TJ RPC111 Homo sapiens genomic clone R-52M1, genomic survey sequence.//0.00015:227:64//AQ052526  
R-HEMBA1006535//HS\_2234\_B1\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525  
R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007  
R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603  
R-HEMBA1006559//Mus musculus PRAJA1 (Prajai) mRNA, complete cds.//3.4e-64:551:78//U06944  
R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pJ404m15, complete sequence.//5.7e-09:266:66//AC002554  
R-HEMBA1006566//HS\_2171\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421  
R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357  
R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032  
R-HEMBA1006583//CIT-HSP-2377M16. TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ11875  
R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709  
R-HEMBA1006597//Homo sapiens PI clone GSP13996 from Sq12, complete sequence.//2.7e-45:371:80//AC005031  
R-HEMBA1006612  
R-HEMBA1006617//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 8822, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737  
R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284  
R-HEMBA1006631//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848  
R-HEMBA1006635//ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572  
R-HEMBA1006639  
R-HEMBA1006643  
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282  
R-HEMBA1006652//Human BAC clone RG308B22 from Tq22-q31, complete sequence.//8.7e-54:334:76//AC002089  
R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390  
R-HEMBA1006665//HS\_3213\_B2\_D04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625  
R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTEL00023.seq.//2.6e-32:212:83//Z96776  
R-HEMBA1006675//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551  
R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608  
R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096  
R-HEMBA1006696  
R-HEMBA1006708  
R-HEMBA1006709//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 715M11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674  
R-HEMBA1006717  
R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//9.9e-18:365:66//AC005828  
R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//2.3e-10:186:67//AC002994

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plete sequence.//1.3e-37:380:75//AC003108  
 R-HEMBA1006754//Homo sapiens chromosome 5, Pl clone 962c5 (LBML H8 7), complete sequence.//2.1e-75:338:85//AC003951  
 R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBML H 161), complete sequence.//1.2e-112:579:95//AC005752  
 R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551  
 R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, c omplete sequence.//2.3e-46:305:87//AC005701  
 R-HEMBA1006780//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-3 9:305:82//AL022323  
 R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61 //AL031317  
 R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, c omplete sequence.//4.1e-43:355:80//AC006120  
 R-HEMBA1006796//HS\_3038\_B2\_H11\_MF CIT Approved Human Genomic Spere Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, gen omic survey sequence.//0.99:158:63//AQ102483  
 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUEN CE, 33 unordered pieces.//8.4e-47:481:75//AC004854  
 R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62\_0\_9, com plete sequence.//3.0e-08:84:90//AC004797  
 R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromo some Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:4 96:76//Z93023  
 R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, c omplete sequence.//0.70:206:65//AC005668  
 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPC13-521E19 (Roswell Pa k Cancer Institute Human PAC library) complete sequence.//1.2e-46: 281:91//AC004217  
 R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence./ /0.61:115:70//AF056074  
 R-HEMBA1006877//Mus musculus mRNA for oxysterol-binding protein, c omplete cds.//3.3e-102:618:87//AB017026  
 R-HEMBA1006885  
 4.2e-14:379:63//AC006839  
 R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic cl one 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395  
 R-HEMBA1006921//Homo sapiens PAC clone DJ0777023 from 7p14-p15, co mplete sequence.//2.1e-68:267:86//AC005154  
 R-HEMBA1006926  
 R-HEMBA1006929//HS\_3244\_A2\_CD1\_T7 CIT Approved Human Genomic Spere Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, geno mic survey sequence.//6.9e-21:191:83//AQ207500  
 R-HEMBA1006936  
 R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853  
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like pr otein.//2.0e-75:371:98//AJ010841  
 R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, co mplete sequence.//0.47:240:63//AC005518  
 R-HEMBA1006973//HS\_2009\_A2\_A12\_MR CIT Approved Human Genomic Spere Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, gen omic survey sequence.//9.6e-05:407:60//AQ232302  
 R-HEMBA1006976//RPC111-49L11.TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701  
 R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 6, co mplete exon 7, partial exon 8, and partial cds for thymopoietin be ta.//1.9e-47:394:79//U18271  
 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic cl one 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406  
 R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558  
 R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, c omplete sequence.//5.6e-41:437:71//AC005277  
 R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:5 56:80//X79088  
 R-HEMBA1007045  
 R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-oter contains EST.//9.9e-27:342:71//Z72006  
 R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056  
 R-HEMBA1007062  
 R-HEMBA1007066  
 R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421\_E\_14, c omplete sequence.//2.0e-66:476:85//AC006141  
 R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, co mplete sequence.//1.0e-38:179:82//AC005325  
 R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUEN CE, 6 unordered pieces.//3.2e-49:551:73//AC006015  
 R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequen ce.//1.0:261:61//AC000385  
 R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQ UENCE, 37 unordered pieces.//0.043:295:62//AC004803  
 R-HEMBA1007113//Homo sapiens (subclone 6\_a8 from P1 H16) DNA seque nce.//1.4e-52:307:87//L43392  
 R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547  
 R-HEMBA1007147//H.sapiens CpG island DNA genomic MseI fragment, cl one 65f1, reverse read cpg65f1.r1a.//0.16:187:64//Z62246  
 R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complet e sequence.//7.6e-108:543:96//AC005239  
 R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, comple te sequence.//0.14:323:58//AC004875  
 R-HEMBA1007174//Homo sapiens opsin 2a mRNA, complete cds.//5.1e-10 3:529:94//AF062085  
 R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC111-372B 4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//5.4e-106:537:96//A C005911  
 R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Rosw ell Park Cancer Institute Human PAC Library) complete sequence.//4.1e-39:262:80//AC003035  
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete c ds.//5.3e-61:332:95//DB6987  
 R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromo some Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//1.9e-50:4 36:81//Z93023  
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cd s.//2.3e-96:471:97//AB018340  
 R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBML H 85), complete sequence.//0.011:349:62//AC004777  
 R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, co mplete sequence.//2.8e-10:224:70//AC004856  
 R-HEMBA1007267//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.4e-53:36 2:86//AC005924  
 R-HEMBA1007273  
 R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete ge nome: segment 4/4.//0.042:454:57//AJ235273  
 R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete ge nome: segment 3/4.//0.99:288:60//AJ235272  
 R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//7.4 e-107:554:95//AL031003  
 R-HEMBA1007300//Caenorhabditis elegans cosmid C4BC5.//0.22:474:59/ /U39994  
 R-HEMBA1007301  
 R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT.//4.9e-08:524:58//Y14425  
 R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segm ent 14/28, WORKING DRAFT SEQUENCE.//3.4e-16:244:71//AP000043  
 R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, com plete sequence.//3.9e-83:383:85//AC005251  
 R-HEMBA1007327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 7706, WORKING DRAFT SEQUENCE.//1.6e-38:533:71//Z96804  
 R-HEMBA1007341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268D13, WORKING DRAFT SEQUENCE.//3.6e-21:394:66//AL0235 13  
 R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete seque nce.//1.7e-15:190:73//AC003080  
 R-HEMBA1007347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone N38G6, WORKING DRAFT SEQUENCE.//2.2e-47:455:77//Z96802  
 R-HEMBA1000005//Homo sapiens 3p21.1-9 PAC RPC14-793P23 (Roswell Pa rk Cancer Institute Human PAC Library) complete sequence.//1.1e-6 2:539:79//AC006208  
 R-HEMBA1000008//Homo sapiens chromosome 17, clone hCIT.211\_P\_7, co mplete sequence.//1.2e-36:285:83//AC003665  
 R-HEMBA1000018//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUEN CE, 5 unordered pieces.//1.2e-51:416:79//AC004820  
 R-HEMBA1000024//Human DNA sequence from BAC 175E3 on chromosome 22 q11.2-oter. Contains ESTs, STSs and polymorphic CA repeat.//3.9e-1 8:211:79//Z95113  
 R-HEMBA1000025//HS\_3064\_B2\_B07\_MF CIT Approved Human Genomic Spere Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, gen omic survey sequence.//5.9e-40:254:90//AQ132765  
 R-HEMBA1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinas

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## 【表490】

a gene similar to yeast suppressor protein SRP40. EST and GSS, complete sequence.//1.5e-32:452:70//Z85986

R-HEM8B1000036//CIT-HSP-2024L15. TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence.//9.3e-63:541:77//B66264

R-HEM8B1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//AF084928

R-HEM8B1000039//Homo sapiens chromosome 17, clone hRKC.401\_0\_9, complete sequence.//2.4e-44:456:68//AC005291

R-HEM8B1000044//Human BAC clone RC016J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064

R-HEM8B1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279810, complete sequence.//3.8e-09:330:63//AC002300

R-HEM8B1000050//Human DNA sequence from PAC 436M11 on chromosome X p22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the R51 gene for retinoblastoma (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

R-HEM8B1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEM8B1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

R-HEM8B1000059//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC005009

R-HEM8B1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEM8B1000089//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

R-HEM8B1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0509 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEM8B1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

R-HEM8B1000113//HS\_3013\_A1\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEM8B1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEM8B1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEM8B1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

R-HEM8B1000144//Homo sapiens chromosome 17, clone hCIT.507\_E\_2, complete sequence.//0.00083:206:66//AC004134

R-HEM8B1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

R-HEM8B1000175

R-HEM8B1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

R-HEM8B1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase-MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

R-HEM8B1000217

R-HEM8B1000218//Homo sapiens 12q24 PAC RPC11-65E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEM8B1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

R-HEM8B1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM8B1000244//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

R-HEM8B1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777

R-HEM8B1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

R-HEM8B1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

R-HEM8B1000266//RPC111-76C20. TV RPC111 Homo sapiens genomic clone 76C20, genomic survey sequence.//1.0:232:59//AQ265533

R-HEM8B1000272//HS\_3032\_B1\_H06\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702

R-HEM8B1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.6e-45:277:72//AC000053

R-HEM8B1000284//Homo sapiens full length insert cDNA clone Y88A05.//6.9e-112:572:96//AF088018

R-HEM8B1000307//Homo sapiens chromosome 17, clone hRKC.471\_L\_13, complete sequence.//5.7e-96:523:93//AC005244

R-HEM8B1000312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693

R-HEM8B1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145

R-HEM8B1000318//Human DNA sequence from PAC 292H14 on chromosome X p21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710

R-HEM8B1000335//Homo sapiens chromosome 5, Pl clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179

R-HEM8B1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147

R-HEM8B1000337//CIT-HSP-2329010. TF CIT-HSP Homo sapiens genomic clone 2329010, genomic survey sequence.//1.2e-31:192:92//AQ035976

R-HEM8B1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24877, complete sequence.//1.9e-39:477:71//AC004605

R-HEM8B1000339//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031658

R-HEM8B1000341//Homo sapiens 12q24 PAC RPC13-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350

R-HEM8B1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644

R-HEM8B1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751

R-HEM8B1000369//Homo sapiens chromosome 4 clone B366024 map 4q25, complete sequence.//9.0e-25:179:79//AC004067

R-HEM8B1000374//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199

R-HEM8B1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675

R-HEM8B1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080

R-HEM8B1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838

R-HEM8B1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052

R-HEM8B1000404//HS\_2246\_A2\_D01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251

R-HEM8B1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.2e-29:358:72//AC000053

R-HEM8B1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069

R-HEM8B1000438//HS\_2239\_B2\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700

R-HEM8B1000441//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207

R-HEM8B1000449//Homo sapiens clone DJ089B018, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920

R-HEM8B1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:65//AC005007

R-HEM8B1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104

R-HEM8B1000480//Human DNA sequence from Fosmid 6587 on chromosome 22q11.2-pter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (Hi

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gh Affinity Sodium-Glucose Cotransporter). complete sequence.//3.4e-36:285:82//Z83849

R-HEM8B1000487

R-HEM8B1000490//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423

R-HEM8B1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023

R-HEM8B1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, GSSs, and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721

R-HEM8B1000510//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397

R-HEM8B1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477

R-HEM8B1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079

R-HEM8B1000530//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//4.2e-74:428:92//AC006236

R-HEM8B1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321

R-HEM8B1000554//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824

R-HEM8B1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds.//0.031:275:60//U53786

R-HEM8B1000564//Homo sapiens chromosome 5, BAC clone 189 (LBML H135), complete sequence.//3.1e-17:227:76//AC005914

R-HEM8B1000573//Borrelia afzelii (strain NT8) DNA, internal transcribed spacer.//0.078:161:63//D84405

R-HEM8B1000575//Homo sapiens chromosome 17, clone hRPC.859\_0\_20, complete sequence.//7.2e-52:260:80//AC003695

R-HEM8B1000586//Human DNA sequence from cosmid Y210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280

R-HEM8B1000589//Homo sapiens chromosome 17, clone hRPC.1064\_E\_11, complete sequence.//1.3e-14:409:65//AC005208

R-HEM8B1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665M22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184

R-HEM8B1000592//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC005831

R-HEM8B1000598//Homo sapiens chromosome 11 pac pDJ159ol, complete sequence.//3.3e-38:407:76//AC000381

R-HEM8B1000623//CIT-HSP-2374P17, TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717

R-HEM8B1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724

R-HEM8B1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80058

R-HEM8B1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176

R-HEM8B1000637//Human BAC clone RC094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085

R-HEM8B1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112

R-HEM8B1000643//HS\_2242\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993

R-HEM8B1000649//Homo sapiens RBP56/NTAF1168 gene, exon 7.//8.3e-63:306:100//AB010061

R-HEM8B1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031

R-HEM8B1000665//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MXA21, complete sequence.//0.98:251:63//AB005247

R-HEM8B1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chromosome X.//6.8e-58:296:85//Z83313

R-HEM8B1000673//CITB1-E1-2506F20, TR CITB1-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731

R-HEM8B1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4. Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584

R-nnnnnnnnnnn/Homo sapiens neuroanl mRNA, complete cds.//2.0e-50:287:93//AF040723

R-HEM8B1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943

R-HEM8B1000706//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380

R-HEM8B1000709//RPC111-79A8.TV RPC111 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374

R-HEM8B1000725//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MGN6, complete sequence.//0.00018:386:60//AB017066

R-HEM8B1000726//Homo sapiens PAC clone DJ1185107 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990

R-HEM8B1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875

R-HEM8B1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069

R-HEM8B1000763//Plasmid Col 1b-P9 (from E.coli K12) colicin 1b promoter region and 5' coding region.//1.0:115:63//K02071

R-HEM8B1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205

R-HEM8B1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046

R-HEM8B1000789//RPC111-2114.TVB RPC11-11 Homo sapiens genomic clone RPC11-2114, genomic survey sequence.//3.0e-09:299:64//B63628

R-HEM8B1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740

R-HEM8B1000794//HS\_3253\_A1\_G06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291

R-HEM8B1000807

R-HEM8B1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542

R-HEM8B1000821

R-HEM8B1000822//CITB1-E1-2517E13.TF CITB1-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944

R-HEM8B1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043

R-HEM8B1000827//Homo sapiens clone DJ0981007, complete sequence.//6.8e-43:319:84//AC006017

R-HEM8B1000831//HS\_3247\_B2\_A09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850

R-HEM8B1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368

R-HEM8B1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283

R-HEM8B1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086

R-HEM8B1000852//HS\_3075\_A2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816

R-HEM8B1000870//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523

R-HEM8B1000876//Human DNA sequence from clone 91J24 on chromosome 6q24. Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474

R-HEM8B1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//AC005621

R-HEM8B1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061

R-HEM8B1000888//CIT-HSP-2282A13, TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

R-HEM8B1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995

R-HEM8B1000893//Homo sapiens BAC clone RC363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492

R-HEM8B1000908//RPC111-13P12.TV RPC11-11 Homo sapiens genomic clone RPC11-11-13P12, genomic survey sequence.//0.98:183:61//B76199

R-HEM8B1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10

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## 【表492】

In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024  
 R-HEM8B1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037  
 R-HEM8B1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-22 4D6 complete sequence.//6.3e-09:536:59//U95739  
 R-HEM8B1000917//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015  
 R-HEM8B1000927  
 R-HEM8B1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228  
 R-HEM8B1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//5.7e-89:544:90//AC003098  
 R-HEM8B1000973//Arabidopsis thaliana chromosome II BAC F219 genomic sequence, complete sequence.//0.038:377:58//AC005560  
 R-HEM8B1000975//Arabidopsis thaliana chromosome II BAC FSH14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234  
 R-HEM8B1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443  
 R-HEM8B1000985//HS\_3184\_A1\_012\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008  
 R-HEM8B1000991  
 R-HEM8B1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//1.4e-42:343:81//AC002368  
 R-HEM8B1001004  
 R-HEM8B1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056  
 R-HEM8B1001011//HS\_3017\_B1\_003\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944  
 R-HEM8B1001014//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662  
 R-HEM8B1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549  
 R-HEM8B1001024//Homo sapiens (subclone 2\_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475  
 R-HEM8B1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527  
 R-HEM8B1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699  
 R-HEM8B1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586  
 R-HEM8B1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014  
 R-HEM8B1001058//Homo sapiens clone UMGCC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187  
 R-HEM8B1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973  
 R-HEM8B1001063//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375  
 R-HEM8B1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803  
 R-HEM8B1001096//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735  
 R-HEM8B1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily A, member 1 (SMN2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577  
 R-HEM8B1001105//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 462023, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431  
 R-HEM8B1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), 5' UTR, ESTs, STS.//1.1e-38:306:84//Z99570  
 R-HEM8B1001117//RPC11-3518.TK RPC1-11 Homo sapiens genomic clone RPC1-11-3518, genomic survey sequence.//1.5e-08:67:100//AQ047113  
 R-HEM8B1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071  
 R-HEM8B1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495  
 R-HEM8B1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//W25077  
 R-HEM8B1001137//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-09, complete sequence.//2.5e-07:334:62//AL010

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 R-HEM8B1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564  
 R-HEM8B1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904  
 R-HEM8B1001153//RPC11-10L7.TP RPC1-11 Homo sapiens genomic clone RPC1-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766  
 R-HEM8B1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070  
 R-HEM8B1001175//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055  
 R-HEM8B1001177  
 R-HEM8B1001182//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226  
 R-HEM8B1001199  
 R-HEM8B1001208  
 R-HEM8B1001209//RPC11-41E13.TP RPC1-11 Homo sapiens genomic clone RPC1-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098  
 R-HEM8B1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LAML), complete sequence.//6.2e-08:412:61//AC005199  
 R-HEM8B1001218//RPC11-13L8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158  
 R-HEM8B1001221//RPC111-62024.TJ RPC111 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950  
 R-HEM8B1001234  
 R-HEM8B1001242  
 R-HEM8B1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377  
 R-HEM8B1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089  
 R-HEM8B1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461  
 R-HEM8B1001267//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain L1KE gene, a alternatively spliced Melanoma-Associated Antigen MAGE-LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046  
 R-HEM8B1001271//Homo sapiens chromosome 17, clone hRPC.349\_A\_8, complete sequence.//3.9e-47:494:75//AC005544  
 R-HEM8B1001282//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428  
 R-HEM8B1001288  
 R-HEM8B1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBML H180), complete sequence.//2.0e-31:301:78//AC005601  
 R-HEM8B1001294//Homo sapiens BAC clone RG060W22 from 7q21, complete sequence.//0.053:283:60//AC003083  
 R-HEM8B1001302  
 R-HEM8B1001304//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396:64//AL033397  
 R-HEM8B1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8 SPN6, genomic survey sequence.//3.4e-42:293:86//AC013777  
 R-HEM8B1001315//Human NFE genomic fragment.//7.5e-30:243:78//W98511  
 R-HEM8B1001317//Homo sapiens chromosome 17, clone hRPC.1028\_K\_7, complete sequence.//2.3e-39:301:82//AC004585  
 R-HEM8B1001326//HS\_3054\_A1\_F12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096  
 R-HEM8B1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//0.037:103:77//D63850  
 R-HEM8B1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229:77//AC003037  
 R-HEM8B1001337  
 R-HEM8B1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551:72//U85056  
 R-HEM8B1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292:99//AF097441  
 R-HEM8B1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326:82//AC004859  
 R-HEM8B1001356//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213:67//Z82207  
 R-HEM8B1001364//HS\_3050\_A2\_F05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ133940  
 R-HEM8B1001366//Homo sapiens chromosome 10 clone CIT987SK-118815 m

## 【0793】



【表493】

ap 10p11.2-10p12.1, complete sequence.//4.1e-37:419:73//AC005876  
 R-HEM81001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//U91326  
 R-HEM81001369//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224:83//AL021686  
 R-HEM81001380//HS\_2267\_B1\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896  
 R-HEM81001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//AF071314  
 R-HEM81001387//Homo sapiens chromosome 9, P1 clone 8660 (LBML H105), complete sequence.//1.0:166:63//AC003953  
 R-HEM81001394//Homo sapiens chromosome 17, clone hRPK.215\_E\_13, complete sequence.//1.4e-55:494:76//AC005549  
 R-HEM81001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:63//AC006204  
 R-HEM81001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//AC002370  
 R-HEM81001426//Homo sapiens 12q24 PAC RPC13-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328:84//AC002350  
 R-HEM81001429//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14: HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160  
 R-HEM81001436  
 R-HEM81001443//HS\_2228\_A1\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934  
 R-HEM81001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339:69//AC005522  
 R-HEM81001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBML H60), complete sequence.//1.1e-39:299:84//AC005355  
 R-HEM81001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:486:59//AE001430  
 R-HEM81001463//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154  
 R-HEM81001464//CIT-HSP-2370C10, TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941  
 R-HEM81001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762  
 R-HEM81001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATPTA) putative Cu<sup>2+</sup>-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801  
 R-HEM81001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046842  
 R-HEM81001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483:76//AC005000  
 R-HEM81001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070  
 R-HEM81001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286:79//Z74581  
 R-HEM81001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169  
 R-HEM81001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394  
 R-HEM81001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-48SG10, complete sequence.//0.34:212:61//AC003049  
 R-HEM81001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-32BA3, complete sequence.//8.0e-40:267:88//AC002301  
 R-HEM81001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225  
 R-HEM81001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194:75//AC004840  
 R-HEM81001585//Human DNA sequence from clone 79086 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677  
 R-HEM81001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//7.2e-30:371:74//AC005236  
 R-HEM81001588//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106  
 R-HEM81001603//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-59, complete sequence.//0.034:302:59//AL010235  
 R-HEM81001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.1e-31:503:68//Z93023  
 R-HEM81001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368  
 R-HEM81001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z68062  
 R-HEM81001635//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//1.5e-23:407:69//AC004075  
 R-HEM81001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368  
 R-HEM81001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506  
 R-HEM81001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344  
 R-HEM81001665//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572  
 R-HEM81001668  
 R-HEM81001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546  
 R-HEM81001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//186429  
 R-HEM81001685//Homo sapiens chromosome 17, clone hRPK.721\_K\_1, complete sequence.//2.6e-43:311:83//AC005411  
 R-HEM81001695  
 R-HEM81001704//CIT-HSP-2324C15, TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704  
 R-HEM81001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851  
 R-HEM81001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020  
 R-HEM81001717//CIT-HSP-2378C19, TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992  
 R-HEM81001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBML H94), complete sequence.//1.8e-10:80:90//AC005613  
 R-HEM81001736//CIT-HSP-2369K6, TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221  
 R-HEM81001747//Homo sapiens cosmid Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671  
 R-HEM81001749//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, complete sequence.//1.4e-60:242:92//AC005829  
 R-HEM81001753//RPC111-59J22, TK RPC111 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046  
 R-HEM81001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130  
 R-HEM81001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2128, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050  
 R-HEM81001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IaAlpha) and major histocompatibility protein class II beta chain (IbBeta) genes, complete cds: butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds: NG12 pseudogene, partial sequence: and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157  
 R-HEM81001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170  
 R-HEM81001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140  
 R-HEM81001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391  
 R-HEM81001812//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882  
 R-HEM81001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996  
 R-HEM81001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209  
 R-HEM81001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328  
 R-HEM81001839  
 R-HEM81001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241  
 R-HEM81001853//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436  
 R-HEM81001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327  
 R-HEM81001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754  
 R-HEM81001869//Homo sapiens chromosome 17, clone HCIT529110, comp

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## 【表494】

lete sequence.//7.0e-37:285:85//AC002553  
R-HEM8B1001872//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGR  
ESS \*\*\* from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//A  
L009027  
R-HEM8B1001874  
R-HEM8B1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complet  
e plasmid sequence.//0.037:406:60//AE001272  
R-HEM8B1001880//Homo sapiens chromosome 17, clone hRPK.235\_1\_10, c  
omplete sequence.//1.3e-49:461:77//AC005922  
R-HEM8B1001899//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGR  
ESS \*\*\* from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z  
98858  
R-HEM8B1001905//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL0223  
45  
R-HEM8B1001906  
R-HEM8B1001908//Genomic sequence from Human 17, complete sequence.  
//2.9e-36:274:76//AC001231  
R-HEM8B1001910//Homo sapiens chromosome 17, clone HCIT39G8, comple  
te sequence.//3.5e-41:408:76//AC003070  
R-HEM8B1001911//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKI  
NG DRAFT SEQUENCE.//6.1e-64:310:89//AJ011929  
R-HEM8B1001915//Mouse mRNA for arylhydrocarbon receptor, complete  
cds.//2.0e-20:220:78//D38417  
R-HEM8B1001921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034  
422  
R-HEM8B1001922//Homo sapiens chromosome 17, clone HCIT421K24, comp  
lete sequence.//6.2e-32:378:74//AC004099  
R-HEM8B1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and  
pDJ239b22, WORKING DRAFT SEQUENCE. 17 unordered pieces.//8.2e-41:  
304:84//AC000406  
R-HEM8B1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge  
ne of hepatocellular colorectal and non-small cell lung cancer, s  
egment 10/11.//8.3e-12:202:69//AB020867  
R-HEM8B1001944//P. falciparum gene for beta subunit RNA polymerase.  
//0.00090:264:62//X75544  
R-HEM8B1001945//Swietenia humilis DNA for simple tandem repeat (24  
2bp).//0.056:224:62//AJ000408  
R-HEM8B1001947//RPC111-60L13.TJ RPC111 Homo sapiens genomic clone  
R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ020335  
R-HEM8B1001950//Human DNA sequence from clone 41SG2 on chromosome  
22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//  
0.57:115:68//Z83846  
R-HEM8B1001952//Homo Sapiens Chromosome X clone bWXD171, WORKING D  
RAFT SEQUENCE. 1 ordered pieces.//5.6e-36:283:84//AC004676  
R-HEM8B1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUEN  
CE. 7 unordered pieces.//8.9e-60:334:82//AC005037  
R-HEM8B1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENC  
E. 2 unordered pieces.//1.9e-56:518:77//AC005077  
R-HEM8B1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LAN  
L), complete sequence.//3.2e-19:157:86//AC005736  
R-HEM8B1001967//Homo sapiens DNA for amyloid precursor protein, co  
mplete cds.//5.7e-68:314:89//D87675  
R-HEM8B1001973//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from P  
AC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ  
009617  
R-HEM8B1001983//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL0344  
17  
R-HEM8B1001988//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034  
420  
R-HEM8B1001990//Homo sapiens full length insert cDNA clone ZC33G0  
3.//7.8e-95:456:98//AF086192  
R-HEM8B1001996  
R-HEM8B1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENC  
E. 26 unordered pieces.//6.4e-26:162:83//AC005055  
R-HEM8B1002002//Human DNA sequence from PAC 2A2 on chromosome X co  
ntains ESTs.//8.2e-83:362:93//Z84816  
R-HEM8B1002005//Homo sapiens chromosome 3p clone RPC15-1034C16, WO  
RKING DRAFT SEQUENCE. 45 unordered pieces.//8.5e-36:291:83//AC0059  
03  
R-HEM8B1002009//Homo sapiens clone DJ0828F13, complete sequence.//  
5.6e-08:307:65//AC004904  
R-HEM8B1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Libr  
ary C Homo sapiens genomic clone Plate-CT 821 Col=19 Row=E, genom  
ic survey sequence.//1.9e-05:375:62//B36336  
R-HEM8B1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic cl  
one 2313E13, genomic survey sequence.//0.34:241:62//AQ028389  
R-HEM8B1002043//Homo sapiens chromosome 21, P1 clone LBL88 (LBML H  
8), complete sequence.//7.4e-35:297:82//AC005612  
R-HEM8B1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBML  
H154), complete sequence.//5.8e-96:582:90//AC005740  
R-HEM8B1002045//Homo sapiens chromosome 19, cosmid F22676, complet  
e sequence.//4.7e-63:575:77//AC005778  
R-HEM8B1002049//Human Chromosome X clone bWXD187, complete sequenc  
e.//1.9e-21:384:64//AC004383  
R-HEM8B1002050//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, co  
mplete sequence.//2.5e-37:368:76//AC005553  
R-HEM8B1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBML  
H170), complete sequence.//0.30:167:65//AC004782  
R-HEM8B1002069//Homo sapiens chromosome 19, cosmid R33516, complet  
e sequence.//2.3e-73:449:84//AC004799  
R-HEM8B1002092//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, c  
omplete sequence.//3.8e-45:307:87//AC005828  
R-HEM8B1002094//Homo sapiens chromosome 19, cosmid R30538, complet  
e sequence.//3.1e-47:457:76//AC005943  
R-HEM8B1002115//HS\_2223\_B1\_G10\_MF CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate-2223 Col=19 Row=N, gen  
omic survey sequence.//3.0e-58:295:98//AQ152279  
R-HEM8B1002139//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus s  
equence.//6.6e-49:283:93//U14573  
R-HEM8B1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUEN  
CE. 5 unordered pieces.//1.1e-45:451:76//AC006006  
R-HEM8B1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16  
map 10q25, complete sequence.//1.3e-57:359:81//AC005881  
R-HEM8B1002189//Human Chromosome 11 pac pDJ392a17, complete sequen  
ce.//4.5e-43:420:77//AC000385  
R-HEM8B1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUEN  
CE. 6 unordered pieces.//8.2e-33:340:64//AC004913  
R-HEM8B1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92  
//180846  
R-HEM8B1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-  
52:415:81//AF015148  
R-HEM8B1002218//, complete sequence.//3.4e-17:178:82//AC005300  
R-HEM8B1002232//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromo  
some 4, BAC clone C0052122: HTGS phase 1, WORKING DRAFT SEQUENCE.  
4 unordered pieces.//1.6e-55:292:88//AC004599  
R-HEM8B1002247//Homo sapiens chromosome 17, clone hRPK.259\_G\_18, c  
omplete sequence.//2.9e-13:227:70//AC005829  
R-HEM8B1002249//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL03173  
3  
R-HEM8B1002254//Human Chromosome X, WORKING DRAFT SEQUENCE. 6 unor  
dered pieces.//6.3e-104:593:91//AC002415  
R-HEM8B1002255//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930  
R-HEM8B1002266//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE  
SS \*\*\* from contig 4-10, complete sequence.//1.3e-09:371:63//AL010  
216  
R-HEM8B1002280//Homo sapiens PAC clone DJ0545C24 from Tq21-q22, co  
mplete sequence.//1.3e-39:247:86//AC004534  
R-HEM8B1002300//Human Chromosome 11 Cosmid cSRL30h11, complete seq  
uence.//4.1e-84:549:86//U73642  
R-HEM8B1002306//Homo sapiens BAC clone RG136M17 from Tp15-p21, com  
plete sequence.//2.5e-10:164:71//AC004129  
R-HEM8B1002327//Homo sapiens BAC clone GS539F22 from Tp12-p14, com  
plete sequence.//0.39:365:59//AC005028  
R-HEM8B1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Libr  
ary C Homo sapiens genomic clone Plate-CT 771 Col=9 Row=N, genomic  
survey sequence.//0.96:180:58//B39313  
R-HEM8B1002340//Homo sapiens PAC clone DJ0659J06 from Tq33-q35, co  
mplete sequence.//7.9e-17:258:73//AC004849  
R-HEM8B1002342//Homo sapiens mRNA for putative thioredoxin-like pr  
otein.//6.9e-96:479:97//AJ010841  
R-HEM8B1002358//Human Xp22 BAC CT-285115 (from CalTech/Research Ge  
netics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and C  
osmid U3585 (from Lawrence Livermore), complete sequence.//2.3e-5  
3:309:83//AC002366  
R-HEM8B1002359//Homo sapiens clone NH0486122, WORKING DRAFT SEQUEN  
CE. 5 unordered pieces.//4.9e-27:350:74//AC005038  
R-HEM8B1002364//Homo sapiens Xp22 PAC RPC11-108M6 (Roswell Park Ca  
ncer Center PAC library) complete sequence.//8.6e-53:302:79//AC003  
036  
R-HEM8B1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapp  
ing to chromosome 11, band p13.//3.2e-38:199:100//X04094  
R-HEM8B1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:12  
0:78//AF072467  
R-HEM8B1002383//Human DNA sequence from cosmid U19H10 on chromosom

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【表495】

e X. Contains ESTs and CA repeat. //0.98:351:58//AL021182  
 R-HEM8B1002387//HS-1052-82-G10-MR. abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence. //2.0e-07:276:67//B41091  
 R-HEM8B1002415//Homo sapiens chromosome 17, clone hRPK.209.D.14, complete sequence. //1.4e-25:202:79//AC005730  
 R-HEM8B1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence. //3.6e-60:401:87//AC004799  
 R-HEM8B1002442//Homo sapiens clone UWCC:r9a from 6p21, complete sequence. //3.1e-51:358:81//AC006046  
 R-HEM8B1002453//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 86D1, WORKING DRAFT SEQUENCE. //1.4e-115:557:98//AL034349  
 R-HEM8B1002457//Human DNA sequence from clone 364122 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence. //6.3e-37:338:80//AL031012  
 R-HEM8B1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence. //9.7e-09:314:64//AE000659  
 R-HEM8B1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project). //0.42:110:74//AL021635  
 R-HEM8B1002489//Salvelinus fontinalis microsatellite sequence SF0-12. //6.6e-06:167:71//U50302  
 R-HEM8B1002492//RPC111-74F21.TK RPC111 Homo sapiens genomic clone R-74F21, genomic survey sequence. //3.1e-14:410:63//AQ238960  
 R-HEM8B1002495//HS\_3220\_A2\_F07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence. //1.3e-24:137:100//AQ180762  
 R-HEM8B1002502//Homo sapiens chromosome 17, clone hRPK.346.K.10, complete sequence. //9.6e-81:538:86//AC006120  
 R-HEM8B1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence. //0.0061:482:57//AL031313  
 R-HEM8B1002510//HS\_2179\_A1\_F03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence. //6.9e-35:423:72//AQ298309  
 R-HEM8B1002520//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 27K12, WORKING DRAFT SEQUENCE. //2.0e-62:201:85//AL033397  
 R-HEM8B1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL HI 39), complete sequence. //0.99:323:58//AC004225  
 R-HEM8B1002531  
 R-HEM8B1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE. //1.0e-61:380:79//AP000009  
 R-HEM8B1002545//RPC111-2F3.TVB RPC111 Homo sapiens genomic clone RPC111-2F3, genomic survey sequence. //3.5e-12:414:63//B63283  
 R-HEM8B1002550  
 R-HEM8B1002556//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0481P14: HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces. //2.6e-62:299:85//AC006160  
 R-HEM8B1002579//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1141E15, WORKING DRAFT SEQUENCE. //1.7e-42:286:88//AL034422  
 R-HEM8B1002582//Homo sapiens clone DJ1119N05, complete sequence. //3.0e-14:426:60//AC004968  
 R-HEM8B1002590//Homo sapiens clone RG132J19, complete sequence. //1.1e-30:392:74//AC005163  
 R-HEM8B1002596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50B115, WORKING DRAFT SEQUENCE. //8.5e-44:335:83//AL02107  
 R-HEM8B1002600//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //2.0e-105:470:96//AC005865  
 R-HEM8B1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence. //1.3e-44:445:77//AC004223  
 R-HEM8B1002603//Homo sapiens clone UWCC:y23c049 from 6p21, complete sequence. //7.0e-40:321:82//AC006162  
 R-HEM8B1002607//CIT-HSP-234707.TF CIT-HSP Homo sapiens genomic clone 234707, genomic survey sequence. //1.1e-44:234:98//AQ060197  
 R-HEM8B1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E5, complete sequence. //7.0e-22:455:65//U91321  
 R-HEM8B1002613//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //3.0e-72:302:85//AC005908  
 R-HEM8B1002614//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //3.8e-10:512:60//AC004801  
 R-HEM8B1002617//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 5 unordered pieces. //6.8e-24:486:63//AC005520  
 R-HEM8B1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence. //2.4e-41:326:83//AC004953  
 R-HEM8B1002635//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces. //2.6e-42:360:80//AC005910  
 R-HEM8B1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence. //9.1e-51:335:87//AF042090  
 R-HEM8B1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds. //0.0011:399:59//AF030694  
 R-HEM8B1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence. //4.1e-55:515:76//AF042090  
 R-HEM8B1002684//Human BAC clone RG066D11 from 7q22, complete sequence. //1.7e-18:504:62//AC002430  
 R-HEM8B1002686//Homo sapiens full length insert cDNA clone ZC65D06. //7.0e-85:413:99//AF086217  
 R-HEM8B1002692//Homo sapiens 12p13.3 BAC RPC111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //9.8e-69:505:82//AC006206  
 R-HEM8B1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.26:390:58//AC004153  
 R-HEM8B1002699//Human NFE genomic fragment. //8.0e-32:226:79//M98511  
 R-HEM8B1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence. //8.6e-43:351:80//B59764  
 R-HEM8B1002705//Plasmodium yoelii rhoptry protein, complete cds. //0.0064:454:59//L27838  
 R-HEM8B1002712//Human DNA sequence from clone 50S813 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence. //9.6e-09:187:67//Z98052  
 R-MAMMA1000009//Homo sapiens clone NH046SM07, WORKING DRAFT SEQUENCE, 7 unordered pieces. //4.1e-21:201:80//AC005037  
 R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence. //4.2e-48:306:82//AF015720  
 R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VTA protein pseudogene, EST, GSS, complete sequence. //1.4e-41:306:86//AL022163  
 R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence. //6.1e-36:281:83//AL031058  
 R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence. //1.3e-67:321:88//AC000090  
 R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence. //6.7e-86:559:86//AC004054  
 R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bca microl. //0.79:63:77//AF025889  
 R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in a intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence. //1.6e-53:397:83//AL021366  
 R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces. //2.0e-37:295:83//AC005057  
 R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces. //7.1e-45:296:88//AC005867  
 R-MAMMA1000085  
 R-MAMMA1000092//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE. //8.2e-34:539:69//AL034410  
 R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91.J.4, complete sequence. //3.4e-39:297:85//AC003976  
 R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5. //2.6e-07:162:67//U69641  
 R-MAMMA1000129//Homo sapiens clone DJ076820, WORKING DRAFT SEQUENCE, 6 unordered pieces. //5.1e-13:141:80//AC004882  
 R-MAMMA1000133  
 R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete

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e sequence. //9.7e-18:171:80//AC005328  
 R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENC  
 E, 7 unordered pieces. //1.2e-49:366:75//AC005000  
 R-MAMMA1000143//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from P  
 AC D9.2, WORKING DRAFT SEQUENCE. //3.9e-56:318:89//AJ009615  
 R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome  
 22q13.1-13.2. Contains the 5' part of the human ortholog of chick  
 on P52 and mouse H74, and a novel gene coding for a protein simila  
 r to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STS  
 s, GSSs, genomic marker D22S418 and putative CpG islands, complete  
 sequence. //2.1e-68:562:78//AL022476  
 R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENC  
 E, 5 unordered pieces. //5.3e-06:408:58//AC005089  
 R-MAMMA1000171//CIT-HSP-2335L20, TR CIT-HSP Homo sapiens genomic cl  
 one 2335L20, genomic survey sequence. //1.5e-42:173:89//AQ037381  
 R-MAMMA1000173  
 R-MAMMA1000175//H. sapiens CpG island DNA genomic MseI fragment, cl  
 one 186C5, reverse read cpg186C5.rtlb. //0.072:90:72//Z57594  
 R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems  
 Human BAC library) complete sequence. //1.5e-44:445:75//AC004552  
 R-MAMMA1000198//Homo sapiens clone c10200968, complete sequence. //1  
 .9e-23:135:85//AF038667  
 R-MAMMA1000221//HS\_3242\_B2\_H02\_T7 CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, geno  
 mic survey sequence. //0.031:167:67//AQ220385  
 R-MAMMA1000221//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 1071N3, WORKING DRAFT SEQUENCE. //4.5e-36:487:71//AL0317  
 28  
 R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromos  
 ome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB  
 Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase c  
 omponent A 1, Choroideremia protein, Tapetochooidal-Dystrophy (T  
 CD) protein). Contains ESTs and an STS, complete sequence. //6.2e-0  
 7:445:59//AL022401  
 R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complet  
 e sequence. //1.6e-25:390:69//AC005266  
 R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chro  
 mosome 22q12. Contains a pseudogene with similarity to part of mou  
 se NINEIN and the KIAA0609 gene for a protein similar to C. elegans  
 K09C8.4. Contains ESTs, GSSs and a gatt repeat polymorphism, com  
 plete sequence. //1.1e-37:327:80//AL008715  
 R-MAMMA1000257//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 1125A11, WORKING DRAFT SEQUENCE. //1.3e-22:281:74//AL034  
 549  
 R-MAMMA1000264//\*\*\* SEQUENCING IN PROGRESS \*\*\* EPM1/APECD region  
 of chromosome 21, clones A69E8, B127P21, B173L3, B23N8, C1242C9, C  
 579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in  
 this region has been discontinued by the Stanford Human Genome Cen  
 ter, WORKING DRAFT SEQUENCE, 50 unordered pieces. //1.7e-29:337:67/  
 AC003656  
 R-MAMMA1000266//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 681N20, WORKING DRAFT SEQUENCE. //7.7e-37:339:80//AL0316  
 70  
 R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, co  
 mplete sequence. //1.2e-40:283:86//AF001549  
 R-MAMMA1000277//CIT-HSP-516K6, TP CIT-HSP Homo sapiens genomic clon  
 e 516K6, genomic survey sequence. //3.0e-29:265:80//B49900  
 R-MAMMA1000278//Sequence 25 from patent US 5708157. //2.6e-39:282:8  
 2//180056  
 R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LA  
 NL), complete sequence. //1.6e-52:295:84//AC004494  
 R-MAMMA1000284//CITB1-E1-2522B20, TF CITB1-E1 Homo sapiens genomic  
 clone 2522B20, genomic survey sequence. //1.8e-11:288:61//AQ280722  
 R-MAMMA1000287  
 R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112\_i\_9, co  
 mplete sequence. //4.1e-16:169:77//AC005553  
 R-MAMMA1000307//RPC111-89L1, TV RPC111 Homo sapiens genomic clone  
 R-89L1, genomic survey sequence. //1.3e-86:429:97//AQ284795  
 R-MAMMA1000309//Homo sapiens hJAG2, del-E6 (JAG2) mRNA, alternative  
 ly spliced isoform of Jagged2, complete cds. //0.00020:384:60//AF02  
 9779  
 R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequ  
 ence. //0.0026:310:60//AF003518  
 R-MAMMA1000313//Human cosmid Xq28\_1A649, complete sequence. //1.5e-  
 26:317:67//U82694  
 R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENC  
 E, 5 unordered pieces. //3.1e-39:277:86//AC004947  
 R-MAMMA1000339//Homo sapiens clone H519.1 Alu-Ya5 sequence. //3.2e-  
 44:180:89//AF015147  
 R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of  
 73 of the complete sequence. //0.97:293:64//AE001388  
 R-MAMMA1000348//Homo sapiens BAC129, complete sequence. //4.4e-27:3  
 65:72//U85195  
 R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252  
 (D97)), complete sequence. //0.73:332:61//AC002493  
 R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, co  
 mplete sequence. //4.6e-80:279:89//AC005189  
 R-MAMMA1000361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 753D4, WORKING DRAFT SEQUENCE. //7.8e-18:346:63//AL03167  
 6  
 R-MAMMA1000372//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone Y214H10, WORKING DRAFT SEQUENCE. //5.3e-40:299:83//AL022  
 344  
 R-MAMMA1000385//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 310013, WORKING DRAFT SEQUENCE. //1.0e-28:225:84//AL0316  
 58  
 R-MAMMA1000388//CIT-HSP-2321D3, TR CIT-HSP Homo sapiens genomic clo  
 ne 2321D3, genomic survey sequence. //4.7e-60:298:99//AQ038102  
 R-MAMMA1000395  
 R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, co  
 mplete sequence. //1.4e-84:276:88//AC004692  
 R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, co  
 mplete sequence. //6.7e-35:360:76//AC002394  
 R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, c  
 omplete sequence. //3.1e-69:327:79//AC004662  
 R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chrom  
 osome Xq13.1-Xq21.2. Contains GSS (BAC end sequence), STS. //3.6e-4  
 1:180:87//AL009028  
 R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENC  
 E, 4 unordered pieces. //3.1e-59:478:77//AC005377  
 R-MAMMA1000421//Human coxIb gene, last exon and flanking sequenc  
 e. //5.3e-53:294:82//X58139  
 R-MAMMA1000422//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 8B22, WORKING DRAFT SEQUENCE. //1.0:252:59//AL031737  
 R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence. //2  
 .0e-50:491:76//AC004816  
 R-MAMMA1000424//Human DNA sequence from PAC 507115 on chromosome X  
 q26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gen  
 e, ESTs, STSs and a polymorphic CA repeat. //3.5e-40:340:80//Z98950  
 R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds. //0.0019:87:7  
 9//AF062484  
 R-MAMMA1000431//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENC  
 E, 5 unordered pieces. //2.0e-58:564:77//AC004821  
 R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete s  
 equence. //3.0e-43:328:83//AC002067  
 R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequenc  
 e. //0.95:209:65//U82672  
 R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1  
 clone: MXK3, complete sequence. //0.99:182:61//AB019236  
 R-MAMMA1000468  
 R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9  
 N34, genomic survey sequence. //1.0e-38:142:88//AC010148  
 R-MAMMA1000478//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 16915, WORKING DRAFT SEQUENCE. //1.3e-37:286:83//Z93015  
 R-MAMMA1000483//CIT-HSP-384B14, TR CIT-HSP Homo sapiens genomic clo  
 ne 384B14, genomic survey sequence. //4.3e-34:158:86//B54637  
 R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, compl  
 ete sequence. //4.2e-98:569:90//AC006130  
 R-MAMMA1000500//Human BRCA1, Rho7 and vat1 genes, complete cds, an  
 d ipf35 gene, partial cds. //1.2e-41:334:79//L78833  
 R-MAMMA1000501//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 153G14, WORKING DRAFT SEQUENCE. //1.4e-38:250:84//AL0311  
 18  
 R-MAMMA1000516//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 424J12, WORKING DRAFT SEQUENCE. //1.3e-43:318:83//Z82207  
 R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome  
 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequenc  
 e. //4.4e-13:202:73//AL031289  
 R-MAMMA1000559//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 16915, WORKING DRAFT SEQUENCE. //2.2e-30:245:83//Z93015  
 R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01\_183\_B\_7  
 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces. //3.6e-39:281:  
 80//U82205  
 R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, comple  
 te cds. //9.2e-19:216:76//U18419  
 R-MAMMA1000576  
 R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112\_H\_10, c  
 omplete sequence. //5.4e-53:297:85//AC005666  
 R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENC  
 E, 4 unordered pieces. //1.2e-35:450:71//AC006018

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【表497】

R-MAMMA1000594//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from c  
osmid 5L5. WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613  
R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clo  
ne 2341F4, genomic survey sequence.//0.83:110:70//AQ057131  
R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUEN  
CE, 4 unordered pieces.//2.6e-50:290:86//AC004956  
R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic cl  
one 2334J18, genomic survey sequence.//0.76:132:65//AQ038364  
R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, p  
artial sequence.//6.8e-06:431:59//U06970  
R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U0  
8573  
R-MAMMA1000623  
R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complet  
e sequence.//3.3e-07:325:63//AC005498  
R-MAMMA1000643//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 39817, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL02365  
6  
R-MAMMA1000664//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromo  
some 4, BAC clone C0326F06: HTGS phase 1, WORKING DRAFT SEQUENCE.  
16 unordered pieces.//1.4e-40:338:81//AC004555  
R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome  
20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) pr  
edicts a gene like the mouse transcription factor RBP-L. MATN4 (m  
atrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:8  
6//AL021578  
R-MAMMA1000670  
R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome  
6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//  
AL031785  
R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:  
247:63//AF054623  
R-MAMMA1000696//Human Chromosome X clone bWXD173, WORKING DRAFT SE  
QUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387  
R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENC  
E, 3 unordered pieces.//3.4e-09:244:66//AC005075  
R-MAMMA1000713//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUEN  
CE, 5 unordered pieces.//3.7e-51:439:74//AC005478  
R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, com  
plete sequence.//2.8e-29:288:75//AC004694  
R-MAMMA1000718//Human Xp22 BAC CT-285115 (from CalTech/Research Ge  
netics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and C  
osmid U3585 (from Lawrence Livermore), complete sequence.//3.0e-3  
7:231:91//AC002366  
R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complet  
e sequence.//1.4e-35:299:81//AC005781  
R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome  
Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogen  
e, YTA protein pseudogene, EST, GSS, complete sequence.//3.9e-59:4  
09:79//AL022163  
R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENC  
E, 2 unordered pieces.//9.4e-29:560:66//AC005077  
R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUEN  
CE, 10 unordered pieces.//2.4e-14:309:68//AC004832  
R-MAMMA1000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL00872  
2  
R-MAMMA1000734//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024  
507  
R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//  
6.6e-41:347:82//U03115  
R-MAMMA1000744//T2708-T7 TAMU Arabidopsis thaliana genomic clone T  
2708, genomic survey sequence.//0.095:367:60//B20150  
R-MAMMA1000746//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromo  
some 4, BAC clone C0135005: HTGS phase 1, WORKING DRAFT SEQUENCE.  
23 unordered pieces.//7.4e-95:569:87//AC004661  
R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter,  
complete sequence.//1.3e-48:295:84//AC003071  
R-MAMMA1000760//Human DNA sequence from clone 879B4 on chromosome  
22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//  
Z82178  
R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, comp  
lete sequence.//1.1e-32:292:80//U73169  
R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22\_M12, W  
ORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412  
R-MAMMA1000776//Human BAC clone G552A01 from 7q21-q22, complete s  
equence.//1.0e-63:429:79//AC002454  
R-MAMMA1000778//Human DNA sequence from 4PTL, Huntington's Diseas  
e Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704  
R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome  
6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:11  
9:74//AL031120  
R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBRI o  
n chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042  
R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complet  
e sequence.//1.1e-36:261:80//AC005339  
R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic c  
lone 2387J3, genomic survey sequence.//0.68:156:65//AQ240807  
R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.725\_0\_12, W  
ORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC0055  
17  
R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-97203, co  
mplete sequence.//1.3e-40:322:77//U91323  
R-MAMMA1000842//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985  
R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4  
unordered pieces.//0.85:394:60//AC004815  
R-MAMMA1000845//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE  
SS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744  
R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete s  
equence.//1.7e-10:115:83//AF030876  
R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete s  
equence.//5.0e-44:352:83//AC004263  
R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complet  
e sequence.//1.8e-10:149:74//AC004611  
R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated r  
egion, partial sequence, clone #16.//8.1e-05:205:66//AF009075  
R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12,  
U115B9 (Lawrence Livermore human cosmid library) complete sequenc  
e.//2.9e-49:421:80//AC002364  
R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-32  
8A3, complete sequence.//9.1e-41:302:83//AC002301  
R-MAMMA1000867//Human BRCA1, Rho7 and vatl genes, complete cds, an  
d ip135 gene, partial cds.//1.9e-17:500:61//L78833  
R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LAN  
L), complete sequence.//1.2e-17:211:74//AC004653  
R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Hu  
man BAC library) complete sequence.//4.7e-09:160:65//AC003658  
R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromo  
some Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.2e-34:3  
54:75//Z93023  
R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-57  
5C2, complete sequence.//1.4e-41:411:74//AC002425  
R-MAMMA1000883  
R-MAMMA1000897  
R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H  
66), complete sequence.//1.3e-73:304:91//AC004506  
R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F1415  
0, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110  
R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ41616, compl  
ete sequence.//1.5e-09:170:71//AC003024  
R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, co  
mplete sequence.//8.3e-13:323:67//AC005247  
R-MAMMA1000921//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL0343  
79  
R-MAMMA1000931//HS\_3227\_B1\_B03\_T7 CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=0, geno  
mic survey sequence.//1.4e-55:443:79//AQ191777  
R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENC  
E, 6 unordered pieces.//2.0e-43:340:84//AC005046  
R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete  
sequence.//1.8e-53:330:84//AC002347  
R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequenc  
e.//1.2e-39:391:74//AC004383  
R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete s  
equence.//4.6e-75:566:81//AC002477  
R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//  
0.013:285:59//AL034559  
R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENC  
E, 10 unordered pieces.//5.2e-45:288:90//AC005096  
R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUEN  
CE, 5 unordered pieces.//2.9e-108:561:96//AC006001  
R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete s  
equence.//3.9e-41:287:87//AC004263  
R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chrom  
osome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and t  
he alternatively spliced SAPK2 gene coding for CSalpha binding prot  
ein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and

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## 【表498】

two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152

R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 787, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219

R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-133BF24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101

R-MAMMA1001008//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929

R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913

R-MAMMA1001030//Homo sapiens full length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074

R-MAMMA1001035//RPC1-1-46G8Sp6 RPC1-1 Homo sapiens genomic clone RPC1-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089

R-MAMMA1001041

R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394

R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-237IK20, TF CIT-HSP Homo sapiens genomic clone 237IK20, genomic survey sequence.//7.2e-65:346:95//AQ111326

R-MAMMA1001073

R-MAMMA1001074//Homo sapiens BAC clone RH0400010 from Y, complete sequence.//8.6e-33:457:69//AC006040

R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:325:62//AC004605

R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203a13 (LBML H155), complete sequence.//1.6e-45:344:84//AC005609

R-MAMMA1001082//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403

R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//115499

R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372\_K\_20, complete sequence.//2.0e-51:267:82//AC005951

R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OC1-5) (GTR2-2), 5' UTR, ESTs, STS.//6.9e-22:178:85//Z99570

R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPK1169K15, complete sequence.//3.0e-19:141:81//AC003963

R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109

R-MAMMA1001133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847

R-MAMMA1001139//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345

R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684

R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235\_I\_10, complete sequence.//9.5e-49:512:74//AC005922

R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-88D1, complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289

R-MAMMA1001161//Human DNA sequence from clone 6B1J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286

R-MAMMA1001162//Human DNA from cosmid DNA MMD8 (f10080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651

R-MAMMA1001181//Human Chromosome X clone bWDX173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.7e-29:351:74//AC004387

R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125

R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662

R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:23:86//U29156

R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748

R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22\_M\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412

R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBML H44), complete sequence.//4.6e-08:442:61//AC004763

R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393

R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708

R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//0.041:277:61//B97762

R-MAMMA1001243

R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862

R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221

R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115

R-MAMMA1001259

R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6.3e-20:226:75//AB014561

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.//1.1e-47:352:85//Z95124

R-MAMMA1001271

R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232:93//X88457

R-MAMMA1001280//Homo sapiens full length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976

R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314

R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730

R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849\_M\_15, complete sequence.//1.5e-38:306:83//AC005703

R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 2 q11.2-qter, contains gene for GTPase-activating-protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838

R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (1-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398

R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614

R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430

R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 2 q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016

R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:89//AC002041

R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-23JAS, complete sequence.//0.99:182:64//AC004685

R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815

R-MAMMA1001388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 508115, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707

R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044

R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805

R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928

R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957

R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBML

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## 【表499】

- H88), complete sequence.//2.8e-09:377:63//AC005179  
 R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//29  
 9126  
 R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, c  
 omplete sequence.//3.4e-17:259:72//AC004047  
 R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from Tq11-q21, com  
 plate sequence.//2.9e-17:231:71//AC004491  
 R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome  
 Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pse  
 udogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:  
 73//AL024493  
 R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific  
 cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequen  
 ce.//3.0e-23:141:96//B04295  
 R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.  
 4e-09:309:64//L31783  
 R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108\_L11,  
 complete sequence.//5.1e-30:286:79//AC005206  
 R-MAMMA1001501  
 R-MAMMA1001502//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL03171  
 4  
 R-MAMMA1001510  
 R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBML H  
 194), complete sequence.//1.5e-09:136:75//AC005352  
 R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:30  
 0:84//AC002418  
 R-MAMMA1001551//Human DNA sequence from PAC 42616 on chromosome 1p  
 34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protei  
 n phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997  
 R-MAMMA1001575  
 R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:5  
 30:78//M61764  
 R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alph  
 a-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F  
 TP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027  
 R-MAMMA1001600//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Ca  
 ncer Institute Human PAC library) complete sequence.//2.1e-18:390:  
 66//AC004216  
 R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosom  
 e 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase  
 (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with pr  
 obable rabGAP domains and Src homology domain 3). Contains ESTs, S  
 TSs, GSSs and a putative CpG island, complete sequence.//1.0:227:6  
 2//AL022238  
 R-MAMMA1001606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL0319  
 85  
 R-MAMMA1001620//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031  
 650  
 R-MAMMA1001627//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090  
 R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399  
 R-MAMMA1001633//Homo sapiens chromosome 10 clone C1987SK-1057L21  
 map 10q25, complete sequence.//2.2e-21:241:70//AC005386  
 R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromo  
 some Xp11.3. Contains EST, STS and GSS, complete sequence.//1.1e-3  
 2:346:74//Z84466  
 R-MAMMA1001649  
 R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4  
 e-68:267:89//AC004811  
 R-MAMMA1001670//Human DNA sequence from PAC 75M13 on chromosome Xq  
 21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands.//1.7e-4  
 9:322:88//Z82216  
 R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complet  
 e sequence.//2.4e-114:575:96//AC005614  
 R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clo  
 ne 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393  
 R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKIN  
 G DRAFT SEQUENCE, 9 unordered pieces.//5.7e-47:533:72//AC004166  
 R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, comple  
 te sequence.//6.6e-12:194:72//AC005261  
 R-MAMMA1001692//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone Y738F9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL0223  
 45  
 R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21,  
 complete sequence.//3.1e-31:436:70//AF110324  
 R-MAMMA1001715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330  
 R-MAMMA1001730  
 R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta  
 tubulin (clone B9T), partial.//2.7e-13:382:63//X60786  
 R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segm  
 ent 21/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050  
 R-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//  
 4.0e-108:566:95//AC006017  
 R-MAMMA1001744  
 R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete  
 sequence.//3.5e-113:564:97//AF070718  
 R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complet  
 e sequence.//3.6e-30:312:75//AC005625  
 R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha  
 isoform (SFD) mRNA, complete cds.//4.7e-34:320:77//AF041338  
 R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4\_G\_17, com  
 plate sequence.//4.7e-10:244:67//AC003688  
 R-MAMMA1001760//RPC111-38L16.TV RPC1-11 Homo sapiens genomic clone  
 RPC1-11-38L16, genomic survey sequence.//1.3e-10:236:64//AQ029432  
 R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42  
 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//  
 0.74:361:60//AC005140  
 R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPC.147\_L13, c  
 omplete sequence.//1.6e-42:416:76//AC005332  
 R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073\_F\_15,  
 complete sequence.//1.4e-13:129:83//AC004686  
 R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69/  
 X85991  
 R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING  
 DRAFT SEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360  
 R-MAMMA1001785//Human chromosome 16p13.11 BAC clone C1987SK-98H8  
 complete sequence.//3.0e-49:282:86//U91319  
 R-MAMMA1001788  
 R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUEN  
 CE, 6 unordered pieces.//9.8e-43:530:71//AC004913  
 R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone C1987SK-A-31  
 9E8, complete sequence.//1.8e-43:324:79//AC004020  
 R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of  
 73 of the complete sequence.//0.65:183:63//AE001432  
 R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENC  
 E, 3 unordered pieces.//1.1e-10:417:62//AC005018  
 R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSMB-32AM7 (Genome System  
 s Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859  
 R-MAMMA1001818  
 R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered  
 pieces.//2.2e-45:340:82//AC004086  
 R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUEN  
 CE, 8 unordered pieces.//1.9e-53:291:85//AC004966  
 R-MAMMA1001836//HS\_3164\_B1\_A02\_MR CIT Approved Human Genomic Sperm  
 Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=B, geno  
 mic survey sequence.//6.5e-08:79:89//AQ185484  
 R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F1  
 8547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-  
 55:209:85//AC003682  
 R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, comple  
 te sequence.//1.6e-16:125:90//AC006144  
 R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SE  
 QUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099  
 R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone C1987SK-A-57  
 5C2, complete sequence.//1.7e-38:308:82//AC002425  
 R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X in  
 activation transcript (XIST) gene, complete sequence.//6.5e-50:283:  
 86//U80460  
 R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORK  
 ING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143  
 R-MAMMA1001868//Plasmodium falciparum chromosome 2, section 54 of  
 73 of the complete sequence.//1.4e-11:495:63//AE001417  
 R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence; WOR  
 KING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117  
 R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6  
 p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1  
 (WAF1, CDKN1A, CDKN1, MDA-6, SD11, PIC1, CAP20) genes. Contains p  
 robable GTPase and receptor genes and ESTs, STSs and CpG islands.//  
 6.9e-44:391:78//Z85996  
 R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosom  
 e 22q12-qter contains ESTs, tRNA.//1.3e-15:181:76//Z82097  
 R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone C1987-SKA-67  
 0B5 -complete genomic sequence, complete sequence.//1.7e-43:283:8  
 6//AC002303  
 R-MAMMA1001907//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL03172

【0800】

【表500】

<p>R-MAMMA1001908//Saccharomyces cerevisiae chromosome IV cosmid 948 1.//2.9e-14:505:60//U28373</p> <p>R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008</p> <p>R-MAMMA1001956//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL03438 0</p> <p>R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149</p> <p>R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128</p> <p>R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071</p> <p>R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525:72//AC004581</p> <p>R-MAMMA1002009//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL02387 9</p> <p>R-MAMMA1002011</p> <p>R-MAMMA1002032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL0312 84</p> <p>R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-17:170:81//AC003954</p> <p>R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865</p> <p>R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:80//U91318</p> <p>R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:75//U91318</p> <p>R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence.//6.6e-48:367:82//AC005962</p> <p>R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.25:139:69//AC005052</p> <p>R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-45:406:78//AC004676</p> <p>R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//2.3e-22:357:64//AC005291</p> <p>R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//AC004263</p> <p>R-MAMMA1002084//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL0316 02</p> <p>R-MAMMA1002093//CIT-HSP-206D9.7F CIT-HSP Homo sapiens genomic clone 206D9.9, genomic survey sequence.//9.7e-17:129:88//B69983</p> <p>R-MAMMA1002108</p> <p>R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete sequence.//0.94:168:64//Z73495</p> <p>R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.8e-40:313:83//AC005670</p> <p>R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:83//AC004953</p> <p>R-MAMMA1002140//Human DNA sequence from PAC 465C10 on chromosome X contains Menkes Disease (ATPTA) putative Cut+transporting P-type ATPase exons 2 to 21, PCAM-B, ESTs.//1.1e-32:477:73//Z94801</p> <p>R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//6.6e-06:130:73//AF027357</p> <p>R-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.0e-19:242:73//AL03144 7</p> <p>R-MAMMA1002153//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0281M17: HTGS phase 1, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.1e-51:291:75//AC006052</p> <p>R-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 608E9, WORKING DRAFT SEQUENCE.//1.2e-53:461:79//AL02234 3</p> <p>R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:82//AC004997</p> <p>R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:81//AL034418</p> <p>R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylyl)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL03158</p>	<p>8</p> <p>R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871</p> <p>R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890</p> <p>R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.2e-23:269:74//AC005821</p> <p>R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:243:68//AC005158</p> <p>R-MAMMA1002219//Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.3e-45:295:8 8//AC004802</p> <p>R-MAMMA1002230//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL0343 79</p> <p>R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253</p> <p>R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//2.8e-119:582:98//AC005666</p> <p>R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600</p> <p>R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-33:571:67//AC006120</p> <p>R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749</p> <p>R-MAMMA1002269//345117.TV CIT978SKA1 Homo sapiens genomic clone A-345117, genomic survey sequence.//4.7e-05:153:69//B15590</p> <p>R-MAMMA1002282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987</p> <p>R-MAMMA1002292//Hordeum vulgare lipoxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358</p> <p>R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568</p> <p>R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPK.1110_E_20, complete sequence.//1.2e-35:281:82//AC004231</p> <p>R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375</p> <p>R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//1.8e-17:296:70//AC005074</p> <p>R-MAMMA1002299//HS_3116_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=N, genomic survey sequence.//4.1e-60:354:91//AQ140526</p> <p>R-MAMMA1002308</p> <p>R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979</p> <p>R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC00621 0</p> <p>R-MAMMA1002312//H. sapiens gene encoding La autoantigen.//1.3e-23:3 82:67//X97869</p> <p>R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:3 23:87//AL031054</p> <p>R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756</p> <p>R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042</p> <p>R-MAMMA1002329//M. musculus mRNA for semaphorin B.//2.0e-12:210:73//X85991</p> <p>R-MAMMA1002332//Homo sapiens PAC clone DJ1139101 from Xq23, complete sequence.//3.4e-46:393:71//AC004973</p> <p>R-MAMMA1002333//HS_3245_A1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759</p> <p>R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549</p> <p>R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPC13-305I20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088</p> <p>R-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022 100</p> <p>R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228</p> <p>R-MAMMA1002353//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:3 02:80//AC002996</p> <p>R-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241</p>
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【表501】

R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//8.3e-28:187:91//AC004662

R-MAMMA1002359//Human DNA sequence from cosmid L11805, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//Z68869

R-MAMMA1002360//HS\_2163\_B2\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213

R-MAMMA1002361//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520

R-MAMMA1002362//H.sapiens PEX gene.//1.8e-40:243:86//Y10196

R-MAMMA1002380//RPC111-73J4.TJ RPC111 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168

R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801

R-MAMMA1002385

R-MAMMA1002392//Human BAC clone RG066D11 from Tq22, complete sequence.//2.0e-37:355:77//AC002430

R-MAMMA1002411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496:65//AL031668

R-MAMMA1002413//Homo sapiens 12q24.2 PAC RPC11-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.3e-15:153:77//AC005146

R-MAMMA1002417//Human DNA sequence from PAC 42616 on chromosome 1p34.1-p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1. ESTs, and a CA repeat.//1.8e-23:508:62//AL020997

R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288:84//U91321

R-MAMMA1002428//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185M5, WORKING DRAFT SEQUENCE.//6.0e-05:130:75//AL034423

R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GS S.//4.8e-18:205:78//AL022396

R-MAMMA1002446//CIT-HSP-202114.TR CIT-HSP Homo sapiens genomic clone 202114, genomic survey sequence.//4.6e-41:387:72//B65379

R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491:82//AC005512

R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188:85//AC003982

R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280:61//U10556

R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310:74//Z83822

R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE. 2 unordered pieces.//1.2e-98:533:93//AC005077

R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560:97//AF055460

R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//2.1e-46:329:84//Z69375

R-MAMMA1002498//Rat mRNA.//0.0068:223:64//M59859

R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139

R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.2e-101:529:95//AF065214

R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//AF041427

R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056

R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence.//9.6e-13:237:67//AC005878

R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence.//9.7e-14:216:73//AQ261427

R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey sequence.//4.6e-25:142:99//AQ279542

R-MAMMA1002573//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 811H13, WORKING DRAFT SEQUENCE.//1.1e-30:250:82//AL023805

R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580

R-MAMMA1002590//H.sapiens CpG island DNA genomic MseI fragment, clone 8d5, forward read cpg8d5.flg.//1.0:114:64//Z63758

R-MAMMA1002597//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1103G7, WORKING DRAFT SEQUENCE.//9.0e-96:459:98//AL034548

R-MAMMA1002598//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//0.79:362:58//AL031847

R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPK.214\_C\_8, complete sequence.//1.3e-46:333:80//AC005803

R-MAMMA1002612//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 269M15, WORKING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395

R-MAMMA1002617//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING DRAFT SEQUENCE.//1.7e-20:308:71//AL031594

R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067

R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPC1P704E14135Q2.//9.0e-113:551:98//AJ010598

R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324:83//AC004050

R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171\_1\_10, complete sequence.//2.7e-80:344:84//AC004687

R-MAMMA1002625//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1056L3, WORKING DRAFT SEQUENCE.//2.6e-34:391:72//AL031727

R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmid R32543, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:345:81//AC003006

R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE. 8 unordered pieces.//1.1e-52:285:92//AC004895

R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666

R-MAMMA1002646//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING DRAFT SEQUENCE.//2.5e-24:285:68//AL023585

R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:237:61//X03424

R-MAMMA1002655//Homo sapiens minisatellite ceb1 repeat region.//0.18:152:65//AF048727

R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870

R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//7.4e-55:298:92//Z92844

R-MAMMA1002671//RPC111-45M10.TK RPC111 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//3.1e-38:410:76//AL022162

R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987

R-MAMMA1002685//HS\_2052\_A1\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=3 Row=0, genomic survey sequence.//1.2e-23:255:75//AQ231087

R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.1e-38:299:83//AC004673

R-MAMMA1002699//Mus musculus intersectin-EH binding protein Ibp1 mRNA, partial cds.//3.3e-05:61:93//AF057285

R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399

R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPC15-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.26:365:62//AC005293

R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995

R-MAMMA1002721//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826

R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710

R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037

R-MAMMA1002744//Human chromosome 8 BAC-clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//U96629

R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPC.136\_H\_19, complete sequence.//2.2e-108:544:97//AC005856

R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055

R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE. 4 unordered pieces.//1.7e-34:305:79//AC005020

R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626

R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete

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【表503】

complete sequence.//3.4e-23:335:72//AC005856  
 R-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//D12646  
 R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154  
 R-NT2RM4000191  
 R-NT2RM4000197//HS\_3241\_A2\_H05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=10 Row=0, genomic survey sequence.//2.8e-86:430:97//AQ206812  
 R-NT2RM4000199//Mus musculus Yp BAC G5MB-368G7 (Genome Systems Mouse BAC Library) complete sequence.//0.0047:193:63//AC006056  
 R-NT2RM4000200  
 R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//2.1e-40:334:76//AC004035  
 R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255  
 R-NT2RM4000215  
 R-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//2.1e-55:303:86//AC005383  
 R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07:198:67//AF003735  
 R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-8-393i15 (BC301323), complete sequence.//1.7e-49:322:88//AC006116  
 R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 7218 in DCCR Region, complete sequence.//0.97:184:66//AC000085  
 R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055  
 R-NT2RM4000290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 39417, WORKING DRAFT SEQUENCE.//1.4e-05:229:65//AL023585  
 R-NT2RM4000324  
 R-NT2RM4000327//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 75N14, WORKING DRAFT SEQUENCE.//3.3e-42:443:75//Z97199  
 R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.4e-64:433:84//AC004826  
 R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630  
 R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//J05066  
 R-NT2RM4000356  
 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542  
 R-NT2RM4000368  
 1.6e-48:348:85//AG006257  
 R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148  
 R-NT2RM4000395//RPC111-8N9, TP RPC111 Homo sapiens genomic clone RPC111-8N9, genomic survey sequence.//1.4e-25:207:75//B71494  
 R-NT2RM4000414//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//7.1e-17:492:64//AL031985  
 R-NT2RM4000421//RPC111-66B1, TK RPC111 Homo sapiens genomic clone R-66B1, genomic survey sequence.//1.8e-40:311:82//AQ241167  
 R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone G5MB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867  
 R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stras) mRNA, complete cds.//1.6e-17:133:78//AF062476  
 R-NT2RM4000457  
 R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952  
 R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461  
 R-NT2RM4000496  
 R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829  
 R-NT2RM4000514//CIT-HSP-2169K4, TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey sequence.//1.5e-20:150:89//B95717  
 R-NT2RM4000515//HS-1024-B2-G01-MR, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556  
 R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790  
 R-NT2RM4000531  
 R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:66//AE001391  
 R-NT2RM4000534//paramecium species 4.5ler mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60//X00909  
 R-NT2RM4000585//HS\_3252\_A2\_G08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890  
 R-NT2RM4000590//CIT-HSP-539024, TV CIT-HSP Homo sapiens genomic clone 539024, genomic survey sequence.//1.7e-38:226:93//B50657  
 R-NT2RM4000595//Human Chromosome X clone bWXD342, complete sequence.//1.0:239:61//AC004072  
 R-NT2RM4000603//RPC111-49P13, TK RPC111 Homo sapiens genomic clone R-49P13, genomic survey sequence.//0.77:139:64//AQ051950  
 R-NT2RM4000611  
 R-NT2RM4000616//HS\_3107\_A2\_B03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034  
 R-NT2RM4000674  
 R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823  
 R-NT2RM4000698  
 R-NT2RM4000700  
 R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039  
 R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence.//0.050:387:58//AL034560  
 R-NT2RM4000733//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//1.0e-107:566:95//AL034379  
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//1.1e-103:536:95//AB018303  
 R-NT2RM4000741//CIT-HSP-2294N4, TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey sequence.//5.2e-41:244:93//AQ006361  
 R-NT2RM4000751//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 537K23, WORKING DRAFT SEQUENCE.//2.7e-28:416:67//AL034405  
 R-NT2RM4000764//Human HepG2 3' region Mbol cDNA, clone hmd3g01m3.//2.1e-33:199:96//D17217  
 R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC Library) complete sequence.//0.00060:241:62//AC002980  
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//2.9e-104:546:94//AB007920  
 R-NT2RM4000787//Homo sapiens, clone hRPK\_3\_A\_1, complete sequence.//5.3e-32:321:77//AC006198  
 R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//1.9e-111:552:97//AC005306  
 R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence.//0.74:364:57//U58675  
 R-NT2RM4000796//Homo sapiens full length insert cDNA clone ZD62D10.//2.7e-105:510:98//AF083348  
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end.//7.7e-27:158:96//M21868  
 R-NT2RM4000813  
 R-NT2RM4000820//, complete sequence.//2.0e-104:432:97//AC005406  
 R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX122, complete sequence.//2.0e-07:166:68//AB012248  
 R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds.//0.073:70:84//M22013  
 R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:237:62//AC004709  
 R-NT2RM4000855  
 R-NT2RM4000887//HS\_3189\_B2\_B08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=16 Row=D, genomic survey sequence.//2.1e-06:114:73//AQ300597  
 R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.//3.8e-46:207:91//AF077058  
 R-NT2RM4000950//Human BAC clone RG341D10 from Tpl5-p21, complete sequence.//1.0:336:60//AC002530  
 R-NT2RM4000971//Human Xq28 cosmid U126G1, U142F2, U6986, U145C10, U169AS, U84H1, U24D12, U80A7, U153E6, L3548S, and RT-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//7.1e-09:259:64//AF011889  
 R-NT2RM4000979  
 R-NT2RM4000996//HS\_3164\_A1\_E02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=I, genomic survey sequence.//2.0e-82:443:94//AQ141622  
 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.2e-112:545:97//AB018272  
 R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//7.9e-113:556:97//AB014539  
 R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes.//1.2e-10:12:0:82//AJ224639  
 R-NT2RM4001047//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 163G9, WORKING DRAFT SEQUENCE.//1.0:158:67//AL008733  
 R-NT2RM4001054//CIT-HSP-2292N8, TR CIT-HSP Homo sapiens genomic clone

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【表504】

ne 2292NB, genomic survey sequence.//5.8e-19:118:97//AQ004096  
 R-NT2RM4001084//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//1.0e-05:271:64//M10296  
 R-NT2RM4001092//CITBI-EI-2524J20.TR CITBI-EI Homo sapiens genomic clone 2524J20, genomic survey sequence.//1.0:186:63//AQ277294  
 R-NT2RM4001116  
 R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from Tpl4-p15, complete sequence.//3.6e-79:468:90//AC004593  
 R-NT2RM4001151//HS\_2270\_B1\_E05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey sequence.//5.5e-62:312:98//AQ163739  
 R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//1.4e-107:536:97//AC005841  
 R-NT2RM4001160//HS\_3015\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=19 Row=P, genomic survey sequence.//7.1e-35:201:95//AQ118712  
 R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201  
 R-NT2RM4001191//HS\_3002\_A1\_F05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791  
 R-NT2RM4001200//Homo sapiens full length insert cDNA clone YL35HD3.//7.5e-69:335:99//AF085857  
 R-NT2RM4001203  
 R-NT2RM4001204  
 R-NT2RM4001217  
 R-NT2RM4001256  
 R-NT2RM4001258  
 R-NT2RM4001309  
 R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPC11-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.00055:183:63//AC004551  
 R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117\_K\_16, complete sequence.//4.5e-21:212:79//AC004757  
 R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence.//3.8e-30:86:89//AQ021084  
 R-NT2RM4001340  
 0.0027:493:60//AC005133  
 R-NT2RM4001344  
 R-NT2RM4001347//CITBI-EI-2506120.TR CITBI-EI Homo sapiens genomic clone 2506120, genomic survey sequence.//6.5e-16:101:99//AQ262797  
 R-NT2RM4001371//CITBI-EI-2503G21.TR CITBI-EI Homo sapiens genomic clone 2503G21, genomic survey sequence.//0.063:140:65//AQ265776  
 R-NT2RM4001382//HS\_3044\_A1\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668  
 R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000  
 R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920  
 R-NT2RM4001411//Rattus norvegicus FcεR1 gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds.//1.7e-55:235:83//U57391  
 R-NT2RM4001412  
 R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence.//1.7e-80:489:89//U69730  
 R-NT2RM4001437//RPC111-56D2.TJ RPC111 Homo sapiens genomic clone R-56D2, genomic survey sequence.//3.8e-43:250:93//AQ081969  
 R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//0.0034:224:63//AC005926  
 R-NT2RM4001454//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//2.4e-33:360:68//AC004075  
 R-NT2RM4001455//HS\_3229\_B1\_E04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence.//1.0:183:61//AQ191289  
 R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.2e-51:451:79//AC005282  
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0585 protein, complete cds.//2.2e-102:547:93//AB014585  
 R-NT2RM4001519//HS\_2208\_A1\_F07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836  
 R-NT2RM4001522//H. sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:246:70//Z29336  
 R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970  
 R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//3.9e-26:329:72//A005910  
 R-NT2RM4001566//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811  
 R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSP01 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//2.0e-35:213:89//AL031663  
 R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317  
 R-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//4.8e-86:565:85//X69942  
 R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120  
 R-NT2RM4001597//HS\_2059\_A1\_G11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136  
 R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334  
 R-NT2RM4001611//Homo sapiens ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936  
 R-NT2RM4001629//RPC111-54G14.TJ RPC111 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173  
 R-NT2RM4001650  
 R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575  
 R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone C1787SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685  
 R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775  
 R-NT2RM4001710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447  
 R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153  
 R-NT2RM4001715//Human DNA sequence from clone 93IK24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430  
 R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF 92 locus.//0.017:93:73//M80527  
 R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123  
 R-NT2RM4001746//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709  
 R-NT2RM4001754//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483  
 R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK 1.//1.9e-18:202:78//Z83868  
 R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.0e-22:236:80//AB018270  
 R-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//4.4e-106:551:95//AC006017  
 R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence.//0.76:279:60//B27099  
 R-NT2RM4001813  
 R-NT2RM4001823  
 R-NT2RM4001828//HS\_3073\_A2\_E01\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey sequence.//1.6e-46:255:96//AQ121030  
 R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:69//U78024  
 R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//AF019184  
 R-NT2RM4001842//Homo sapiens clone RC228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-07:332:61//AC005077  
 R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4.8e-30:235:85//AF046633

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【表505】

R-NT2RM4001858//HS\_3244\_B1\_F10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence.//3.0e-40:263:89//AQ252798  
R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CA LC.//5.0e-119:592:97//Y17711  
R-NT2RM4001876//Megastigmus wachlii dinucleotide microsatellite, clone MWA47CT.//0.13:134:64//AJ001069  
R-NT2RM4001880  
R-NT2RM4001905//HS\_2016\_B1\_H11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877  
R-NT2RM4001922//HS\_2228\_B2\_B07\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498  
R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34\_M\_24, complete sequence.//0.26:325:63//AC004562  
R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081\_P\_3, complete sequence.//2.9e-85:421:98//AC005207  
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162  
R-NT2RM4001953//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 47384, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826  
R-NT2RM4001965//CIT-HSP-385N14, TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey sequence.//5.7e-69:532:81//B55044  
R-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330  
R-NT2RM4001979//Homo sapiens full length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241  
R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161  
R-NT2RM4001987  
R-NT2RM4002013  
R-NT2RM4002018  
R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBML H195), complete sequence.//3.6e-42:277:89//AC005353  
R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from Tq11.23-7q21, complete sequence.//0.83:476:57//AC006204  
R-NT2RM4002054  
R-NT2RM4002062//Human mitochondrial epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659  
R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267  
R-NT2RM4002066//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:54:68//U80742  
R-NT2RM4002067//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832  
R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758  
R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.031:403:57//AC005504  
R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383  
R-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646  
R-NT2RM4002128//Human HepG2 partial cDNA, clone hnd2e12m5.//2.0e-26:186:90//D17000  
R-NT2RM4002140  
R-NT2RM4002145//Homo sapiens full length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247  
R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562  
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535  
R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74\_E\_22, complete sequence.//8.0e-43:302:85//AC005696  
R-NT2RM4002189  
R-NT2RM4002194//Human Cosmid g5129g129 from Tq31.3, complete sequence.//0.29:382:60//AC003960  
R-NT2RM4002205//Spirioplasmavirus (SpV1-RBA2 B) complete genome.//3.5e-05:432:56//X51344  
R-NT2RM4002213  
R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//AC004448  
R-NT2RM4002251  
R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from Tq13-p14, complete sequence.//2.3e-58:299:85//AC004837  
R-NT2RM4002266//H.sapiens CpG island DNA genomic MseI fragment, clone 179f11, forward read cpg179f11.f1la.//0.72:97:69//Z57487  
R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-49:405:84//AC005069  
R-NT2RM4002281//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531  
R-NT2RM4002287  
R-NT2RM4002294//Homo Sapiens Chromosome X clone bWDX171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.98:208:65//AC004676  
R-NT2RM4002301//HS\_2028\_A1\_E10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2028 Col=19 Row=I, genomic survey sequence.//0.94:321:57//AQ233262  
R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPI3G20 and other exonuclease). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822  
R-NT2RM4002339//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569:68//AB002317  
R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709  
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549  
R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417  
R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316  
R-NT2RM4002390  
R-NT2RM4002409//RPC111-45M10.TK RPC111 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411  
R-NT2RM4002438  
R-NT2RM4002446//Human DNA sequence from clone 350A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008  
R-NT2RM4002452  
R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LA NL), complete sequence.//0.99:171:64//AC004034  
R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5C1, ATP5C2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545  
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255  
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591  
R-NT2RM4002493//CIT-HSP-2296C24, TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882  
R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//U84711  
R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//3.9e-11:334:63//AC002368  
R-NT2RM4002527  
R-NT2RM4002532//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985  
R-NT2RM4002534  
R-NT2RM4002567//Homo sapiens chromosome 7 clone UWCC:g1564a040 from Tq14-15, complete sequence.//2.2e-26:181:76//AC005271  
R-NT2RM4002571  
R-NT2RM4002593//CIT-HSP-2303L15, TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579  
R-NT2RM4002623//Homo sapiens clone UWCC:g1564a209 from Tq14-15, complete sequence.//0.0014:670:55//AC005862  
R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422  
R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6 q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205  
R-NT2RP2000008//RPC111-41G16, TP RPC111 Homo sapiens genomic clone RPC111-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090  
R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098  
R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290  
R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749  
R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pigment cell-specific transcription).//0.88:210:60//D26163  
R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758

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【表506】

R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds.//6.0e-10:137:79//D42148  
 R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H 169), complete sequence.//3.1e-76:381:98//AC005754  
 R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 7 3 of the complete sequence.//2.3e-06:380:60//AE001372  
 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97//AF050079  
 R-NT2RP2000079//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549  
 R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338  
 R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21:226:76//AC005048  
 R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873  
 R-NT2RP2000098//Human BAC clone RG33F24 from Tq11.2-q21, complete sequence.//0.34:132:65//AC004015  
 R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973  
 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-74:386:95//AB018356  
 R-NT2RP2000120//CITBI-E1-2503MB, TR CITBI-E1 Homo sapiens genomic clone 2503MB, genomic survey sequence.//5.1e-05:87:77//AQ263909  
 R-NT2RP2000126  
 R-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827  
 R-NT2RP2000147  
 R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626  
 R-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924  
 R-NT2RP2000161//CIT-HSP-2045P7, TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728  
 R-NT2RP2000175  
 R-NT2RP2000183  
 R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60\_A\_24, complete sequence.//4.3e-39:306:83//AC005325  
 R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155  
 R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-15 ZES, complete sequence.//7.3e-55:306:94//AC004382  
 R-NT2RP2000232  
 R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAC) mRNA, complete cds.//7.6e-13:144:75//U88401  
 R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4Q25, complete sequence.//9.6e-63:410:86//AC004066  
 R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726  
 R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from Tq11.23-q21, complete sequence.//2.5e-11:163:72//AC004894  
 R-NT2RP2000258//Arabidopsis thaliana chromosome 11 BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077  
 R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA A-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179  
 R-NT2RP2000274//CIT-HSP-237901, TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409  
 R-NT2RP2000288  
 R-NT2RP2000289  
 R-NT2RP2000297//Homo sapiens full length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165  
 R-NT2RP2000298  
 R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310  
 R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-113:580:96//AL022398  
 R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.4e-47:367:77//AC006039  
 R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunit 1 (1-4, 4L, 5-6): cytochrome oxidase subunits (1-3): adenosine triphosphatase subunits (6,8): cytochrome b: transfer RNA: ribosomal RNA (large and small subunits).//4.9e-08:494:58//L04272  
 R-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds.//3.4e-46:262:94//U83981  
 R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.0e-07:334:61//AC002993  
 R-NT2RP2000414//Mouse DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone BAC394, WORKING DRAFT SEQUENCE.//7.0e-08:98:83//AJ004828  
 R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640\_1\_15, complete sequence.//0.99:150:62//AC005324  
 R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//4.6e-19:142:90//AF102265  
 R-NT2RP2000438//RPC111-62113, TK RPC111 Homo sapiens genomic clone 62113, genomic survey sequence.//3.1e-06:103:79//AQ199572  
 R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from Tp14-p15, complete sequence.//2.0e-22:276:73//AC004691  
 R-NT2RP2000459//CIT-HSP-2013N9, TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence.//5.5e-27:205:87//B53940  
 R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.//6.0e-12:119:84//AC001234  
 R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1.//0.48:201:64//D10170  
 R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.//3.6e-07:472:59//AF033929  
 R-NT2RP2000516  
 R-NT2RP2000523//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//2.3e-61:317:97//AL022318  
 R-NT2RP2000603//Homo sapiens mRNA for NCM3 import factor, complete cds.//6.6e-29:167:97//AB005543  
 R-NT2RP2000617  
 R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//2.5e-64:335:96//AB014514  
 R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATPSG2, ATPSG3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.8e-28:383:70//Z92545  
 R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-2B P pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.0093:110:70//AL021997  
 R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds.//0.73:301:60//U89796  
 R-NT2RP2000668  
 R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE.//2.8e-11:256:66//AP000015  
 R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.036:176:69//AC002346  
 R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from Tp15, complete sequence.//2.7e-110:555:96//AC004540  
 R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs and GSSs, and a ca repeat polymorphism, complete sequence.//2.6e-18:319:68//AL023775  
 R-NT2RP2000758//CIT-HSP-507A14, TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence.//1.0:189:60//B50590  
 R-NT2RP2000764  
 R-NT2RP2000809//Human BAC clone RG356F09 from Tp21, complete sequence.//1.7e-24:215:81//AC004002  
 R-NT2RP2000812//CIT-HSP-2281C3, TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//9.5e-32:176:97//B99575  
 R-NT2RP2000814//paramecium species 5.87 mt dna dimer: replication init. region.//0.0077:418:57//K00916  
 R-NT2RP2000816//F. rubripes GSS sequence, clone 011H02a6, genomic survey sequence.//0.61:52:73//AL011013  
 R-NT2RP2000819  
 R-NT2RP2000841//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 43408, WORKING DRAFT SEQUENCE.//0.00012:181:70//AL033504  
 R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from renin-expressing kidney tumor cell line, partial sequence.//3.7e-27:388:72//U13370  
 R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849\_1\_15, c

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## 【表507】

complete sequence.//0.0022:200:68//AC005703  
R-NT2RP2000863  
R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412  
R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//0.0028:221:62//AB020875  
R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266  
R-NT2RP2000938//Homo sapiens full length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336  
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298  
R-NT2RP2000965  
R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393  
R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597\_M12, complete sequence.//5.4e-93:484:95//AC005277  
R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:318:62//AE001372  
R-NT2RP2001036//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 410B1, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732  
R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42.0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140  
R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029  
R-NT2RP2001070//CITBI-EI-2503F4.TF CITBI-EI Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973  
R-NT2RP2001094//Mycoplasma mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mtld) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140  
R-NT2RP2001119  
R-NT2RP2001127//Homo sapiens HRHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348  
R-NT2RP2001137//Homo sapiens DNA sequence from clone S11B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-I48), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. C contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394  
R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//U01838  
R-NT2RP2001168  
R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB007949  
R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//BB9680  
R-NT2RP2001196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134  
R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//8.5e-15:278:68//AL022153  
R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SMRNP-associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995  
R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey sequence.//8.0e-108:547:96//AQ081110  
R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.//0.0052:350:58//M76713  
R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353  
R-NT2RP2001277//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y59A8, WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870  
R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709  
R-NT2RP2001295//Homo sapiens BAC clone NH0491803 from T2p1-p15, complete sequence.//0.59:218:62//AC005041  
R-NT2RP2001312//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 349A12, WORKING DRAFT SEQUENCE.//0.12:117:64//AL033520  
R-NT2RP2001327//Caenorhabditis elegans cosmid R0403, complete sequence.//0.31:119:66//Z70212  
R-NT2RP2001328//HS\_2213\_A1\_007\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=13 Row=G, genomic survey sequence.//1.7e-22:200:83//AQ136874  
R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:509:56//AL034560  
R-NT2RP2001378//H. sapiens DNA sequence.//0.94:147:63//Z22404  
R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:97//AF091433  
R-NT2RP2001392//Mycococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//0.079:178:62//L19301  
R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//3.4e-60:351:90//Z93242  
R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83//D17294  
R-NT2RP2001420//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 110B011, WORKING DRAFT SEQUENCE.//1.0e-44:246:85//AL034419  
R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//3.7e-05:417:61//AL031273  
R-NT2RP2001427//Human Chromosome 11 Cosmid cSR134e5, complete sequence.//0.94:287:59//U73643  
R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.2e-31:299:77//AF046702  
R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds.//7.8e-75:548:83//D17447  
R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPC11-22B16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-06:452:59//AC004801  
R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.1e-08:218:67//AC004846  
R-NT2RP2001450  
R-NT2RP2001467//Human BAC clone RG343P13 from Tq31, complete sequence.//3.8e-31:254:83//AC002465  
R-NT2RP2001506//C. barati p-47, nttnh, bont genes.//1.2e-06:415:60//Y12091  
R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:155:63//AL034559  
R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALARI.//2.1e-104:545:95//Y14494  
R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175\_E5, complete sequence.//7.0e-16:283:68//AC004596  
R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, genomic sequence, complete sequence.//7.7e-16:108:96//AF037222  
R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//0.052:112:66//B73597  
R-NT2RP2001569//CIT-HSP-2335F8.TR CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey sequence.//6.0e-78:383:98//AQ042029  
R-NT2RP2001576//Homo sapiens sulfonyleurea receptor (SUR2) gene, exon 37.//0.33:135:66//AF061322  
R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63//L15407  
R-NT2RP2001597//HS\_3016\_B2\_F06\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3016 Col=12 Row=L, genomic survey sequence.//5.3e-45:310:87//AQ118854  
R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855\_D21, complete sequence.//0.015:445:58//AC006079  
R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.5e-16:413:63//AF009326  
R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, complete cds.//0.11:190:63//AF034626  
R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//3.0e-26:157:81//AC004125  
R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.0e-58:305:96//AC004472  
R-NT2RP2001678//Human BAC clone RG222A16 from Tq31, complete sequence.//0.95:107:66//AC002385  
R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds.//8.8e-05:211:63//U76758  
R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from T2p15, complete sequence.//4.7e-68:352:97//AC004079  
R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CIT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346:59//B40914  
R-NT2RP2001740//HS\_3213\_A2\_002\_T7 CIT Approved Human Genomic Sperm

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Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162:82//AQ175104

R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312:77//D16583

R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC26 2482), complete sequence.//2.3e-100:435:97//AC004783

R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9.//0.031:261:60//W23468

R-NT2RP2001861

R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194:77//134189

R-NT2RP2001876

R-NT2RP2001883//Human DNA sequence from clone 612618 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//5.0e-111:485:97//AL031864

R-NT2RP2001900

R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382:77//U07563

R-NT2RP2001926//HS\_3180\_B2\_F02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138:80//AQ185415

R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:60//AC005504

R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378:59//AF020280

R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.6e-85:409:100//AC005033

R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140:64//AB002388

R-NT2RP2001969

R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307:98//B99575

R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1M20 (ESSAII project).//0.031:282:61//AL022140

R-NT2RP2002025

R-NT2RP2002032//CITB1-E1-2502C19.TF CITB1-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285:95//AQ264715

R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain.//1.1e-08:389:61//D88270

R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPI111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-49:264:97//AC006206

R-NT2RP2002046//Human BAC clone GS119P05 from Tq21, complete sequence.//0.0023:429:61//AC004011

R-NT2RP2002047//P. falciparum PK1 gene.//0.00015:239:62//X83707

R-NT2RP2002058//HS\_2183\_A1\_G01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185:84//AQ022560

R-NT2RP2002066//G.gallus microsatellite DNA (LE10222 (=T15ivD04)).//0.18:102:70//Z83792

R-NT2RP2002070//P. falciparum major merozoite surface antigen (PMMS A) mRNA, complete cds, isolate FC27.//0.95:192:61//M19143

R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182:86//AF052183

R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97:90//AL009178

R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376:89//AJ007509

R-NT2RP2002105

R-NT2RP2002124//RPI111-75J16.TJ RPI111 Homo sapiens genomic clone R-75J16, genomic survey sequence.//0.58:191:64//AQ266779

R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//0.0065:294:61//AC005913

R-NT2RP2002154

R-NT2RP2002172//RPI111-90C20.TJ RPI111 Homo sapiens genomic clone R-90C20, genomic survey sequence.//0.049:160:65//AQ282591

R-NT2RP2002185//CIT-HSP-2341115.TF CIT-HSP Homo sapiens genomic clone 2341115, genomic survey sequence.//6.0e-36:230:90//AQ053355

R-NT2RP2002192//HS\_2222\_B1\_F08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence.//1.9e-15:249:71//AQ178491

R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//4.7e-35:438:73//AF032872

R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence.//0.00057:468:57//D31785

R-NT2RP2002219//HS\_2058\_A1\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence.//3.4e-55:512:77//AQ234380

R-NT2RP2002231//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-31, complete sequence.//1.5e-06:398:61//Z98557

R-NT2RP2002252//Sequence 11 from patent US 5624818.//3.3e-91:553:87//141141

R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//3.0e-14:132:84//AF005418

R-NT2RP2002259//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 118J21, WORKING DRAFT SEQUENCE.//1.6e-96:548:91//AL033527

R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 B7F, complete sequence.//5.1e-06:391:60//AC004605

R-NT2RP2002292//Genomic sequence from Human 13, complete sequence.//0.91:159:64//AC001226

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.3e-101:527:94//AF069532

R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//0.00052:389:59//AE001408

R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds.//2.3e-112:567:95//AF093668

R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA.//1.5e-22:323:73//L23204

R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//3.7e-102:600:89//AF038958

R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:399:59//AC005308

R-NT2RP2002408//HS\_2212\_A1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence.//9.6e-35:231:88//AQ184632

R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.//2.8e-39:308:82//AL021877

R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA.//0.022:102:71//M74225

R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, a predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.00099:354:59//Z99289

R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE.//0.0015:219:67//AP000013

R-NT2RP2002475

R-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//3.1e-113:605:92//AB005289

R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 2. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//0.32:210:64//Z98047

R-NT2RP2002503//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//4.0e-86:429:98//AC006213

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//2.7e-105:583:91//AB018334

R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//0.14:406:58//AJ223323

R-NT2RP2002537//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 500L14, WORKING DRAFT SEQUENCE.//2.8e-16:188:78//AL023583

R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA.//4.7e-108:571:93//AF009314

R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//1.1e-103:422:95//AC005316

R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds.//1.8e-36:526:67//M27878

R-NT2RP2002595

R-NT2RP2002606//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 2705, WORKING DRAFT SEQUENCE.//7.2e-10:211:71//AL033529

R-NT2RP2002609

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R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence.//2.9e-05:566:60//Z98551

R-NT2RP2002621//Human DNA sequence from PAC 341110 on chromosome 6 q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo) gene, ESTs and STSs.//1.1e-38:348:78//Z97352

R-NT2RP2002643//Homo sapiens chromosome 11 clone pTb15.28 map 11p15.4-p15.5, genomic survey sequence.//1.2e-35:414:66//AF074030

R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//1.3e-77:403:95//AC005384

R-NT2RP2002701

R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778

R-NT2RP2002710//P. falciparum serine rich protein (SERP I) gene.//0.84:135:67//J03983

R-NT2RP2002727//, complete sequence.//1.0:363:59//AC005815

R-NT2RP2002736//Arabidopsis thaliana chromosome 11 BAC T17M13 genomic sequence, complete sequence.//0.44:267:60//AC004138

R-NT2RP2002740//Homo sapiens xp22 BAC GSHB-600C8 (Genome Systems Human BAC library) complete sequence.//0.0016:474:60//AC004674

R-NT2RP2002741//HS\_3051\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence.//1.1e-38:217:86//AQ106283

R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPC11-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395

R-NT2RP2002752//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494

R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-100:496:97//AC004882

R-NT2RP2002769//parametium species 5.311 nt dna dimer: replication init. region.//7.4e-10:404:60//K00917

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:341:94//AF070537

R-NT2RP2002800//RPC111-37C8, TV RPC1-11 Homo sapiens genomic clone RPC1-11-37C8, genomic survey sequence.//4.9e-60:321:95//AQ029850

R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078

R-NT2RP2002857//HS\_3026\_B2\_H07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence.//8.9e-06:242:62//AQ128697

R-NT2RP2002862//RPC111-42115, TJ RPC111 Homo sapiens genomic clone R-42115, genomic survey sequence.//1.5e-44:270:85//AQ052700

R-NT2RP2002880//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL022318

R-NT2RP2002891

R-NT2RP2002925//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395

R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556

R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140

R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//1.0:275:61//AC005701

R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483

R-NT2RP2002979//RPC111-20F13, TPK RPC1-11 Homo sapiens genomic clone RPC1-11-20F13, genomic survey sequence.//0.88:110:72//AQ008132

R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140

R-NT2RP2002986//Human DNA sequence from clone 1147016 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542

R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24\_A\_23, complete sequence.//1.3e-51:283:88//AC005968

R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21.//4.3e-11:430:63//AL021307

R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA A-Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887

R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2/10.//3.5e-33:271:82//AB020870

R-NT2RP2003073

R-NT2RP2003099//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914

R-NT2RP2003108

R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378

R-NT2RP2003121//HS\_2238\_A1\_E08\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence.//0.00055:324:61//AQ293058

R-NT2RP2003125

R-NT2RP2003129

R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084

R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879

R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581

R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018\_M\_14, complete sequence.//2.2e-71:467:86//AC005823

R-NT2RP2003177

R-NT2RP2003194//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597

R-NT2RP2003206//P. falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877

R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551

R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence.//1.0:311:60//AB016888

R-NT2RP2003243//CIT-HSP-2368D12, TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738

R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NG05) mRNA, complete cds.//1.3e-38:273:83//L38481

R-NT2RP2003272//Homo sapiens clone UGCC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187

R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525

R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831

R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261

R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079

R-NT2RP2003295//HS\_2053\_B1\_A10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251

R-NT2RP2003297//Arabidopsis thaliana chromosome 11 BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332

R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960

R-NT2RP2003329//C. reinhardtii psbB 5' flanking region.//0.79:161:59//X59731

R-NT2RP2003339//RPC111-57H15, TK RPC111 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039

R-NT2RP2003347//RPC111-15B19, TV RPC1-11 Homo sapiens genomic clone RPC1-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357

R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84//U91321

R-NT2RP2003391//HS\_2255\_B2\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937

R-NT2RP2003393//RPC111-44K6, TJ RPC111 Homo sapiens genomic clone R-44K6, genomic survey sequence.//3.9e-31:290:79//AQ020481

R-NT2RP2003394//Yeast mitochondrial ox13 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//X14910

R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, partial cds.//0.32:174:66//U81429

R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536

R-NT2RP2003445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//4.4e-99:585:89//AL023808

R-NT2RP2003446

R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559

R-NT2RP2003480//Homo sapiens full length insert cDNA clone ZE09A1.//4.7e-111:540:98//AF086540

R-NT2RP2003499

R-NT2RP2003506

R-NT2RP2003511

R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460

【0810】

【表510】

R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/ PDGF2) mRNA, complete cds.//1.5e-60:518:79//M12783  
 R-NT2RP2003522//HS\_2182\_A1\_D05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304  
 R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPC14-B16N1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//1.5e-37:328:80//AC005841  
 R-NT2RP2003543//HS\_3028\_A2\_C12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957  
 R-NT2RP2003559//Homo sapiens full length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055  
 R-NT2RP2003564  
 R-NT2RP2003581  
 R-NT2RP2003596//HS\_2163\_B1\_D11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143  
 R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067  
 R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507  
 R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//5.1e-37:561:68//AJ006215  
 R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.0053:395:58//Z76735  
 R-NT2RP2003687//Human BAC clone RG222A16 from Tq31, complete sequence.//8.0e-10:205:67//AC002385  
 R-NT2RP2003691//HS\_3252\_A2\_A11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ19783  
 R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey sequence.//3.9e-43:431:75//AQ035000  
 R-NT2RP2003704  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097  
 R-NT2RP2003713//Human DNA sequence from PAC 41186 on chromosome X.//0.64:169:67//Z84470  
 R-NT2RP2003714//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//4.6e-11:152:73//Z95704  
 R-NT2RP2003727//H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631  
 R-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.2e-109:547:96//AC004951  
 R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-42 7H10, complete sequence.//4.1e-109:545:97//AC004626  
 R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019  
 R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468  
 R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete cds.//0.96:446:58//D87956  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437  
 R-NT2RP2003777  
 R-NT2RP2003781//HS\_3109\_B1\_B04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence.//1.3e-60:346:92//AQ186749  
 R-NT2RP2003793  
 R-NT2RP2003840  
 R-NT2RP2003857//HS\_2205\_A2\_H12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence.//8.1e-22:127:99//AQ151299  
 R-NT2RP2003859//RPC111-37C8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-37C8, genomic survey sequence.//8.3e-60:320:95//AQ029850  
 R-NT2RP2003871//HS\_3210\_A1\_C08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence.//8.6e-09:322:61//AQ175028  
 R-NT2RP2003885//RPC111-7M10.TP RPC1-11 Homo sapiens genomic clone RPC1-11-7M10, genomic survey sequence.//4.7e-67:380:92//B72214  
 R-NT2RP2003912//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//1.2e-33:379:75//AL023693  
 R-NT2RP2003952  
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.3e-114:568:97//AB014458  
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1.1e-107:540:97//AB007916  
 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.7e-114:568:96//AB018347  
 R-NT2RP2003984  
 R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.6e-99:551:92//AC000382  
 R-NT2RP2003988  
 R-NT2RP2004014  
 R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//4.9e-114:568:97//AC004780  
 R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence.//0.11:195:64//AQ258389  
 R-NT2RP2004066//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555  
 R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308  
 R-NT2RP2004098//H.sapiens CpG island DNA genomic MseI fragment, clone 133h3, reverse read cpg133h3.r1la.//7.9e-25:140:100//Z64530  
 R-NT2RP2004124  
 R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964  
 R-NT2RP2004152//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776  
 R-NT2RP2004165//Anthodiaris crassispina mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021  
 R-NT2RP2004170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B31108: HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064  
 R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047  
 R-NT2RP2004187//RPC111-59E12.TK RPC111 Homo sapiens genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120  
 R-NT2RP2004194  
 R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D001bE2, genomic survey sequence.//1.6e-22:178:71//AL026601  
 R-NT2RP2004207//Homo sapiens BAC clone GS421103 from Xq25-q26, complete sequence.//0.19:175:64//AC005023  
 R-NT2RP2004226//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808  
 R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524  
 R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//8.7e-108:563:94//AB015718  
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1), mRNA, complete cds.//1.1e-101:530:93//AF039687  
 R-NT2RP2004242  
 R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280  
 R-NT2RP2004270//Lycopersicon esculentum ldh2 gene.//0.98:259:61//Y10603  
 R-NT2RP2004300//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913  
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416  
 R-NT2RP2004321//Caenorhabditis elegans cosmid F4788, complete sequence.//0.0078:333:61//Z77662  
 R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from Tq35-q36, complete sequence.//1.4e-75:306:86//AC005229  
 R-NT2RP2004347//RPC111-90N11.TJ RPC111 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548  
 R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans CO2C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010  
 R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433  
 R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16AF3, genomic survey sequence.//2.1e-05:128:67//AL000528  
 R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPC111-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065  
 R-NT2RP2004389//HS\_2183\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969

【表511】

R-NT2RP2004392//*Ceratovacuna* sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993

R-NT2RP2004396//*Homo sapiens* BAC clone RG135C18 from Tq21, complete sequence.//6.4e-111:572:96//AC005164

R-NT2RP2004399//*Arabidopsis thaliana* chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085

R-NT2RP2004400//HS\_3238\_A2\_H11\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3238 Col=22 Row=0, genomic survey sequence.//5.1e-23:162:89//AQ211412

R-NT2RP2004412//*Saccharomyces douglasii* mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514

R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DDC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718

R-NT2RP2004476//*Rattus norvegicus* activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3' UTR.//5.3e-99:600:90//AF030091

R-NT2RP2004490//*Homo sapiens* chromosome 16, P1 clone 94-10H (LAML), complete sequence.//3.9e-115:575:97//AC005591

R-NT2RP2004512//*Plasmodium falciparum* MAL3P3, complete sequence.//0.00034:517:58//Z98547

R-NT2RP2004523//*Homo sapiens* clone DJ0800C07, complete sequence.//1.8e-115:571:97//AC004890

R-NT2RP2004538//*Homo sapiens* BAC clone RG318C11 from Tpl4-p15, complete sequence.//1.7e-47:322:87//AC005091

R-NT2RP2004551//*Homo sapiens* Xp22: bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184

R-NT2RP2004568//TTC20-Sp6 TAMU *Arabidopsis thaliana* genomic clone TTC20, genomic survey sequence.//0.70:446:54//B08766

R-NT2RP2004580//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768

R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP *Homo sapiens* genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976

R-NT2RP2004594//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-A-24 BFT, complete sequence.//5.3e-10:493:62//AC004605

R-NT2RP2004600//*Homo sapiens* full length insert cDNA clone ZED4E06.//2.1e-70:343:99//AF085522

R-NT2RP2004602//*Homo sapiens* full length insert cDNA clone YW26E09.//2.0e-96:528:93//AF085033

R-NT2RP2004614

R-NT2RP2004655//*Homo sapiens* mRNA for leucine rich protein.//7.3e-117:587:96//AJ006291

R-NT2RP2004664//*Homo sapiens* mRNA for KIAA0460 protein, partial cds.//1.8e-105:520:96//AB007929

R-NT2RP2004675//*Homo sapiens* ELN gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds.//3.4e-22:197:79//U63721

R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661

R-NT2RP2004689//*Homo sapiens* mRNA for KIAA0625 protein, partial cds.//1.6e-118:600:96//AB014525

R-NT2RP2004709//*Homo sapiens* full length insert cDNA clone ZD42A08.//3.5e-14:139:86//AF086259

R-NT2RP2004710//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 126A5, WORKING DRAFT SEQUENCE.//6.9e-117:592:96//AL031447

R-NT2RP2004736//*Homo sapiens* mRNA for KIAA0478 protein, complete cds.//4.2e-117:594:96//AB007947

R-NT2RP2004743//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC005505

R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1 p36.2-1p36.3.//2.0e-81:568:84//Z97988

R-NT2RP2004775//*Anopheles quadrimaculatus* NADH dehydrogenase subunit its (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.0e-08:365:62//L04272

R-NT2RP2004791//*Homo sapiens* chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//7.8e-111:541:98//AC005216

R-NT2RP2004799//*Homo sapiens* ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//2.5e-114:564:96//AF058953

R-NT2RP2004802

R-NT2RP2004815//*Homo sapiens* H beta 58 homolog mRNA, complete cds.//2.7e-118:584:97//AF054179

R-NT2RP2004841//Human BAC clone RG308B22 from Tq22-q31, complete sequence.//4.0e-46:447:72//AC002089

R-NT2RP2004861//*Plasmodium falciparum* MAL3P5, complete sequence.//0.19:189:66//AL034556

R-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//1.1e-08:330:61//AC004383

R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP *Homo sapiens* genomic clone 2374L4, genomic survey sequence.//0.99:129:65//AQ110571

R-NT2RP2004959//*Plasmodium falciparum* MAL3P6, complete sequence.//0.014:402:61//Z98551

R-NT2RP2004961//RPC111-45P2.TK RPC111 *Homo sapiens* genomic clone 45P2, genomic survey sequence.//9.3e-90:453:97//AQ202282

R-NT2RP2004962//*Caenorhabditis elegans* DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y40H4, WORKING DRAFT SEQUENCE.//0.017:291:61//AL022573

R-NT2RP2004967//*Homo sapiens* clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.6e-52:496:77//AC005077

R-NT2RP2004978//*Homo sapiens* chromosome 19, cosmid F23269, complete sequence.//0.088:322:63//AC005614

R-NT2RP2004982//*Homo sapiens* BAC clone BXD85E05 from Z2q12.1-pter, complete sequence.//0.025:339:61//AC003071

R-NT2RP2004985//T31H24TF TAMU *Arabidopsis thaliana* genomic clone T31H24, genomic survey sequence.//0.40:111:70//B78148

R-NT2RP2004999//*Homo sapiens* clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//0.23:157:68//AC005682

R-NT2RP2005000

R-NT2RP2005001//*Homo sapiens* mRNA for KIAA0615 protein, complete cds.//3.0e-111:577:95//AB014515

R-NT2RP2005003//*Homo sapiens* Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC Library) complete sequence.//2.4e-21:246:77//AC004673

R-NT2RP2005012//*Homo sapiens* SEC63 (SEC63) mRNA, complete cds.//9.5e-115:568:97//AF100141

R-NT2RP2005018//HS\_3108\_B1\_E09\_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3108 Col=17 Row=J, genomic survey sequence.//1.9e-31:222:89//AQ104050

R-NT2RP2005020//*Rattus norvegicus* cationic amino acid transporter-1 (CAT-1) mRNA, complete cds.//6.6e-41:566:73//U70476

R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP *Homo sapiens* genomic clone 516A2, genomic survey sequence.//4.1e-31:357:75//B49897

R-NT2RP2005037

R-NT2RP2005038//Sequence 5 from patent US 5552281.//2.2e-32:178:98//J25644

R-NT2RP2005108//*Mus musculus* orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.7e-23:475:67//AF009326

R-NT2RP2005116//*Homo sapiens* mRNA for KIAA0664 protein, partial cds.//8.4e-104:518:97//AB014564

R-NT2RP2005126//*H. sapiens* mRNA for RNA helicase (Myc-regulated dead box protein).//1.4e-67:464:85//X98743

R-NT2RP2005139

R-NT2RP2005140//*Leishmania mexicana amazonensis* kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//7.9e-08:460:60//U00101

R-NT2RP2005144//*Homo sapiens* chromosome 12p13.3 clone RPC111-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//2.5e-103:519:96//AC005911

R-NT2RP2005147//*Homo sapiens* clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.068:100:75//AC004971

R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 *Homo sapiens* genomic clone 2506A8, genomic survey sequence.//0.90:113:71//AQ262104

R-NT2RP2005162//*Homo sapiens* chromosome 17, clone HCIT307A16, complete sequence.//5.0e-14:183:75//AC003041

R-NT2RP2005168//*Homo sapiens* mRNA for E1B-55kDa-associated protein.//7.5e-100:513:95//AJ007509

R-NT2RP2005204

R-NT2RP2005227//*Homo sapiens* PAC clone DJ0905J08 from Tpl2-p14, complete sequence.//7.2e-119:583:97//AC005189

R-NT2RP2005239//*Homo sapiens* mRNA for putative tRNA splicing protein, partial.//8.4e-62:312:98//AJ010952

R-NT2RP2005254//*Homo sapiens* DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/cytoplasmic 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs.//5.7e-09:328:62//Z99297

R-NT2RP2005270//*Plasmodium falciparum* MAL3P8, complete sequence.//2.3e-05:355:61//AL034560

R-NT2RP2005276//Genomic sequence for *Arabidopsis thaliana* BAC F17F8, complete sequence.//0.0014:541:58//AC000107

R-NT2RP2005287//*Cavia porcellus* zinc finger protein (zfoC1) mRNA, complete cds.//4.4e-69:459:86//L26335

R-NT2RP2005288//*Homo sapiens* RCC1-like G exchanging factor RLG mRNA

【表512】

A. complete cds.//7.4e-124:594:98//AF060219  
 R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//1.5e-110:545:96//AJ007590  
 R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//1.1e-12:554:61//U00101  
 R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, ES T, GSS, STS, CpG island, complete sequence.//9.5e-15:218:77//AL022069  
 R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence.//2.0e-72:478:88//L06804  
 R-NT2RP2005336//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//7.3e-33:139:82//U14567  
 R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome X q25-q26.3, contains STS.//0.094:451:60//Z97629  
 R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-11:89:96//AJ010841  
 R-NT2RP2005360//Homo sapiens clone RG023115, WORKING DRAFT SEQUENCE. 1 unordered pieces.//0.046:266:60//AC005049  
 R-NT2RP2005383//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//6.0e-41:226:86//AC005695  
 R-NT2RP2005407  
 R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region.//0.039:169:63//L10835  
 R-NT2RP2005441//CIT-HSP-2338P5. TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//3.0e-38:263:88//AQ055548  
 R-NT2RP2005453//CIT-HSP-2367N1. TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence.//0.67:409:59//AQ079845  
 R-NT2RP2005457//Homo sapiens partial XPC gene, exon 2.//2.0e-42:315:82//X71342  
 R-NT2RP2005464//CIT-HSP-2359C16. TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence.//1.0:251:60//AQ075816  
 R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, PI clone DS08616, complete sequence.//0.25:288:62//AC005457  
 R-NT2RP2005472//Chlorarachnion COMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clip protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNA HEL) genes, complete cds.//1.0:356:59//U58510  
 R-NT2RP2005476//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MALIP3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746  
 R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE. 1 unordered pieces.//6.2e-71:187:100//AC006030  
 R-NT2RP2005491//paramécie species 5.311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917  
 R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE. 12 unordered pieces.//1.3e-25:208:82//AC005051  
 R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722  
 R-NT2RP2005498  
 R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269\_G\_24, complete sequence.//1.7e-29:252:76//AC005828  
 R-NT2RP2005509//CIT-HSP-2060J6. TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979  
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:570:94//AF092563  
 R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432  
 R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61//AC004911  
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.7e-106:560:94//AJ012449  
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963  
 R-NT2RP2005549//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//0.91:287:58//AJ011929  
 R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPC15-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804  
 R-NT2RP2005557//Homo sapiens PAC clone DJ1200123 from 7p15, complete sequence.//8.2e-22:236:76//AC004996  
 R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE. 7 unordered pieces.//7.2e-45:286:85//AC006146  
 R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148  
 R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126  
 R-NT2RP2005620  
 R-NT2RP2005622//jd432 Trypanosome Shotgun W13 genomic Trypanosoma brucei genomic clone 1187, genomic survey sequence.//0.010:308:58//B13538  
 R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996  
 R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Sc ca2) gene, complete cds.//0.030:370:60//AF063937  
 R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398  
 R-NT2RP2005651  
 R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908  
 R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984  
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-IR) mRNA, complete cds.//1.8e-89:434:98//AF089814  
 R-NT2RP2005683//jd432 Trypanosome Shotgun W13 genomic Trypanosoma brucei genomic clone 1187, genomic survey sequence.//0.037:283:58//B13538  
 R-NT2RP2005690//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUENCE. 5 unordered pieces.//1.5e-38:295:83//AC005478  
 R-NT2RP2005694//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-106, complete sequence.//0.0026:414:57//AL010210  
 R-NT2RP2005701  
 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342  
 R-NT2RP2005719//Caenorhabditis elegans cosmid LLL1, complete sequence.//0.83:275:61//Z82277  
 R-NT2RP2005722//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985  
 R-NT2RP2005723  
 R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE. 3 unordered pieces.//2.6e-64:503:82//AC004842  
 R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE. 8 unordered pieces.//2.5e-09:261:64//AC000384  
 R-NT2RP2005748//RPC111-64K11.TK RPC111 Homo sapiens genomic clone 64K11, genomic survey sequence.//0.00039:215:66//AQ239313  
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868  
 R-NT2RP2005753//Homo sapiens 1-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516  
 R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098  
 R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672  
 R-NT2RP2005773//HS\_2168\_B1\_G12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414  
 R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310  
 R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623  
 R-NT2RP2005784//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423  
 R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147\_L\_13, complete sequence.//6.3e-16:481:63//AC005332  
 R-NT2RP2005812//Caenorhabditis elegans cosmid F15810.//0.81:147:63//AF036696  
 R-NT2RP2005815  
 R-NT2RP2005835  
 R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873  
 R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047  
 R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308

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【表513】

R-NT2RP2005859//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* SS \*\*\* from contig 3-83, complete sequence.//0.0097:363:59//AL010152

R-NT2RP2005868//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* SS \*\*\* from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971

R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//L11316

R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661

R-NT2RP2005908

R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840

R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudo gene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289

R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616

R-NT2RP2006023//HS\_2176\_B1\_C10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148

R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369

R-NT2RP2006043//Polistes annularis (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835

R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140

R-NT2RP2006069

R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0044:333:61//AC004709

R-NT2RP2006098//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* SS \*\*\* from contig 3-77, complete sequence.//4.1e-09:393:62//AL010151

R-NT2RP2006100//HS\_2020\_A2\_H02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=0, genomic survey sequence.//8.3e-53:304:92//AQ228761

R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NH E-3) mRNA, complete cds.//1.5e-16:199:79//M85300

R-NT2RP2006141

R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:76//AC002045

R-NT2RP2006184//RPC111-6016.TP RPC1-11 Homo sapiens genomic clone RPC1-11-6016, genomic survey sequence.//0.52:273:61//B49539

R-NT2RP2006186//Homo sapiens mRNA for KIAA654 protein, partial cds.//1.9e-108:553:95//AB014554

R-NT2RP2006196//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* SS \*\*\* from contig 3-57, complete sequence.//4.2e-05:420:59//AL008981

R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//2.1e-100:409:96//AC006057

R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X96484

R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707

R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:89//U91318

R-NT2RP2006258//Human PAC clone DJ0899821 from 7p15-p21, complete sequence.//2.2e-08:283:63//AC004008

R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:68//X97630

R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF035262

R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey sequence.//1.2e-27:215:65//B17768

R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U72761

R-NT2RP2006323//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 702J19, WORKING DRAFT SEQUENCE.//2.8e-104:524:96//AL033531

R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:78//AC004893

R-NT2RP2006334

R-NT2RP2006365//RPC111-72115.TK RPC111 Homo sapiens genomic clone R-72115, genomic survey sequence.//2.6e-35:217:92//AQ267043

R-NT2RP2006393//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B13E4: HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046

R-NT2RP2006436//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//3.2e-42:184:86//AL022345

R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568

R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:60//AE001423

R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098

R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266

R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222

R-NT2RP2006472//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1172A22, WORKING DRAFT SEQUENCE.//5.4e-12:407:62//AL034386

R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216

R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:58//AE001370

R-NT2RP2006565//Sus scrofa SCAMPI gene, exon 9.//1.5e-13:292:68//AJ23742

R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//AC004660

R-NT2RP2006573//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64//U50532

R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds.//1.6e-19:448:64//U22015

R-NT2RP3000002//Human DNA sequence from cosmid M104C7 on chromosome 22, complete sequence.//4.4e-14:501:63//Z82246

R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.9e-115:560:97//AJ011972

R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//3.9e-57:402:83//AC005995

R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence.//1.0:158:66//AC005697

R-NT2RP3000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.7e-32:411:69//AL033522

R-NT2RP3000055//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1000N6, WORKING DRAFT SEQUENCE.//7.9e-17:309:69//AL034378

R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds.//2.9e-07:516:60//D88192

R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence.//1.7e-27:186:90//AC005630

R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds.//0.0051:289:59//U23155

R-NT2RP3000109//HS\_3065\_A2\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

R-NT2RP3000134//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P3, WORKING DRAFT SEQUENCE.//0.027:414:57//AL031746

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//3.8e-115:578:96//AB011164

R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332\_H\_18, complete sequence.//1.3e-67:354:95//AC005746

R-NT2RP3000186

R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeats.//2.5e-31:295:78//Z82899

R-NT2RP3000207//Homo sapiens chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence.//0.016:305:61//AC004514

R-NT2RP3000220//RPC111-6307.TJ RPC111 Homo sapiens genomic clone R-6307, genomic survey sequence.//0.25:118:66//AQ201832

R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195.//3.2e-11:440:59//X15063

R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1.//0.81:114:64//U19530

R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1-27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence.//4.8e-73:352:86//AL023279

R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192\_H\_23, complete sequence.//0.025:131:66//AC005726

【表514】

R-NT2RP3000252  
R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence.//0.67:119:66//B34879  
R-NT2RP3000267  
R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//1.2e-23:424:69//D29766  
R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence.//0.55:414:59//AL008970  
R-NT2RP3000320//HS\_3056\_A1\_C03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence.//4.1e-32:214:89//AQ134064  
R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//1.5e-22:265:75//U78090  
R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence.//0.68:460:57//Z98551  
R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase.//1.4e-19:137:90//X97544  
R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence.//0.0014:118:72//AQ278177  
R-NT2RP3000350  
R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.8e-55:320:75//AC006039  
R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds.//0.18:275:61//AB011124  
R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634  
R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence.//0.015:184:63//B31814  
R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185  
R-NT2RP3000418//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510821, WORKING DRAFT SEQUENCE.//6.2e-15:445:65//AL031885  
R-NT2RP3000433  
R-NT2RP3000439  
R-NT2RP3000441  
R-NT2RP3000449//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018012, WORKING DRAFT SEQUENCE.//1.6e-43:300:76//AL031650  
R-NT2RP3000451//3' untranslated region of human mRNA for a K+ channel protein.//0.71:101:66//E13519  
R-NT2RP3000456//Human Xq28 cosmid U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24012, U80A7, U153E6, L354B5, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//AF011889  
R-NT2RP3000484//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 120G22, WORKING DRAFT SEQUENCE.//0.61:326:58//AL031847  
R-NT2RP3000487//Sequence 32 from patent US 5476781.//8.6e-08:409:61//116692  
R-NT2RP3000512//RPC111-60F15.TK RPC111 Homo sapiens genomic clone R-60F15, genomic survey sequence.//2.2e-68:379:93//AQ201516  
R-NT2RP3000526//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783  
R-NT2RP3000527//HS\_3228\_A1\_H07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=D, genomic survey sequence.//4.5e-30:184:93//AQ209131  
R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence.//0.67:88:68//AQ248538  
R-NT2RP3000542//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 12684, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316  
R-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.1e-107:548:95//AC006012  
R-NT2RP3000562//HS\_2041\_B1\_E08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence.//9.5e-55:279:98//AQ230207  
R-NT2RP3000578//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-105, complete sequence.//0.0060:356:58//AL010212  
R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666  
R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377  
R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077  
R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.02:2:491:56//AC005505  
R-NT2RP3000596//HS\_3025\_A1\_D11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452  
R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560  
R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F209D0, complete sequence.//5.6e-115:554:98//AC006128  
R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414  
R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262  
R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115  
R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379  
R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmid R31240, R30272 and R28549 containing the EKL, GCDH, CRT, and RAD23A genes, genomic sequence.//1.0e-43:408:77//AD000092  
R-NT2RP3000661//F.rubripes GSS sequence, clone 148D22bB9, genomic survey sequence.//2.7e-17:234:69//AL005927  
R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645  
R-NT2RP3000685//HS\_3007\_A2\_F02\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425  
R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551  
R-NT2RP3000736  
R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655  
R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368  
R-NT2RP3000759//HS\_2055\_A2\_D09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828  
R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209\_J\_20, complete sequence.//2.0e-20:293:72//AC005822  
R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551  
R-NT2RP3000826//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315  
R-NT2RP3000836//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344  
R-NT2RP3000841//Homo sapiens, clone hRPK.1\_A\_1, complete sequence.//0.20:226:61//AC006196  
R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781  
R-NT2RP3000847//\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572  
R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014  
R-NT2RP3000852//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297  
R-NT2RP3000859  
R-NT2RP3000865//Human DNA sequence from clone 23X20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153  
R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097  
R-NT2RP3000869//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731  
R-NT2RP3000875//H.sapiens/Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311  
R-NT2RP3000901  
R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348  
R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.0092:456:58//AL034559  
R-NT2RP3000919  
R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-2

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【表515】

4.375:71//X84407  
 R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855\_D\_21, c complete sequence.//0.36:186:62//AC006079  
 R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140  
 R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial s equence.//1.1e-07:330:64//U32857  
 R-NT2RP3001007//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE SS \*\*\* from contig 4-82, complete sequence.//0.045:286:61//AL01025 5  
 R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp 11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymor phic CA repeats.//2.3e-56:348:91//Z95125  
 R-NT2RP3001057//H. sapiens HZF4 mRNA for zinc finger protein.//8.2 e-84:531:86//X78927  
 R-NT2RP3001081//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE SS \*\*\* from MALP3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031 746  
 R-NT2RP3001084  
 R-NT2RP3001096  
 R-NT2RP3001107  
 R-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ10k5 contain ing human DNA polymerase gamma (polg) gene, complete sequence.//7. 4e-62:272:73//AC005316  
 R-NT2RP3001111  
 R-NT2RP3001113  
 R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, co mplete sequence.//7.2e-112:550:97//AC005189  
 R-NT2RP3001116//CIT-HSP-2282K23. TR CIT-HSP Homo sapiens genomic cl one 2282K23, genomic survey sequence.//0.00013:160:69//AQ002011  
 R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protei n, first coding exon of dynamin 2 (DYN11). ESTs, STS, GSS, CpG Isl and, complete sequence.//5.9e-99:497:96//AL031864  
 R-NT2RP3001120  
 R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.// 0.035:266:56//AL034559  
 R-NT2RP3001133  
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cd s.//8.1e-114:549:97//ABD18305  
 R-NT2RP3001141//Homo sapiens chromosome 17, clone HCIT187M2, compl ete sequence.//0.69:198:63//AC004448  
 R-NT2RP3001150//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034 379  
 R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//2.9e-116:56 3:98//AJ006266  
 R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 ge nomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44: 227:62//AC004688  
 R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785  
 R-NT2RP3001216//RPC111-18C15.TPC RPC1-11 Homo sapiens genomic clon e RPC1-11-18C15, genomic survey sequence.//7.0e-29:167:97//B88077  
 R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827  
 R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromo some 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS w ith a CA repeat polymorphism, complete sequence.//2.7e-08:390:62// AL021326  
 R-NT2RP3001236//RPC111-25C17.TKBR RPC1-11 Homo sapiens genomic clo ne RPC1-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ0140 03  
 R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) ge ne, complete cds.//2.9e-21:438:63//L06237  
 R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chrom osome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398  
 R-NT2RP3001253//HS\_3002\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=0, gen omic survey sequence.//0.98:190:63//AQ251982  
 R-NT2RP3001260  
 R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUEN CE, 2 unordered pieces.//0.012:509:57//AC004936  
 R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, co mplete sequence.//2.2e-22:134:87//AC005589  
 R-NT2RP3001274//Sequence 11 from Patent W09517522.//0.0058:133:66// A45341  
 R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq2 1. Contains CA repeats, STS.//4.4e-55:558:76//Z96811  
 R-NT2RP3001307//HS\_2058\_A1\_C06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, gen omic survey sequence.//7.2e-33:260:86//AQ305868  
 R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848  
 R-NT2RP3001325  
 R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:1 84:64//M86367  
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete c ds.//1.2e-112:566:96//AB007920  
 R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105  
 R-NT2RP3001355  
 R-NT2RP3001374//HS\_2184\_A2\_C04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, geno mic survey sequence.//3.7e-10:101:84//AQ024647  
 R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence.//7.4e-07:279:63//AE001397  
 R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complet e sequence.//4.4e-75:382:97//AC005785  
 R-NT2RP3001392//HS\_3078\_B2\_D05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, gen omic survey sequence.//1.0:164:64//AQ140587  
 R-NT2RP3001396//RPC111-63N18.TJ RPC111 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544  
 R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, com plete cds.//1.8e-10:193:72//U49046  
 R-NT2RP3001399  
 R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequ ence.//0.0011:392:60//Z68160  
 R-NT2RP3001420//Human BAC clone GS165104 from 7q21, complete seque nce.//3.7e-29:412:74//AC002379  
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104: 550:94//AF052158  
 R-NT2RP3001427//Caenorhabditis elegans cosmid K1105.//0.39:174:64// U53152  
 R-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//1.4e-94:533:91//U69668  
 R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chrom osome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), com plete sequence.//2.5e-12:415:61//AL009029  
 R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21. 1, complete sequence.//5.6e-36:358:77//AC004903  
 R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100: 499:97//AF070630  
 R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUEN CE, 2 unordered pieces.//4.0e-47:295:86//AC004906  
 R-NT2RP3001457  
 R-NT2RP3001459  
 R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b rRNA-mRNA chimera, clone:24.//0.33:150:66//D13030  
 R-NT2RP3001490//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE SS \*\*\* from contig 3-103, complete sequence.//2.3e-08:483:60//AL01 0208  
 R-NT2RP3001495//Human oxidoreductase (HMCNA56) mRNA, complete cds. //4.4e-60:338:93//U13395  
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T RCB (TRCB) mRNA, complete cds.//2.1e-110:549:97//AF064801  
 R-NT2RP3001527//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//5.3e-32:310:78//AL034 549  
 R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:28 0:93//AC002420  
 R-NT2RP3001538  
 R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mR NA, complete cds.//7.8e-16:391:62//U38292  
 R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 ge nomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.000 26:456:58//AC004688  
 R-NT2RP3001587//Homo sapiens HRHFB2115 mRNA, partial cds.//5.6e-0 8:86:88//ABD15337  
 R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096\_C\_20, complete sequence.//0.066:360:60//AC005410  
 R-NT2RP3001607//CIT-HSP-2010M8. TR CIT-HSP Homo sapiens genomic clo ne 2010M8, genomic survey sequence.//0.041:194:67//B53490  
 R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinic acid synthase (erythr oid); 6-aminolevulinic acid synthase. (EC 2.3.1.37). 6-phosphofruct o-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46

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【表516】

), ESTs and STS.//0.69:151:64//Z83821	7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//7.0e-109:552:96//AC005844
R-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.4e-46:354:83//AL021808	R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029
R-NT2RP3001629//H.sapiens simple DNA sequence region clone wgl10.//0.99:137:63//X76572	R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987
R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149	R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779
R-NT2RP3001642	R-NT2RP3002007
R-NT2RP3001646//HS_3218_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence.//2.6e-32:215:91//AQ303003	R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A 2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//AL022322
R-NT2RP3001671//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-88, complete sequence.//0.018:262:61//AL010157	R-NT2RP3002033
R-NT2RP3001672	R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537
R-NT2RP3001676//Homo sapiens cosmid Q9504, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905	R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence.//0.82:362:57//Z98877
R-NT2RP3001678//RPC111-50C17.TK RPC111 Homo sapiens genomic clone R-50C17, genomic survey sequence.//0.15:232:62//AQ116359	R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence.//0.010:185:63//Z87006
R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//7.8e-104:549:95//AB020860	R-NT2RP3002057
R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//AC006019	R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002
R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:433:59//AE001415	R-NT2RP3002063
R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//AF053523	R-NT2RP3002081//HS_3082_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence.//4.2e-25:344:73//AQ122260
R-NT2RP3001712//CITB1-E1-2516N9.TF CITB1-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence.//1.5e-95:456:99//AQ279562	R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//2.6e-23:212:80//AC006210
R-NT2RP3001716//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.0012:346:58//AC004617	R-NT2RP3002102//Homo sapiens BAC clone RG290C13 from 7q21, complete sequence.//0.43:168:64//AC004746
R-NT2RP3001724//Human HepG2 3' region Mbol cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273	R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence.//3.5e-08:110:78//AQ059071
R-NT2RP3001730//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111822, WORKING DRAFT SEQUENCE.//7.6e-43:409:76//Z98200	R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds.//0.11:534:55//U80077
R-NT2RP3001739	R-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//4.1e-108:551:96//AL031710
R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279	R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulator Y Protein, complete cds.//6.8e-62:347:80//AB003503
R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence.//8.8e-06:102:78//AQ113378	R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds.//0.77:281:63//U46857
R-NT2RP3001764	R-NT2RP3002165
R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican).//0.99:166:66//X54232	R-NT2RP3002166//D.sargus satellite DNA (clone PSE3).//0.81:124:62//Z48711
R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928	R-NT2RP3002173
R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//U13262	R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence.//1.3e-35:305:81//B36980
R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962	R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3.//0.0024:393:61//AF100669
R-NT2RP3001819	R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 2 2q12-qter contains ESTs.//0.30:217:63//Z82189
R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410	R-NT2RP3002255
R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694	R-NT2RP3002273//Homo sapiens BAC clone 393122 from 8q21, complete sequence.//0.84:463:57//AF070717
R-NT2RP3001855	R-NT2RP3002276//HS_2260_A1_WF_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence.//0.0017:198:63//AQ292491
R-NT2RP3001896//CIT9785K-A-636F10.TV CIT9785K Homo sapiens genomic clone A-636F10, genomic survey sequence.//0.0012:68:82//AQ116409	R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17.//7.4e-93:510:93//X13546
R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950	R-NT2RP3002304//Human BAC clone GS188P18, complete sequence.//6.3e-09:477:59//AC000115
R-NT2RP3001915//Human BAC clone RG367017 from 7p15-p21, complete sequence.//0.018:144:66//AC002486	R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.087:388:58//AC004688
R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142	R-NT2RP3002343
R-NT2RP3001929	R-NT2RP3002351//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.20:489:56//AC004617
R-NT2RP3001931//Homo sapiens full length insert cDNA clone YU73B1.//1.0e-110:562:96//AF087969	R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (7-17A) gene.//2.4e-104:516:94//Y15164
R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome X q13.1-q13.3.//0.38:386:56//Z95328	R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//4.7e-102:524:95//AB014578
R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:61//AC004500	R-NT2RP3002484
R-NT2RP3001944//Bos taurus clone CSM056 satellite DNA sequence.//0.0095:76:78//U03836	R-NT2RP3002501//Human DNA sequence from PAC 92W18, BRCA2 gene region on chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS.//5.2e-17:232:75//Z73359
R-NT2RP3001959//Homo sapiens chromosome 12p13.3 clone RPC111-350L	R-NT2RP3002512

【0817】



【表517】

R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey sequence.//0.81:266:58//AQ057387

R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272

R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12.//0.95:381:56//AJ002479

R-NT2RP3002566//HS\_2036\_A1\_D08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627

R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE. 4 unordered pieces.//5.1e-15:213:73//AC004956

R-NT2RP3002590//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNX3, complete sequence.//0.00010:431:59//AB019236

R-NT2RP3002602//Mus musculus stannin gene, complete cds.//1.6e-20:339:70//AF030522

R-NT2RP3002603

R-NT2RP3002631//Homo sapiens chromosome 21 PAC RPCIP704A9190Q2.//1.0:241:59//AJ006997

R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NH E-3) mRNA, complete cds.//6.8e-24:331:76//M85300

R-NT2RP3002660//H. sapiens partial gene for progesterone receptor and Alu element DNA.//9.8e-43:273:82//Z49816

R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA, partial sequence.//0.60:300:59//J82072

R-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.2e-20:399:66//AL023704

R-NT2RP3002682//RPC111-44K6.TJ RPC111 Homo sapiens genomic clone R-44K6, genomic survey sequence.//4.7e-09:122:77//AQ202481

R-NT2RP3002687//P. falciparum complete gene map of plastid-like DNA (IR-B).//1.1e-07:494:59//X95276

R-NT2RP3002688//Human TSL RNA sequence.//2.7e-32:290:79//X01037

R-NT2RP3002701

R-NT2RP3002713//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//0.95:334:59//AL031427

R-NT2RP3002763//HUMAN WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567

R-NT2RP3002770//R.drowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710

R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence.//0.78:354:59//AC004822

R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.1e-20:161:77//AF003528

R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972

R-NT2RP3002818//HS\_3053\_A2\_A08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3053 Col=16 Row=A, genomic survey sequence.//0.19:220:60//AQ135025

R-NT2RP3002861//P. falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276

R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165:64//AC005256

R-NT2RP3002876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 50024, WORKING DRAFT SEQUENCE.//2.6e-59:311:96//AL034380

R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.6e-24:422:63//AC003035

R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314

R-NT2RP3002911//Homo sapiens BAC clone GS16A23 from 7p21, complete sequence.//3.1e-16:471:64//AC005014

R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500

R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBML H 169), complete sequence.//3.4e-111:566:96//AC005754

R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:58//AE001391

R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666

R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482

R-NT2RP3002978//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 455J7, WORKING DRAFT SEQUENCE.//4.8e-05:249:63//AL031733

R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.0097:246:67//Z97195

R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds: snRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds: and unknown genes.//1.9e-24:188:78//AF109905

R-NT2RP3003032//Arabidopsis thaliana (clone DM1) DNA retrotransposon on Tall-1 integration site.//5.3e-07:376:63//L47211

R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165\_1\_16, complete sequence.//1.4e-13:323:66//AC005669

R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone h11-10).//3.8e-42:265:91//Y16708

R-NT2RP3003068//HS\_3214\_B2\_G09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=18 Row=N, genomic survey sequence.//0.025:207:64//AQ181894

R-NT2RP3003071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013

R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153

R-NT2RP3003121//Homo sapiens full length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348

R-NT2RP3003133//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985

R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646

R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995

R-NT2RP3003150

R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human BAC Library) complete sequence.//5.5e-42:289:74//AC005294

R-NT2RP3003185//HS\_2058\_A1\_H03\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence.//0.025:52:94//AQ231298

R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, complete sequence.//4.8e-40:349:79//AC005701

R-NT2RP3003197//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 364I1, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319

R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904

R-NT2RP3003204//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183

R-NT2RP3003212//Homo sapiens full length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173

R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307

R-NT2RP3003242//Homo sapiens chromosome 7 clone UMGc:3586A160 from 7p14-15, complete sequence.//1.0:346:57//AC005272

R-NT2RP3003251//Homo sapiens BAC clone RCG60N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083

R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862

R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3blm5.//9.4e-47:302:89//D17022

R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983

R-NT2RP3003290//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662

R-NT2RP3003301

R-NT2RP3003302//CIT-HSP-2319H19.TR CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950

R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505

R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660

R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287

R-NT2RP3003330//Homo sapiens full length insert cDNA Y124C02.//4.4e-96:458:99//AF075015

R-NT2RP3003344//HS\_3235\_B2\_H09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203

R-NT2RP3003346

R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834

【表518】

R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.9e-97:481:94//AC005519

R-NT2RP3003384//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-10:226:71//AC004820

R-NT2RP3003385

R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type I Cytoskeletal 18 (KRT18, C YK18, K18, CK18) pseudogene and an STS, complete sequence.//2.8e-40:496:72//AL031585

R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:68//L23204

R-NT2RP3003411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 438L4, WORKING DRAFT SEQUENCE.//1.0:180:61//Z97635

R-NT2RP3003427//RPC111-45J23.TJ RPC111 Homo sapiens genomic clone R-45J23, genomic survey sequence.//0.82:162:69//AQ195566

R-NT2RP3003433//Homo sapiens BAC clone MH0044G14 from 7q11.23-21.1, complete sequence.//1.1e-10:379:61//AC006031

R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//1.1e-95:478:96//AF004828

R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.3e-100:527:93//AB018268

R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-08:495:59//AE001398

R-NT2RP3003500//W. suavis mitochondria ATP9 gene.//0.0074:514:59//X77238

R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTC)n repeat-containing mRNA.//1.3e-31:217:88//U00952

R-NT2RP3003552

R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds.//0.98:321:61//AF057019

R-NT2RP3003564

R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22 q12.1 contains STS.//0.0015:507:59//AL008638

R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//1.2e-39:359:79//AC003007

R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence.//0.014:539:58//AL034560

R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinate, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, 5 TSS, GSSs and a putative CpG island, complete sequence.//1.8e-44:48:77//AL022238

R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401\_0\_9, complete sequence.//0.34:257:62//AC005291

R-NT2RP3003659//O. fuscipennis 16S rRNA gene, partial.//0.021:145:65//Z93701

R-NT2RP3003665//HS\_3078\_B2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, genomic survey sequence.//1.3e-75:397:95//AQ140580

R-NT2RP3003672

R-NT2RP3003686

R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence.//6.4e-17:464:62//AC002452

R-NT2RP3003716//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 774G10, WORKING DRAFT SEQUENCE.//0.00072:425:62//AL034410

R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//1.7e-101:492:97//AB018300

R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987SK-SK502C10, complete sequence.//3.7e-07:217:66//AC003009

R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//8.1e-26:456:68//Z98052

R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey sequence.//4.9e-09:117:77//B01736

R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds.//2.8e-105:551:95//AF077754

R-NT2RP3003805

R-NT2RP3003809//Homo sapiens full length insert cDNA clone Y295A01.//3.6e-106:533:97//AF085107

R-NT2RP3003819//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34606, WORKING DRAFT SEQUENCE.//6.0e-44:288:81//Z84487

R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA.//0.0014:410:58//M64404

R-NT2RP3003828

R-NT2RP3003831//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//2.3e-41:289:85//U14567

R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.6e-108:541:97//AF070611

R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//1.5e-46:457:74//AC002980

R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence.//3.5e-06:356:62//Z98547

R-NT2RP3003870//Homo sapiens full length insert cDNA clone ZD75H11.//8.2e-09:68:98//AF085402

R-NT2RP3003876//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018D12, WORKING DRAFT SEQUENCE.//0.0027:180:66//AL031650

R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Tdd-3 tandem array.//0.029:234:62//X53439

R-NT2RP3003918

R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds.//0.00087:164:67//AF029215

R-NT2RP3003989

R-NT2RP3003992//Sequence 1 from patent US 5591825.//0.56:235:59//I33465

R-NT2RP3004013//HS\_3018\_A1\_G09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=17 Row=W, genomic survey sequence.//0.00026:421:60//AQ119904

R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s DS03465 (D149) and DS08544 (D187)), complete sequence.//4.8e-12:308:62//AC004532

R-NT2RP3004041//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 598F2, WORKING DRAFT SEQUENCE.//0.42:190:64//AL021579

R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//3.6e-21:332:69//AC006130

R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.0e-05:476:57//AC005308

R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence.//2.0e-86:486:93//AC005784

R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence.//5.3e-11:230:69//AC002525

R-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-93:551:92//AC005038

R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPC15-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-104:317:100//AC006064

R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus).//0.73:168:60//U36532

R-NT2RP3004145//Homo sapiens full length insert cDNA clone ZE09H03.//2.3e-89:427:99//AF086542

R-NT2RP3004148//Arabidopsis thaliana chromosome 11 BAC T188 genomic sequence, complete sequence.//0.013:134:70//U78721

R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//3.8e-10:101:87//AC004081

R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//1.5e-06:442:57//AC005533

R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.7e-07:220:69//D29763

R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//7.3e-89:504:92//D42052

R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence.//0.018:353:59//Z81498

R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//4.5e-06:407:60//AE001415

R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//2.8e-105:534:97//AC005385

R-NT2RP3004253//RPC111-78J12.TJ RPC111 Homo sapiens genomic clone R-78J12, genomic survey sequence.//4.0e-64:382:90//AQ281324

R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-60:417:84//AF013967

R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds.//2.7e-43:528:73//AF092536

R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPK.1110\_E\_20, complete sequence.//1.4e-06:435:62//AC004231

R-NT2RP3004341//CITB1-E1-2503F11.TR CITB1-E1 Homo sapiens genomic clone 2503F11, genomic survey sequence.//0.0018:210:65//AQ263365

R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//7.1e-46:340:83//AC005695

R-NT2RP3004349//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//9.4e-29:263:79//AL020995

R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp 11.3-p11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.0e-67:422:90//Z95125

R-NT2RP3004399//HS\_3046\_A1\_E02\_MR CIT Approved Human Genomic Sperm

【表519】

Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=1, genomic survey sequence.//0.00014:186:67//AQ137619  
 R-NT2RP3004424//RPC111-59114.TJ RPC111 Homo sapiens genomic clone R-59114, genomic survey sequence.//7.4e-71:370:95//AQ201461  
 R-NT2RP3004428//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y56A7. WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282  
 R-NT2RP3004451//Arabidopsis thaliana chromosome 11 BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824  
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917  
 R-NT2RP3004466  
 R-NT2RP3004470//Homo sapiens chromosome 5, BAC clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895  
 R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504  
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925  
 R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024  
 R-NT2RP3004490//Homo sapiens PAC clone 165H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982  
 R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023  
 R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357  
 R-NT2RP3004504//M. musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260  
 R-NT2RP3004507  
 R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H1 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518  
 R-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316  
 R-NT2RP3004544  
 R-NT2RP3004566  
 R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709  
 R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083  
 R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946  
 R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234  
 R-NT2RP3004617  
 R-NT2RP3004618//F2H16TF. IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414  
 R-NT2RP3004670//Homo sapiens CN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase 6 (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679  
 R-NT2RP4000008//H. sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749  
 R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388  
 R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015  
 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266  
 R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b1 n DCCR Region, complete sequence.//0.56:462:58//AC000074  
 R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0021:460:60//AC005506  
 R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648  
 R-NT2RP4000109//Homo sapiens mRNA for NEGF5, partial cds.//3.5e-106:536:96//AB011538  
 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952  
 R-NT2RP4000147  
 R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681  
 R-NT2RP4000151  
 R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//AF016439  
 R-NT2RP4000167//RPC111-59L8.TX RPC111 Homo sapiens genomic clone R-59L8, genomic survey sequence.//6.2e-26:163:93//AQ200049  
 R-NT2RP4000185  
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.

...//4.6e-99:505:96//AB014600  
 R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300  
 R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//AC005261  
 R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//AC004081  
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470  
 R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727  
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092  
 R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.26:124:69//AQ043515  
 R-NT2RP4000290//ORF 5' of ECLF2... ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368  
 R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384  
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524  
 R-NT2RP4000323//S. cerevisiae telomeric sequence DNA, clone YLP108C A-2-i.//0.048:107:69//M34311  
 R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972  
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281  
 R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195  
 R-NT2RP4000370//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//9.9e-25:348:72//AC005154  
 R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901  
 R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//0.066:197:63//AC006080  
 R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527  
 R-NT2RP4000417//Homo sapiens full length insert cDNA clone ZD52B1 0.//9.6e-96:468:97//AF086313  
 R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO 1), FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026  
 R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505  
 R-NT2RP4000449//HS\_2037\_B2\_A09\_T7 CIT Approved Human Genom Spem Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047  
 R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271  
 R-NT2RP4000457  
 R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082  
 R-NT2RP4000481  
 R-NT2RP4000500  
 R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140  
 R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007  
 R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021058  
 R-NT2RP4000519  
 R-NT2RP4000524  
 R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138\_P\_22, complete sequence.//0.99:158:66//AC005697  
 R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e n DCCR Region, complete sequence.//1.0:309:59//AC000078  
 R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene.

【表520】

complete cds.//0.0031:126:72//AF052695	2.//3.3e-09:153:74//AF086247
R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161	R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086
R-NT2RP4000614//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013	R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H 192), complete sequence.//9.9e-84:435:96//AC005216
R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468.F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666	R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859
R-NT2RP4000648//CIT-HSP-230017, TR CIT-HSP Homo sapiens genomic clone 230017, genomic survey sequence.//0.22:110:68//AQ012747	R-NT2RP4001064//H. sapiens NOS2 gene, exon 15.//0.71:183:61//X85771
R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5' LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443	R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213
R-NT2RP4000704//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824	R-NT2RP4001079//Homo sapiens mRNA for putative Ca <sup>2+</sup> -transporting ATPase, partial.//2.4e-118:574:98//AJ010953
R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c1 n DGCR Region, complete sequence.//2.2e-70:448:88//AC000080	R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429
R-NT2RP4000728//CIT-HSP-2310K14, TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669	R-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164
R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765	R-NT2RP4001095//Homo sapiens cosmid IM0525, LC1233, Qc3C1, LB143 9, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626
R-NT2RP4000781//P. cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds.//1.0:392:59//D12503	R-NT2RP4001100//Human DNA sequence from cosmid UB5A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//8.7e-41:389:78//Z78021
R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037	R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629
R-NT2RP4000833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808	R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298
R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660	R-NT2RP4001126//HS_3146_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093
R-NT2RP4000855	R-NT2RP4001138
R-NT2RP4000865//Homo sapiens chromosome 17, clone HRC905N1, complete sequence.//1.5e-78:479:88//AC003098	R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668
R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616	R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095
R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153	R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067
R-nnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006	R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone to 144a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412
R-nnnnnnnnnnn//H. sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398	R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468
R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975	R-NT2RP4001174//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996
R-NT2RP4000927//epstein-barr virus simple repeat array (ir3).//0.0012:367:61//J02079	R-NT2RP4001206//P. falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924
R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MCL19, complete sequence.//1.0:138:68//AB006698	R-NT2RP4001207
R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 2, complete sequence.//0.45:288:62//Z82197	R-NT2RP4001210//CIT-HSP-2042D13, TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772
R-NT2RP4000955//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302	R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593
R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528	R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635
R-NT2RP4000975	R-NT2RP4001228//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745
R-NT2RP4000979//HS_3009_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957	R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L, genomic survey sequence.//0.0033:301:63//AQ126918
R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011NT.01_dilPD, partial cds.//0.11:219:62//U44882	R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389
R-NT2RP4000989//Sequence 3D from patent US 5552281.//3.5e-25:154:97//125669	R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426
R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694	R-NT2RP4001274//RPC111-24021, TKBF RPC11-11 Homo sapiens genomic clone RPC11-11-24021, genomic survey sequence.//3.9e-25:142:99//AQ013887
R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003	R-NT2RP4001276//Homo sapiens full length insert cDNA clone ZD5SD1 0.//1.2e-10:90:92//AF086334
R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence.//2.8e-38:241:90//AQ168515	R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//7.7e-23:466:66//AF009326
R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023	R-NT2RP4001315//CIT-HSP-2312C6, TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence.//0.88:305:62//AQ018036
R-NT2RP4001010//Homo sapiens full length insert cDNA clone ZD38E1	R-NT2RP4001339
	R-NT2RP4001345
	R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00082:260:59//AB003097
	R-NT2RP4001353//RPC111-55N17, TJ RPC111 Homo sapiens genomic clone 55N17, genomic survey sequence.//0.74:106:66//AQ081821

【表521】

R-NT2RP4001372	R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629
R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//1.5e-09:473:60//AC006080	R-NT2RP4001725//Human Chromosome 3 pac pDJ70111, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380
R-NT2RP4001375	R-NT2RP4001730//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735
R-NT2RP4001379//CIT-HSP-2335A10, TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence.//9.4e-41:441:75//AQ040083	R-NT2RP4001739//RPC111-74E7.TJ RPC111 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408
R-NT2RP4001389//Homo sapiens PAC clone DJ0740002 from 7p14-p15, complete sequence.//2.4e-22:276:73//AC004691	R-NT2RP4001753//H. sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//U78926
R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140	R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316
R-NT2RP4001414	R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020
R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272	R-NT2RP4001803//HS_3087_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405
R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308	R-NT2RP4001822
R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220	R-NT2RP4001823
R-NT2RP4001474	R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Kiotho ESTs and CoG island.//4.1e-14:136:83//Z92540
R-NT2RP4001483	R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372
R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:61//L34027	R-NT2RP4001849//P. falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983
R-NT2RP4001502//HS_2187_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2187 Col=19 Row=F, genomic survey sequence.//1.3e-20:183:81//AQ214108	R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548
R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.15:333:62//AC005916	R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014
R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226	R-NT2RP4001896
R-NT2RP4001529//Mus domesticus nuclear binding factor NF209 mRNA, complete cds.//9.5e-34:337:80//U20086	R-NT2RP4001901
R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.0027:336:63//AC004710	R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146
R-NT2RP4001551//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119	R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//W55523
R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//Z82212	R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157
R-NT2RP4001567//RPC111-61A2.TJ RPC111 Homo sapiens genomic clone R-61A2, genomic survey sequence.//0.0072:180:60//AQ200771	R-NT2RP4001950//RPC111-69C18.TJ RPC111 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641
R-NT2RP4001568	R-NT2RP4001953//Homo sapiens DNA sequence from PAC 95883 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CoG island.//6.6e-70:325:84//Z93023
R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GR11), 12S ribosomal RNA, and apocytobchrome b (Cytb) genes, primary transcripts, and cytochrome c oxidase subunit III (COIII) gene, complete cds.//1.6e-09:555:56//U14181	R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148
R-NT2RP4001574//HS_2247_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345	R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3' UTR region.//1.0e-46:242:98//U25276
R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of act in mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RINGS), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CoG islands, ESTs, STSs, and GSSs, complete sequence.//1.1e-118:567:98//AL031228	R-NT2RP4002018//RPC111-76123.TV RPC111 Homo sapiens genomic clone R-76123, genomic survey sequence.//7.9e-89:438:97//AQ268536
R-NT2RP4001592//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 101BD12, WORKING DRAFT SEQUENCE.//2.5e-09:370:61//AL031650	R-NT2RP4002047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297
R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364	R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353
R-NT2RP4001614	R-NT2RP4002058//RPC111-6901.TJ RPC111 Homo sapiens genomic clone R-6901, genomic survey sequence.//0.23:163:64//AQ268418
R-NT2RP4001634//Homo sapiens full length insert cDNA clone YU73B1.1.//5.8e-101:526:94//AF087969	R-NT2RP4002071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386
R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151	R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6 q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375
R-NT2RP4001644//M. musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092	R-NT2RP4002078//RPC111-79116.TV RPC111 Homo sapiens genomic clone R-79116, genomic survey sequence.//3.3e-87:452:95//AQ283131
R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384	R-NT2RP4002081
R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397	R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619
	R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.//6.8e-62:320:95//AQ111163
	R-NT2RP4002791//Human PAC clone DJ318C15 from 1q23, complete sequence.//0.022:435:61//AC002476
	R-NT2RP4002888//Homo sapiens BAC clone RGD67E13 from 7q21, complete sequence.//6.0e-56:660:71//AC002383
	R-NT2RP4002905//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.0017:533:57//AL008972
	R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934

【0822】

【表522】

R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25. c  
omplete sequence.//2.1e-43:326:74//AC005510  
R-OVARC1000006//HS\_2253\_B1\_F01\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, geno  
mic survey sequence.//3.7e-35:191:98//AQ069124  
R-OVARC1000013//HS\_2212\_A2\_G06\_MF CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, gen  
omic survey sequence.//0.14:212:63//AQ210584  
R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome X  
q25 contains STS.//0.0053:356:62//Z80232  
R-OVARC1000017  
R-OVARC1000035//RPC111-65E1.TJ RPC111 Homo sapiens genomic clone  
R-65E1, genomic survey sequence.//3.3e-05:236:63//AQ237194  
R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chrom  
osome 22q11.21-12.1. Contains an immunoglobulin LIKE gene and a ps  
eudogene similar to Beta Crystallin. Contains ESTs, STSs, CDSs and  
tags and tat repeat polymorphisms, complete sequence.//2.7e-48:32  
5:82//AL008721  
R-OVARC1000092//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 27K12. WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL03339  
7  
R-OVARC1000068//P. falciparum complete gene map of plastid-like DNA  
(IR-B).//0.00038:553:58//X95276  
R-OVARC1000071//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 596C15. WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031  
387  
R-OVARC1000085//DNA encoding component HCS of human proteasome.//  
2.7e-65:366:92//E03413  
R-OVARC1000087//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic cl  
one 2172N17, genomic survey sequence.//0.80:285:59//B94391  
R-OVARC1000091  
R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic cl  
one 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520  
R-OVARC1000106  
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein  
(OA48-18) mRNA, complete cds.//2.6e-100:495:97//AF069250  
R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:3  
92:80//X71342  
R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, co  
mplete sequence.//0.00020:243:65//U95740  
R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 a  
sp 10q25, complete sequence.//1.8e-16:370:67//AC005385  
R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic  
clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492  
R-OVARC1000151//M. musculus GEG-154 mRNA.//9.8e-21:192:81//X71642  
R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clo  
ne 2336F6, genomic survey sequence.//0.050:176:62//AQ042932  
R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 g  
enomic sequence. WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7  
e-08:534:58//AC005506  
R-OVARC1000198//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromo  
some 4, BAC clone C0366H07: HTGS phase 1, WORKING DRAFT SEQUENCE,  
28 unordered pieces.//5.2e-111:556:96//AC004604  
R-OVARC1000209//B1acus sp. 16S ribosomal RNA gene, partial sequenc  
e.//0.55:165:67//AF003501  
R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484  
R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, com  
plete sequence.//6.2e-38:193:82//AC005670  
R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha  
mRNA, complete cds.//1.1e-25:312:73//AF060194  
R-OVARC1000288//Human HepG2 3' region Mbol cDNA, clone hmd1d01m3./  
/5.4e-07:128:70//D17131  
R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, co  
mplete sequence.//1.7e-10:100:88//AC005971  
R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X525  
74  
R-OVARC1000309  
R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUEN  
CE, 12 unordered pieces.//6.5e-83:453:94//AC005236  
R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C  
(LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614  
R-OVARC1000335//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromo  
some 4, BAC clone C0483123: HTGS phase 1, WORKING DRAFT SEQUENCE,  
7 unordered pieces.//0.034:429:60//AC005690  
R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:  
61//AF020308  
R-OVARC1000384//D. discoideum glycoprotein 24 A and B (GP24A and GP  
24B) genes, complete cds.//0.48:296:62//W27588  
R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740  
containing NEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:28  
5:87//AD000812  
R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic cl  
one 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720  
R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3  
X10, genomic survey sequence.//1.8e-32:296:75//AC002388  
R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//  
2.0e-48:354:77//AC005378  
R-OVARC1000427//D. discoideum vegetative specific gene V18 gene for  
ribosomal protein.//2.5e-09:370:59//X15382  
R-OVARC1000431//HS\_2199\_A2\_E02\_T7 CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=1, geno  
mic survey sequence.//1.3e-34:186:98//AQ093722  
R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80  
//L06662  
R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.  
1, complete sequence.//0.0054:337:61//AC006043  
R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic cl  
one 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381  
R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete c  
ds.//1.1e-77:418:94//AB014583  
R-OVARC1000461//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417  
R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (AR  
F-GEPI) mRNA, complete cds.//1.1e-81:489:91//AF023451  
R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 l  
ocus, complete sequence.//0.0088:98:72//AC004526  
R-OVARC1000473//Homo sapiens full length insert cDNA clone Y153C1  
0.//3.2e-92:317:100//AF085851  
R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//  
2.7e-70:502:84//D07671  
R-OVARC1000486//Dictyostelium discoideum fusc (fusC) gene, partial  
cds.//0.52:411:58//AF019984  
R-OVARC1000496  
R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete s  
equence.//3.8e-17:294:71//AC005005  
R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENC  
E, 17 unordered pieces.//4.5e-109:547:96//AC005024  
R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complet  
e sequence.//3.0e-46:264:93//AC004510  
R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.0063:417:  
59//U49831  
R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chrom  
osome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, ES  
T, GSS, STS, CpG island, complete sequence.//1.5e-39:144:92//AL022  
069  
R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complet  
e sequence.//1.5e-81:429:96//AC005197  
R-OVARC1000564//Homo sapiens chromosome 17, clone HRPCK837J1, compl  
ete sequence.//0.83:301:58//AC004223  
R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the  
ALD locus containing the genes for creatine transporter (SLC6A8),  
CDM, adrenoleukodystrophy (ALD), Nat-isocitrate dehydrogenase gam  
ma subunit (IDH), and translocin-associated protein delta (TRAP) g  
enes, complete cds, plexin related protein (PLEXR) and serine kina  
se (SK) genes, partial cds, Xq28lul gene and cytochrome C (CCp) ps  
eudogene.//2.4e-44:300:88//U52111  
R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, co  
mplete sequence.//6.4e-48:436:78//AF001549  
R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complet  
e sequence.//2.7e-32:313:78//AC005952  
R-OVARC1000605  
R-OVARC1000622//Homo sapiens PAC clone DJ0942116 from 7q11, comple  
te sequence.//6.2e-43:328:83//AC006012  
R-OVARC1000640//High throughput sequencing of human chromosome 12,  
WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC0058  
40  
R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete c  
ds.//1.6e-29:162:100//AB011162  
R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42  
0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//  
0.50:270:60//AC005140  
R-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein M  
yr 7.//1.4e-83:549:86//AJ001713  
R-OVARC1000681//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL0344  
24  
R-OVARC1000689//Schistocerca americana Antennapedia homeotic prote  
in (Antp) mRNA, complete cds.//0.90:230:61//U32943  
R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H  
169), complete sequence.//5.1e-15:133:85//AC005754

【表523】

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130\_H\_16, c  
omplete sequence.//6.9e-48:525:73//AC005585  
R-OVARC1000730//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, gen  
omic survey sequence.//0.00019:198:63//AQ093513  
R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA  
(IR-B).//0.98:154:65//X95276  
R-OVARC1000769//Human coagulation factor XI gene, intron 2, partia  
l, clone pTZ18R.//2.0e-30:187:78//M21185  
R-OVARC1000771  
R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77/  
/A63552  
R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter,  
complete sequence.//7.8e-111:567:95//AC004542  
R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cd  
s.//1.3e-17:119:95//L15189  
R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBML  
H171), complete sequence.//2.3e-51:482:78//AC005574  
R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CA  
LC.//3.6e-105:536:95//Y17711  
R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LA  
ML), complete sequence.//2.7e-107:538:96//AC004494  
R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:57  
9:98//AF045584  
R-OVARC1000862//M.musculus F1t mRNA.//2.3e-20:346:73//X71978  
R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of  
73 of the complete sequence.//9.1e-08:427:58//AE001416  
R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA,  
complete cds.//5.6e-34:357:78//U20086  
R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homo  
log (GAD3) mRNA, partial cds.//0.47:305:60//U21801  
R-OVARC1000886  
R-OVARC1000891//HS\_3082\_A2\_F04\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, geno  
mic survey sequence.//1.1e-16:187:79//AQ122500  
R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome  
Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ES  
Ts and GSSs, complete sequence.//7.2e-07:476:60//AL020989  
R-OVARC1000912  
R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WO  
RKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150  
R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk  
In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471  
R-OVARC1000936//HS\_2195\_A2\_C12\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, gen  
omic survey sequence.//2.4e-76:463:90//AQ191108  
R-OVARC1000937//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 250010, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716  
R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific b  
inding protein, complete cds.//3.5e-62:526:78//AB005549  
R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1)  
gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribos  
omal gene, partial sequence, mitochondrial genes encoding mitochon  
drial products.//0.018:212:61//U61169  
R-OVARC1000959//CIT-HSP-2371K16, TR CIT-HSP Homo sapiens genomic cl  
one 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323  
R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, com  
plete sequence.//7.5e-44:353:81//AC005021  
R-OVARC1000971//H.sapiens DNA for repeat unit locus D185S1 (285 b  
p).//2.2e-07:223:70//X91255  
R-OVARC1000984  
R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome  
1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, B  
eta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca2+/Calmodulin dep  
endent Protein Kinase LIKE gene. Contains ESTs, STSS, GSSs, genom  
ic marker D15491 and a ca repeat polymorphism, complete sequence.//  
1.3e-06:179:70//AL023754  
R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457\_L\_16, c  
omplete sequence.//5.8e-71:332:87//AC003957  
R-OVARC1001000//HS\_3032\_B1\_G11\_MF CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, gen  
omic survey sequence.//5.1e-51:257:99//AQ096695  
R-OVARC1001004//Homo sapiens from UMGCC:Y18c282 from 6p21, complete  
sequence.//5.5e-92:473:96//AC004190  
R-OVARC1001010//RPC111-10P1.TV RPC1-11 Homo sapiens genomic clone  
RPC1-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813  
R-OVARC1001011//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUEN  
CE, 6 unordered pieces.//7.9e-18:219:69//AC005520  
R-OVARC1001032//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL0223

45  
R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBML H8  
D), complete sequence.//1.4e-18:451:64//AC005220  
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.  
3e-99:501:96//AF099149  
R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096\_G\_20,  
complete sequence.//9.7e-17:180:78//AC005410  
R-OVARC1001044  
R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal pr  
oteins L41.//3.7e-15:124:88//Z12962  
R-OVARC1001055//Homo sapiens, clone hRPK.15\_A\_1, complete sequenc  
e.//2.0e-30:292:76//AC006213  
R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:9  
2//176237  
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, p  
artial cds.//2.3e-95:463:98//AF082657  
R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA,  
complete cds.//0.92:272:59//U47276  
R-OVARC1001074//HS\_2205\_A1\_D07\_MF CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, gen  
omic survey sequence.//1.3e-35:205:94//AQ184530  
R-OVARC1001085  
R-OVARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (c  
lone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q  
7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897  
R-OVARC1001113//Homo sapiens diaphanous 1 (DIA1) mRNA, complete c  
ds.//1.0e-73:386:95//AF051782  
R-OVARC1001117//Homo sapiens chromosome 7 clone UWCC:g3586a160 fro  
m Tpl4-15, complete sequence.//6.1e-37:314:81//AC005272  
R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBML H  
73), complete sequence.//1.5e-44:390:77//AC005372  
R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete ge  
nome: segment 1/4.//0.81:461:57//AJ235270  
R-OVARC1001161//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL0316  
80  
R-OVARC1001162//CIT-HSP-2171J2, TR CIT-HSP Homo sapiens genomic clo  
ne 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781  
R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUEN  
CE, 15 unordered pieces.//1.3e-28:427:70//AC004963  
R-OVARC1001169//RPC111-36P6.TV RPC1-11 Homo sapiens genomic clone  
RPC1-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859  
R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Hu  
man BAC library) complete sequence.//8.8e-39:301:85//AC002549  
R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:  
83//U67213  
R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete s  
equences.//9.1e-41:516:72//AC005907  
R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g  
4, complete sequence.//1.2e-14:134:85//AC004796  
R-OVARC1001200//ALS-85 kDa insulin-like growth factor binding prot  
ein-3 complex acid-labile subunit (baboons, liver, mRNA Partial, 1  
818 nt).//0.12:345:60//S83462  
R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//  
0.66:257:59//M36794  
R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124\_H\_2, co  
mplete sequence.//1.4e-41:284:87//AC006071  
R-OVARC1001243//HS\_2055\_B2\_C01\_MR CIT Approved Human Genomic Sperm  
Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, geno  
mic survey sequence.//0.59:83:75//AQ243142  
R-OVARC1001261//Crocodilus porosus mRNA for transthyretin.//0.93:1  
21:66//AJ223148  
R-OVARC1001268  
R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//  
0.0031:295:62//Z98551  
R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LA  
ML), complete sequence.//1.6e-107:544:97//AC004494  
R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPC11-199J3 (Roswell P  
ark Cancer Institute Human PAC Library) complete sequence.//0.025:  
402:59//AC006062  
R-OVARC1001296//Homo sapiens echinoderm microtubule-associated pro  
tein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018  
R-OVARC1001306//Sequence 13 from patent US 5624818.//5.4e-85:577:8  
4//141142  
R-OVARC1001329//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402  
R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.  
1, complete sequence.//0.19:256:59//AC004862  
R-OVARC1001339//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park  
Cancer Institute Human PAC Library) complete sequence.//2.5e-49:36

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【表524】

6:83//AC004242  
 R-OVARC1001341//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 695020, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818  
 R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874  
 R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBML H190), complete sequence.//2.8e-46:424:78//AC005350  
 R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//134297  
 R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786\_0\_4, complete sequence.//0.20:335:60//AC005863  
 R-OVARC1001369  
 R-OVARC1001372//S. scrofa DNA for myogenin 3' flanking region (285 bp).//6.9e-29:249:83//X89210  
 R-OVARC1001376//Homo sapiens BAC clone RG139P11 from Tq11-q21, complete sequence.//2.1e-50:491:73//AC004491  
 R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156\_L\_14, complete sequence.//9.3e-20:422:60//AC005821  
 R-OVARC1001391  
 R-OVARC1001399  
 R-OVARC1001417//Homo sapiens EXLW1 mRNA, complete cds.//9.9e-110:561:95//AB006651  
 R-OVARC1001419//CIT-HSP-2362F16, TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668  
 R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157  
 R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341  
 R-OVARC1001442  
 R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//2.3e-19:181:81//AC002086  
 R-OVARC1001476//CITB1-E1-2517B6, TR CITB1-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence.//0.24:308:59//AQ278655  
 R-OVARC1001480//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 75304, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676  
 R-OVARC1001489//E. caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546  
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507  
 R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13 F4 complete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039  
 R-OVARC1001525//Homo sapiens clone NHD215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036  
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//AB016488  
 R-OVARC1001547  
 R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retro pseudogene.//5.9e-33:216:92//AF031165  
 R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418  
 R-OVARC1001610//HS\_3070\_A2\_A06\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523  
 R-OVARC1001611//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423  
 R-OVARC1001615//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone 310013, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658  
 R-OVARC1001668//HS\_3228\_A2\_E12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379  
 R-OVARC1001702//CITB1-E1-2501P16, TR CITB1-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965  
 R-OVARC1001703  
 R-OVARC1001711//CITB1-E1-2502N10, TF CITB1-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194  
 R-OVARC1001726//CIT-HSP-232001, TF CIT-HSP Homo sapiens genomic clone 232001, genomic survey sequence.//0.021:170:62//AQ038145  
 R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (p1).//2.5e-72:422:90//X05276  
 R-OVARC1001745//Human DNA sequence from clone 796111 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257  
 R-OVARC1001762//S. cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166  
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670  
 R-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575  
 R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279  
 R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066  
 R-OVARC1001795  
 R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337  
 R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat at polymorphism, complete sequence.//3.0e-112:581:95//AL023694  
 R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type I Cytoskeletal 18 (KRT18, C YK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585  
 R-OVARC1001813//CITB1-E1-2508J18, TR CITB1-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046  
 R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086  
 R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688  
 R-OVARC1001846//CIT-HSP-2014F15, TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905  
 R-OVARC1001861//M. musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350  
 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611  
 R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein n, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//9.1e-20:206:80//AL031864  
 R-OVARC1001880//RPC111-42115, TJ RPC111 Homo sapiens genomic clone 42115, genomic survey sequence.//3.9e-50:287:88//AQ052700  
 R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123\_L\_14, complete sequence.//6.1e-13:457:63//AC003950  
 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.5e-86:346:90//AF061749  
 R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//7.2e-89:421:100//AF072246  
 R-OVARC1001911//Homo sapiens full length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315  
 R-OVARC1001916  
 R-OVARC1001928  
 R-OVARC1001942//S. cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166  
 R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP32 9, envelope glycoprotein V3 region (env) gene, partial cds.//0.14:173:64//U58826  
 R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:63//M99593  
 R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112\_M\_10, complete sequence.//8.2e-38:385:75//AC005666  
 R-OVARC1001987  
 R-OVARC1001989//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 from clone Y57G11, WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841  
 R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//5.0e-42:298:86//AL031286  
 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934  
 R-OVARC1002056//Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.//0.23:210:61//AC004411  
 R-OVARC1002082//Homo sapiens clone DJ096SK10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.4e-99:546:92//AC006015  
 R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome X q25-Xq26. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174  
 R-OVARC1002127  
 R-OVARC1002138//CIT-HSP-2290018, TF CIT-HSP Homo sapiens genomic clone 2290018, genomic survey sequence.//2.4e-07:316:62//AQ003988  
 R-OVARC1002143//RPC111-54M8, TJ RPC111 Homo sapiens genomic clone 54M8, genomic survey sequence.//2.3e-35:220:90//AQ083241  
 R-OVARC1002156



## 【表525】

R-OVARC1002158//CITBI-E1-251404.TF CITBI-E1 Homo sapiens genomic clone 251404, genomic survey sequence.//1.6e-12:140:79//AQ265720  
R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey sequence.//5.0e-59:291:99//AQ020420  
R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060  
R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z37981  
R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507  
R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557  
R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, pl clone: T1212 and T1601, WORKING DRAFT SEQUENCE.//2.8e-44:405:77//D83253  
R-PLACE1000031//Homo sapiens clone UNGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//AC006162  
R-PLACE1000040//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y105C5, WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855  
R-PLACE1000048//Human BAC clone RG210104, complete sequence.//4.7e-83:518:89//AC002462  
R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505  
R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154  
R-PLACE1000066  
R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.2e-87:456:95//AC005848  
R-PLACE1000081  
R-PLACE1000094//RPC111-91K6.TV RPC111 Homo sapiens genomic clone R-91K6, genomic survey sequence.//2.3e-83:409:98//AQ282619  
R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746\_E\_8, complete sequence.//1.8e-06:420:57//AC005358  
R-PLACE1000142  
R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//AF058291  
R-PLACE1000185  
R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//8.2e-80:410:97//AQ022149  
R-PLACE1000214//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-09, complete sequence.//1.6e-05:548:59//AL008989  
R-PLACE1000236//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 695020, WORKING DRAFT SEQUENCE.//2.2e-16:118:91//AL032818  
R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122  
R-PLACE1000292//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 111822, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98200  
R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281\_F\_24, complete sequence.//1.8e-16:598:62//AC004706  
R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//AC005326  
R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//8.7e-09:492:58//AC005278  
R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 7 3 of the complete sequence.//0.59:354:59//AE001364  
R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtr1) mRNA, complete cds.//0.55:65:84//AF073997  
R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-17:152:83//AC005015  
R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K21N1, complete sequence.//0.51:346:58//AB020742  
R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009  
R-PLACE1000421//HS\_2251\_B2\_G12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=24 Row=M, genomic survey sequence.//1.4e-82:430:95//AQ192807  
R-PLACE1000424//Human PAC clone DJ15N1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//AC002073  
R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:76//AF015724  
R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227\_G\_15, complete sequence.//1.0e-54:429:81//AC005899  
R-PLACE1000453//Murine genomic DNA: partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//0.65:103:72//AF059580  
R-PLACE1000481//Human DNA sequence from clone 960017 on chromosome Xp11.21-11.22 Contains EST, CA repeat (DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166  
R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//3.2e-17:221:72//U35245  
R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00045:480:60//AC005308  
R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//AC004790  
R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409  
R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302  
R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799\_N\_11, complete sequence.//1.5e-37:414:74//AC005323  
R-PLACE1000588//Human guanylate binding protein isoform 1 (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542  
R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506  
R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2 MIT, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV3J0S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059  
R-PLACE1000610//HS\_3071\_A1\_C05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341  
R-PLACE1000636//HS\_3220\_B2\_E09\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157  
R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265  
R-PLACE1000656//Homo sapiens mRNA for JMA protein, complete CDS (clone IMAGE 546750 and LNLCL110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896  
R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219  
R-PLACE1000712//Homo sapiens full length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408  
R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300  
R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547  
R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791  
R-PLACE1000755//HS\_2183\_B1\_H11\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202  
R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847  
R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548  
R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970  
R-PLACE1000793  
R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNARI1.//5.1e-26:348:72//AF039904  
R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081  
R-PLACE1000849//Homo sapiens full length insert cDNA clone Z055010.//1.4e-13:93:96//AF086334  
R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunit its (1-4, 4L, 5-6): cytochrome oxidase subunits (1-3): adenosine triphosphatase subunits (6,8): cytochrome b: transfer RNA: ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272  
R-PLACE1000863  
R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505  
R-PLACE1000931//RPC111-66P7.TK RPC111 Homo sapiens genomic clone R-66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489  
R-PLACE1000948//RPC111-64K15.TK RPC111 Homo sapiens genomic clone

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【表526】

R-64K15, genomic survey sequence.//6.6e-06:258:62//AQ239337  
 R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112\_J\_9, complete sequence.//8.3e-20:223:76//AC005553  
 R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506  
 R-PLACE1000979  
 R-PLACE1001000//CIT-HSP-229718.TF CIT-HSP Homo sapiens genomic clone 229718, genomic survey sequence.//7.0e-07:64:95//AQ004997  
 R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607  
 R-PLACE1001010  
 R-PLACE1001015//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 150C2, WORKING DRAFT SEQUENCE.//1.5e-16:452:63//AL022318  
 R-PLACE1001024//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 417M14, WORKING DRAFT SEQUENCE.//0.99:186:63//AL024498  
 R-PLACE1001036//Homo sapiens clone DJ1136C02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377  
 R-PLACE1001062//Homo sapiens chromosome 17, clone hC1T54K19, complete sequence.//7.3e-16:119:84//AC003664  
 R-PLACE1001076  
 R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696  
 R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07:302:62//AC005139  
 R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372  
 R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480  
 R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22\_M\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412  
 R-PLACE1001168//HS\_2036\_A1\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=0, genomic survey sequence.//0.40:144:63//AQ230662  
 R-PLACE1001171  
 R-PLACE1001185  
 R-PLACE1001238//Human coxVib gene, last exon and flanking sequence.//3.4e-36:349:76//X58139  
 R-PLACE1001241//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-20, complete sequence.//0.11:258:61//AL008972  
 R-PLACE1001257//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone B4P3: HTCS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016  
 R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448  
 R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839  
 R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129  
 R-PLACE1001294//M.musculus CEG-154 mRNA.//1.3e-22:472:65//X71642  
 R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682  
 R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286  
 R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480  
 R-PLACE1001351//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399  
 R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927  
 R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615  
 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030  
 R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319  
 R-PLACE1001387  
 R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355  
 R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22\_M\_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412  
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087  
 R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202\_H\_3, complete sequence.//0.12:53:84//AC006241  
 R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDH, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocin-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lul gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111  
 R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130  
 R-PLACE1001468//HS\_3050\_A2\_D07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920  
 R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//7.2e-17:180:80//AC002368  
 R-PLACE1001502//RPC111-24F2.TP RPC111 Homo sapiens genomic clone RPC111-24F2, genomic survey sequence.//0.15:203:66//B84401  
 R-PLACE1001503//HS\_2183\_A1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613  
 R-PLACE1001517//Homo sapiens hCAAI mRNA, complete cds.//6.4e-56:339:90//AB006969  
 R-PLACE1001534//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667  
 R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165\_L\_16, complete sequence.//2.6e-18:171:82//AC005669  
 R-PLACE1001551  
 R-PLACE1001570//M.capricolus DNA for CONTIG NC188.//0.0043:305:57//Z33135  
 R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860  
 R-PLACE1001603//Homo sapiens KED5 protein mRNA, complete cds.//1.5e-40:295:84//AF064605  
 R-PLACE1001610//Homo sapiens clone RH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037  
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174  
 R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878  
 R-PLACE1001634//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791  
 R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651\_L\_9, complete sequence.//2.6e-83:441:95//AC005971  
 R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8.//0.91:115:69//Z79253  
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.5e-111:545:97//AF069250  
 R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077  
 R-PLACE1001705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716  
 R-PLACE1001716//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349  
 R-PLACE1001720  
 R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120  
 R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261  
 R-PLACE1001740//Homo sapiens BAC clone GS114109 from Tpl4-p15, complete sequence.//5.3e-11:249:67//AC006027  
 R-PLACE1001745  
 R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509  
 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243  
 R-PLACE1001756//Human BAC clone RG302F04 from Tq31, complete sequence.//0.074:344:62//AC002463  
 R-PLACE1001761  
 R-PLACE1001771//Homo sapiens full length insert cDNA clone ZD79C1.//4.4e-57:298:96//AF086426  
 R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711  
 R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 g

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【表527】

enomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710  
R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//4.1e-92:463:95//AF058953  
R-PLACE1001821//Homo sapiens Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567  
R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351  
R-PLACE1001869  
R-PLACE1001897//Mus musculus homeobox protein (Dlx5) mRNA, complete cds.//0.0043:207:64//AF033011  
R-PLACE1001912//RPC111-25F23.TKBR RPC1-11 Homo sapiens genomic clone RPC1-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567  
R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671  
R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642\_C\_21, complete sequence.//0.9e-248:60//AC005245  
R-PLACE1001983//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y4DH7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389  
R-PLACE1001989//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 968D22, WORKING DRAFT SEQUENCE.//1.4e-44:376:80//AL023755  
R-PLACE1002046//CITBI-EI-2520J24.TF CITBI-EI Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117  
R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900  
R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438  
R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//9.7e-06:414:60//AC004763  
R-PLACE1002073  
R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4, complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302  
R-PLACE1002115//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344  
R-PLACE1002119//Mus musculus IERS (Iers) mRNA, complete cds.//5.1e-67:442:86//AF079527  
R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162  
R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome X q27-q28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706  
R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC6A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849  
R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785  
R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456  
R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome X p22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RSI gene for retinosischisis (X-linked, juvenile) 1 (KLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056  
R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152  
R-PLACE1002227//Homo sapiens BAC clone BX085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071  
R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907  
R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255  
R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0023:549:58//AC005505  
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271  
R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329  
R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5D06.//2.4e-71:411:92//D16939  
R-PLACE1002433//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984  
R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542  
R-PLACE1002438//CITBI-EI-2501M20.TF.1 CITBI-EI Homo sapiens genomic clone 2501M20, genomic survey sequence.//0.70:247:61//AQ242104  
R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22: segment 1/3.//0.00060:471:59//AJ229041  
R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//2.5e-10:98:81//AC004854  
R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262  
R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATPSG2, ATPSG3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545  
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2 A (STAM2) mRNA, complete cds.//1.1e-53:307:91//AF042273  
R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551  
R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey sequence.//3.2e-42:297:85//AQ037614  
R-PLACE1002514//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE.//7.8e-16:221:73//Z95114  
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256  
R-PLACE1002532//Homo sapiens BAC clone RG30DE22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//AC004774  
R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//0.0042:489:60//D16253  
R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178  
R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:292:84//AC006084  
R-PLACE1002583//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//3.1e-17:517:61//AF045555  
R-PLACE1002591  
R-PLACE1002598//Caenorhabditis elegans cosmid Y37DBA, complete sequence.//0.080:308:60//AL032626  
R-PLACE1002604//Human cosmid LL12NC01-8BA9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:65//U63313  
R-PLACE1002625//HS\_2233\_B2\_H04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663  
R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//AF079765  
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-77:390:97//AF068180  
R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656  
R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//173723  
R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library) complete sequence.//0.0098:197:64//AC005185  
R-PLACE1002772//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:82//AC006145  
R-PLACE1002782  
R-PLACE1002794  
R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey sequence.//6.0e-50:250:100//AQ034981  
R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279  
R-PLACE1002816//Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-59:339:93//AC004466  
R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-78:413:95//W27877  
R-PLACE1002839//Homo sapiens PAC clone DJ0015123 from 22, complete sequence.//6.5e-25:301:74//AC004819  
R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey sequence.//0.0011:210:61//AQ040519  
R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049  
R-PLACE1002881  
R-PLACE1002908//HS\_3064\_A1\_D04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985  
R-PLACE1002941  
R-PLACE1002962

【表528】

R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721

R-PLACE1002991//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 958022, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755

R-PLACE1002993//Homo sapiens PAC clone DJ089E09 from 7q11.23-q21.1, complete sequence.//0.56-72//AC004921

R-PLACE1002996//HS\_2064\_A1\_A05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211

R-PLACE1003025//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//0.26-428:58//AC006145

R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700\_M\_6, complete sequence.//1.3e-95:465:98//AC005920

R-PLACE1003044

R-PLACE1003092//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266

R-PLACE1003100//HS\_2244\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=0, genomic survey sequence.//2.3e-42:288:86//AQ084224

R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885

R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558

R-PLACE1003145

R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616

R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence.//2.4e-05:390:60//AB015479

R-PLACE1003176

R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095

R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551

R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139

R-PLACE1003238//Homo sapiens full length insert cDNA clone ZD79H1.1.//7.6e-114:567:96//AF086432

R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416

R-PLACE1003256//Homo sapiens chromosome 17, clone HC1T421K24, complete sequence.//1.0e-45:328:85//AC004099

R-PLACE1003258

R-PLACE1003296//Diphtheria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952

R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.7e-91:458:96//M27877

R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Np60). Contains ESTs, complete sequence.//4.3e-34:370:71//Z82243

R-PLACE1003342//CIT-HSP-2311D21, TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460

R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153

R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715

R-PLACE1003361

R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805

R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174

R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050\_D\_4, complete sequence.//1.2e-62:434:83//AC004771

R-PLACE1003375//Dictyostelium discoideum golgolin (gol) gene, complete cds.//0.042:263:57//U89350

R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//1.7e-83:429:96//AB020878

R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85\_B\_7, complete sequence.//2.4e-13:175:76//AC005695

R-PLACE1003420//Homo sapiens PAC clone DJ088G15 from 7q33-q35, complete sequence.//2.1e-05:340:61//AC005587

R-PLACE1003454//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-64, complete sequence.//0.47:411:58//AL009014

R-PLACE1003478//M. capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125

R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.6e-37:319:81//AC006080

R-PLACE1003516//CIT-HSP-2295M19, TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence.//1.0e-40:251:90//AQ007480

R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:163:89//AF064859

R-PLACE1003521//HS\_3252\_A2\_G05\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence.//0.00017:274:60//AQ221562

R-PLACE1003528//HS\_2041\_B1\_B07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence.//6.6e-40:219:83//AQ230483

R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01404

R-PLACE1003553//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297

R-PLACE1003566

R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965

R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome X q21.1.//3.5e-18:287:68//Z99571

R-PLACE1003584

R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032

R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066

R-PLACE1003596//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597

R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200

R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081

R-PLACE1003611

R-PLACE1003618//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451

R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688

R-PLACE1003638//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312

R-PLACE1003669//HS\_3054\_A2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=1, genomic survey sequence.//0.014:265:61//AQ132713

R-PLACE1003704//HS\_3213\_A1\_D12\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence.//0.80:195:61//AQ176784

R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067

R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607

R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-44:505:73//AL022336

R-PLACE1003738//H. sapiens DNA sequence.//0.93:185:60//Z22357

R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023

R-PLACE1003762//Homo sapiens chromosome 17, clone HC1T39G8, complete sequence.//4.6e-13:134:79//AC003070

R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//5.4e-12:189:71//AC005919

R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//AC004160

R-PLACE1003783

R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.//5.6e-15:204:74//AC004659

R-PLACE1003795//CIT-HSP-2374C8, TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//7.0e-37:234:89//AQ14933

## 【表529】

- R-PLACE1003833//Homo sapiens full length insert cDNA clone ZE15CO 6.//4.4e-59:313:95//AF086558
- R-PLACE1003850
- R-PLACE1003858
- R-PLACE1003864
- R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 in DGCR Region, complete sequence.//8.7e-33:285:81//AC000072
- R-PLACE1003885
- R-PLACE1003886
- R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, c complete sequence.//0.73:127:65//AC004069
- R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810
- R-PLACE1003903//Homo sapiens full length insert cDNA clone ZD78D1 1.//8.1e-74:369:97//AF086422
- R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6), gene, exons 6 and 7 and complete cds.//0.56:247:61//U73520
- R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete se quence.//0.67:213:63//Z99281
- R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosom e Xp11, contains ESTs.//8.7e-49:342:85//Z74022
- R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030
- R-PLACE1003968//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE SS \*\*\* from contig 4-62, complete sequence.//1.3e-07:245:65//AL010 247
- R-PLACE1004104
- R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0 e-07:336:61//AC002485
- R-PLACE1004118//HS\_3092\_B1\_B01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=D, geno mic survey sequence.//0.80:207:60//AQ128151
- R-PLACE1004128//Rattus norvegicus guanine nucleotide binding prote in beta 4 subunit mRNA, partial cds.//1.8e-06:193:66//AF022085
- R-PLACE1004149//HS\_2253\_A2\_F11\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=22 Row=K, gen omic survey sequence.//2.4e-59:315:95//AQ129711
- R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswel l Park Cancer Institute Human PAC Library) containing Arylsulfatas e D and E genes, complete sequence.//8.3e-53:299:76//AC005295
- R-PLACE1004161
- R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:9 3//AJ010071
- R-PLACE1004197//RPC111-69N15.TK RPC111 Homo sapiens genomic clone R-69N15, genomic survey sequence.//0.0078:170:65//AQ265515
- R-PLACE1004203//Homo sapiens semaphorin L (SEMA1) mRNA, complete c ds.//3.4e-105:501:98//AF030698
- R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromo some 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS w ith a CA repeat polymorphism, complete sequence.//6.1e-65:373:86// ALD21326
- R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21. 1, complete sequence.//0.011:383:61//AC006031
- R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.4e-09:576:59//AC004470
- R-PLACE1004258//HS\_3034\_A1\_B12\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=23 Row=C, gen omic survey sequence.//1.4e-35:359:77//AQ128936
- R-PLACE1004270//CITB1-E1-2504K14, TR CITB1-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108
- R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234
- R-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) m RNA, complete cds.//4.4e-106:581:91//AF084830
- R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 g enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.5 9:231:60//AC005308
- R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700\_H\_6, co mplete sequence.//5.8e-31:340:75//AC005920
- R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENC E, 1 unordered pieces.//6.4e-90:572:86//AC005095
- R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1. 9e-113:590:94//Y11588
- R-PLACE1004336//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033 383
- R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protei n CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153
- R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clo ne 2287M8, genomic survey sequence.//0.47:173:61//AQ000837
- R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic cl one 2316J11, genomic survey sequence.//0.035:109:69//AQ037817
- R-PLACE1004388//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE SS \*\*\* from contig 3-82, complete sequence.//4.2e-06:381:60//AL010 149
- R-PLACE1004405//Homo sapiens clone G5512121, WORKING DRAFT SEQUENC E, 9 unordered pieces.//0.20:270:60//AC005027
- R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, co mplete sequence.//1.3e-96:516:94//AC005532
- R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, comp lete sequence.//5.8e-10:279:65//AL031296
- R-PLACE1004437//Human NADH-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial prote in, complete cds.//2.9e-88:516:88//U49283
- R-PLACE1004451//HS\_2258\_B2\_F01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, geno mic survey sequence.//0.82:172:61//AQ221189
- R-PLACE1004460
- R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspar late transcarbamylase-dihydroorotase (CAD) gene, exons 1 and 2.// 1.2e-24:311:62//M31621
- R-PLACE1004471//Homo Sapiens Chromosome X clone bWID75, complete s equence.//2.1e-34:333:70//AC004389
- R-PLACE1004473
- R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial AtT region.//1.0e-08:485:60//U11584
- R-PLACE1004506
- R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427
- R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071
- R-PLACE1004518
- R-PLACE1004548//Homo sapiens Xp22 BAC GS-551019 (Genome Systems Hu man BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride ch annel 4 gene, complete sequence.//4.9e-40:245:80//AC003666
- R-PLACE1004550
- R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation spe cificity factor.//2.7e-82:532:86//X75931
- R-PLACE1004629//Homo sapiens chromosome 7 clone UMGCG3586a230 fro m 7p14-15, complete sequence.//0.015:437:59//AC004800
- R-PLACE1004645//CIT-HSP-2370D6, TR CIT-HSP Homo sapiens genomic clo ne 2370D6, genomic survey sequence.//0.033:76:75//AQ110136
- R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete se quence.//2.0e-23:237:79//AF036876
- R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPC111-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequenc e.//7.1e-09:94:87//AC005343
- R-PLACE1004664//RPC111-79G23, TV RPC111 Homo sapiens genomic clone R-79G23, genomic survey sequence.//2.2e-81:433:94//AQ283692
- R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putativ e M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263: 74//U07561
- R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606
- R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge ne of hepatocellular colorectal and non-small cell lung cancer, s egment 3/11.//1.3e-96:498:95//AB020860
- R-PLACE1004686
- R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge ne of hepatocellular colorectal and non-small cell lung cancer, s egment 2/11.//2.1e-33:290:80//AB020859
- R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequ ence.//1.0:195:60//ALD21448
- R-PLACE1004716//CITB1-E1-2519C14, TR CITB1-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965
- R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.// 0.0022:360:60//AC005507
- R-PLACE1004736
- R-PLACE1004740
- R-PLACE1004743//Homo sapiens ubiquitin-protein ligase E3-alpha (UB R1) mRNA, partial cds.//5.4e-105:575:92//AF061556
- R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, compl ete sequence.//9.0e-26:317:76//AC002523
- R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds./ /8.5e-88:437:96//AF084367
- R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:13

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## 【表530】

8:65//AP000010  
R-PLACE1004793//Human endogenous retrovirus HERV-K (HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3' LTR.//5.1e-58:313:80//U60269  
R-PLACE1004804//Homo sapiens mRNA for KIAA0506 protein, partial cds.//5.8e-98:580:88//AB011178  
R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140  
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250  
R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//AC004126  
R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468\_F\_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666  
R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bax gene, complete sequence.//2.7e-14:156:79//AC003669  
R-PLACE1004836//HS\_2270\_A2\_H10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=0, genomic survey sequence.//8.6e-51:267:96//AQ164110  
R-PLACE1004838//CIT-HSP-2343E10. TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544  
R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//192820  
R-PLACE1004858//Human Chromosome X clone bWXD342, complete sequence.//0.57:344:59//AC004072  
R-PLACE1004885//HS\_3235\_B2\_E07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193  
R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577  
R-PLACE1004902  
R-PLACE1004913//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209  
R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.00084:373:60//AC004605  
R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936  
R-PLACE1004934//Homo sapiens clone RG052N11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00030:198:66//AC005683  
R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788  
R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494  
R-PLACE1004972  
R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970  
R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308  
R-PLACE1004985//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522  
R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-q32, complete sequence.//2.7e-56:158:99//AC004925  
R-PLACE1005027  
R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775  
R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//8.1e-87:301:98//AC005867  
R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584  
R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556  
R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293\_K\_20, complete sequence.//2.1e-42:384:68//AC005495  
R-PLACE1005086//RPC111-30H10.TV RPC1-11 Homo sapiens genomic clone RPC1-11-30H10, genomic survey sequence.//0.13:112:67//B87788  
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401  
R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476  
R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:32:84//U85195  
R-PLACE1005111//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845  
R-PLACE1005128  
R-PLACE1005146  
R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140  
R-PLACE1005176//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018  
R-PLACE1005181//HS\_2182\_B2\_B05\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=0, genomic survey sequence.//4.9e-05:193:65//AQ030787  
R-PLACE1005187//Arabidopsis thaliana chromosome 11 BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161  
R-PLACE1005206//Homo sapiens full length insert cDNA YN66A06.//5.3e-64:343:93//AF075043  
R-PLACE1005232//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476  
R-PLACE1005243  
R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132  
R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067  
R-PLACE1005277//CITB1-E1-2514D4.TF CITB1-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720  
R-PLACE1005287//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744  
R-PLACE1005305//HS\_3180\_B2\_002\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443  
R-PLACE1005308  
R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383  
R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960  
R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794  
R-PLACE1005335//Human Chromosome 3 pac pDJ701i1, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380  
R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68//U85195  
R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401\_0\_9, complete sequence.//3.0e-44:434:77//AC005291  
R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991  
R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//AC002477  
R-PLACE1005467//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING DRAFT SEQUENCE.//1.1e-40:328:81//Z93014  
R-PLACE1005471//Human DNA sequence from clone 39SP12 on chromosome 1q24-25. Contains the TIGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310  
R-PLACE1005477//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//0.020:216:66//AL023693  
R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//2.8e-44:327:70//AC005392  
R-PLACE1005481//Homo sapiens chromosome 17, clone hRPC.1164\_0\_3, complete sequence.//4.2e-23:284:74//AC004703  
R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631  
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185  
R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468  
R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.3e-76:395:86//AP000038  
R-PLACE1005530//C. familiaris CA repeat sequence (isolate).//0.023:90:75//X86184  
R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:64//AL025928

## 【0831】

【表531】

R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215\_P\_18, c complete sequence.//0.069:305:60//AC005969  
R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117\_B\_12, c complete sequence.//4.3e-105:587:91//AC004707  
R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequ ence.//1.5e-17:274:67//AC003971  
R-PLACE1005584//Homo sapiens PAC clone DJ1186CD1 from 7q21.2-q31. 1, complete sequence.//2.7e-15:191:77//AC004991  
R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, compl ete sequence.//6.4e-90:453:96//AC004126  
R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//U72788  
R-PLACE1005611//Borrelia burgdorferi plasmid cpl8, OspE (ospE) gen e, partial cds.//0.059:473:56//U42599  
R-PLACE1005623//Homo sapiens full length insert cDNA clone ZD76B0 3.//1.6e-113:575:95//AF086405  
R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-79:270:94//AC0058 40  
R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequen ce.//8.2e-56:441:83//AC002382  
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, co mplete cds.//3.2e-110:585:93//AF083255  
R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628\_E\_12, c complete sequence.//8.6e-08:505:58//AC005701  
R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//3.2e-27:307: 72//Z82203  
R-PLACE1005698//344822.TV C1T978SKAI Homo sapiens genomic clone A- 344822, genomic survey sequence.//0.030:91:70//B15144  
R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II (COL2A1) gene.//5.2e-10:587:59 //L10171  
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810  
R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, comple te cds.//2.2e-21:270:72//U15635  
R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219: 64//U64601  
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-4 5:268:87//D42087  
R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in ce ll proliferation.//0.030:91:78//X07024  
R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complet e sequence.//1.4e-69:391:92//AC004827  
R-PLACE1005803  
R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete s equence.//1.8e-21:175:75//AC002530  
R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971\_F\_3, WO RKING DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150  
R-PLACE1005834//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE SS \*\*\* from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL03174 5  
R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8 e-10:182:69//Y00763  
R-PLACE1005850  
R-PLACE1005851//Homo sapiens clone DJ0789105, WORKING DRAFT SEQUEN CE, 2 unordered pieces.//5.5e-06:318:63//AC004887  
R-PLACE1005876//B. taurus mRNA for cleavage and polyadenylation spe cificity factor.//6.7e-28:366:72//X75931  
R-PLACE1005884//Human DNA sequence from cosmid Y526F1, between mar kers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:5 4//Z70281  
R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 g enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00 94:449:59//AC005139  
R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21, genomic survey sequence.//4.8e-84:494:89//AQ261347  
R-PLACE1005923//RPC111-65N9.TJ RPC111 Homo sapiens genomic clone R-65N9, genomic survey sequence.//8.3e-97:520:93//AQ237243  
R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78// AL022719  
R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete se quence.//0.0035:176:62//AL032654  
R-PLACE1005934  
R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence.//0.00021:272:62//AF069716  
R-PLACE1005951  
R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349: 60//U37429  
R-PLACE1005955//Human HepG2 3' region Mbol cDNA, clone hmd1d0m3./ /8.3e-08:128:70//D17131  
R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence: tRNA-Val gene, complete sequence: and small sub unit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//7.0e-09:549:59//AF044863  
R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1 e-51:394:81//AB002086  
R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC111-407G 6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC0 05866  
R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10p13.//5.9 e-27:299:74//U15177  
R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequen ce.//3.5e-07:164:67//AF046375  
R-PLACE1006011//Mus musculus poly-(ADPribozyl)-transferase homolog PARP mRNA, complete cds.//1.1e-32:266:83//AF072521  
R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31a 1 n DGCR Region, complete sequence.//1.8e-17:164:82//AC000077  
R-PLACE1006037//Mus musculus B6D2F1 clone 2C118 mRNA.//2.0e-49:55 7:72//U01139  
R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13: 128:81//X99906  
R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUEN CE, 3 unordered pieces.//3.3e-18:220:74//AC004885  
R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, c omplete CDS.//0.0050:271:63//AJ005122  
R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C 1-31D6. Pl clone DS08879, complete sequence.//0.43:178:65//AC00545 4  
R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, co mplete sequence.//7.5e-13:222:68//AC004849  
R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.// 0.00019:455:59//Z98551  
R-PLACE1006157//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRE SS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034 557  
R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01.124\_D\_3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:5 .86:96//AC006103  
R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ro Ret gene, and sodium phosphate transporter (NPT3) gene, complete c ds.//1.0e-28:342:75//U91328  
R-PLACE1006167//Homo sapiens full length insert cDNA clone ZE14E0 4.//4.6e-77:426:93//AF085555  
R-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82// X14972  
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-1 16:597:95//AF091433  
R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//AC004410  
R-PLACE1006196  
R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence. //8.4e-44:332:85//AC000398  
R-PLACE1006223//Human DNA sequence from cosmid U74C11, between mar kers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:21 5:61//Z73362  
R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequ ence.//9.7e-13:358:63//Z98877  
R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.// 0.00019:538:58//AL008970  
R-PLACE1006239//Homo sapiens BAC clone RG18D07 from 7q31, complet e sequence.//3.1e-96:497:95//AC004142  
R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUEN CE, 1 unordered pieces.//0.029:499:56//AC006034  
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cd s.//9.2e-96:499:95//AB014548  
R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087  
R-PLACE1006288//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL03132 0  
R-PLACE1006318  
R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.// 1.0:426:57//AL034560  
R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq 21.//0.96:173:66//AL008987  
R-PLACE1006357//P. falciparum complete gene map of plastid-like DNA

【表532】

(IR-B).//1.9e-07:491:58//X95276  
 R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398  
 R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630  
 R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LA NL), complete sequence.//3.7e-101:574:91//AC004232  
 R-PLACE1006382  
 R-PLACE1006385//Mus musculus interseitin-EH binding protein lbp2 mRNA, partial cds.//1.4e-50:350:86//AF057286  
 R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854  
 R-PLACE1006414//Homo sapiens 12p13.3 PAC RPC15-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804  
 R-PLACE1006438//Homo sapiens full length insert cDNA YH73H06.//7.6e-73:422:90//AF074985  
 R-PLACE1006445//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726  
 R-PLACE1006469  
 R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152  
 R-PLACE1006482//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 447CA, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977  
 R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180\_P\_B, complete sequence.//0.78:44:95//AC005972  
 R-PLACE1006508//R. norvegicus BSP gene.//1.0:206:60//X86100  
 R-PLACE1006521//RPC111-13L8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158  
 R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197  
 R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934  
 R-PLACE1006540//Homo sapiens clone UMCC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209  
 R-PLACE1006552//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865  
 R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC58 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710  
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//2.9e-116:590:95//U97670  
 R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050  
 R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331  
 R-PLACE1006629//Homo sapiens chromosome 19, cosmid F209D0, complete sequence.//2.8e-25:343:70//AC006128  
 R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038  
 R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882  
 R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024  
 R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS. complete sequence.//0.56:226:63//AL022154  
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:485:98//AF038172  
 R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626  
 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622  
 R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984  
 R-PLACE1006782//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865  
 R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599  
 R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083  
 R-PLACE1006800//HS\_2270\_B1\_D02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793  
 R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507  
 R-PLACE1006815//HS\_3028\_B1\_B04\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174  
 R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062  
 R-PLACE1006829  
 R-PLACE1006860  
 R-PLACE1006867//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378  
 R-PLACE1006878//Homo sapiens full length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155  
 R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LA NL), complete sequence.//1.3e-38:283:85//AC004232  
 R-PLACE1006901  
 R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203  
 R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665M22 (Genome Systems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184  
 R-PLACE1006932  
 R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74//Z86061  
 R-PLACE1006958//Mouse mRNA for germ cell specific protein APC-1, complete cds.//9.5e-85:590:83//D49482  
 R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349\_A\_8, complete sequence.//6.7e-42:295:86//AC005544  
 R-PLACE1006962//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//1.1e-19:302:71//AC002349  
 R-PLACE1006966//HS\_2219\_B2\_C02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequence.//0.019:180:63//AQ145873  
 R-PLACE1006989  
 R-PLACE1007014  
 R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPC13-45482, 3, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845  
 R-PLACE1007045//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693  
 R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895  
 R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL021368  
 R-PLACE1007105//Mus musculus muskulin mRNA, complete cds.//2.7e-32:379:73//U72194  
 R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688  
 R-PLACE1007112//Cynops cornifex cytb gene.//0.020:427:58//AJ228479  
 R-PLACE1007132//Homo sapiens full length insert cDNA YH7TE09.//5.7e-107:535:96//AF074987  
 R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050  
 R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283  
 R-PLACE1007226  
 R-PLACE1007238  
 R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495  
 R-PLACE1007242//CITB1-E1-2512M9.TF CITB1-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454  
 R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970  
 R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908  
 R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394\_K\_10, complete sequence.//4.4e-10:135:74//AC006080  
 R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291  
 R-PLACE1007282//B. garinii (strain T1st) p83/100 gene (partial).//0.95:183:60//X81533  
 R-PLACE1007286//RPC111-13L8.TV RPC1-11 Homo sapiens genomic clone



## 【表533】

RPC1-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158  
 R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q 24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAM IN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195  
 R-PLACE1007317//Drosophila dasycnemis 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253  
 R-PLACE1007342  
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EB BP) mRNA, complete cds.//3.7e-65:367:91//AF096870  
 R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507  
 R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709  
 R-PLACE1007385//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261  
 R-PLACE1007402//HS\_2055\_A2\_D03\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824  
 R-PLACE1007409//Homo sapiens mitoxanthrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771  
 R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594  
 R-PLACE1007450//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 54820, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304  
 R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081  
 R-PLACE1007460  
 R-PLACE1007478//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.0e-08:335:60//AC004241  
 R-PLACE1007484  
 R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373  
 R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559  
 R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110\_E\_20, complete sequence.//1.2e-79:387:96//AC004231  
 R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682  
 R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381  
 R-PLACE1007544  
 R-PLACE1007547//Human laminin alpha 4 chain (LAMA4-1) mRNA, complete cds.//4.0e-17:108:97//U77706  
 R-PLACE1007557//Human BAC clone RG343P13 from Tq31, complete sequence.//2.2e-45:390:77//AC002465  
 R-PLACE1007583//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 545L17, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665  
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179  
 R-PLACE1007618  
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176  
 R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840  
 R-PLACE1007645//Homo sapiens full length insert cDNA clone ZD76G10, //0.0080:96:77//AF086408  
 R-PLACE1007649//CIT-HSP-2308A18, TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149  
 R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 7 of the complete sequence.//0.0041:470:57//AE001367  
 R-PLACE1007688  
 R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044  
 R-PLACE1007697  
 R-PLACE1007705//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662  
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MPI) mRNA, complete cds.//1.8e-73:374:96//AF061243  
 R-PLACE1007725//Caenorhabditis elegans cosmid F38A5, //0.070:186:60//U70854  
 R-PLACE1007729//Human endogenous retrovirus HERV-K (HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3' LTR.//3.8e-53:415:81//U60269  
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585  
 R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169  
 R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560  
 R-PLACE1007746//T. brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.//0.28:386:58//M14820  
 R-PLACE1007791//D. discoideum gene for protein kinase.//0.17:263:60//Z37981  
 R-PLACE1007807//Human DNA sequence from clone 87808 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116  
 R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//AF017104  
 R-PLACE1007829//Human BAC clone GS16S104 from Tq21, complete sequence.//0.0052:455:61//AC002379  
 R-PLACE1007843//P. falciparum complete gene map of plastid-like DNA (1R-A).//0.0050:447:57//X95275  
 R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//2.2e-11:570:95//AP000010  
 R-PLACE1007852//HS\_3028\_B2\_F04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey sequence.//1.3e-12:209:71//AQ131021  
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6.6e-110:574:94//AB018309  
 R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//1.6e-43:551:70//AL022162  
 R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.6e-22:222:78//AC005754  
 R-PLACE1007897//HS\_3113\_B2\_E04\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequence.//2.9e-72:381:95//AQ186905  
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487, //8.8e-88:460:95//AB007956  
 R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095  
 R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157  
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530  
 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529  
 R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262  
 R-PLACE1007990//E. tenella antigen LPW61 mRNA, partial cds.//0.043:273:63//M30933  
 R-PLACE1008000//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346  
 R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628  
 R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840  
 R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592  
 R-PLACE1008080//Arabidopsis thaliana chromosome 11 BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232  
 R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036  
 R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157  
 R-PLACE1008122//Homo sapiens chromosome 17, clone hRPC.142\_H\_19, complete sequence.//1.9e-11:384:63//AC005919  
 R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955  
 R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06, //7.4e-47:320:86//D16939  
 R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849  
 R-PLACE1008181//Caenorhabditis elegans cosmid C31H2, //0.055:358:60//U41748

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R-PLACE1008198  
R-PLACE1008201//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102  
R-PLACE1008209//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549  
R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688  
R-PLACE1008244//P. falciparum P.195 gene.//0.11:212:66//A04562  
R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611  
R-PLACE1008275  
R-PLACE1008280//Homo sapiens chromosome 7 clone WNGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272  
R-PLACE1008309//Human at-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308  
R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886  
R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176  
R-PLACE1008331//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226  
R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEAS) mRNA, 3' UTR.//2.5e-98:556:90//AF036145  
R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336  
R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011  
R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471\_L13, complete sequence.//1.0e-46:282:82//AC005244  
R-PLACE1008398//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417  
R-PLACE1008401//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0366H07: HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604  
R-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//1.5e-101:521:95//D086326  
R-PLACE1008405//Human cosmid CRI-JC2015 at D10S289 in 10p13.//6.8e-22:328:71//U15177  
R-PLACE1008424  
R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//7.5e-101:505:96//AB020864  
R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576  
R-PLACE1008437//H. sapiens genomic DNA (PAC B38L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335  
R-PLACE1008455  
R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526  
R-PLACE1008465//CIT978SK-A-28A11.TYE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696  
R-PLACE1008488  
R-PLACE1008524//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34821, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778  
R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555  
R-PLACE1008532  
R-PLACE1008533  
R-PLACE1008568//HS\_3218\_B2\_08\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=M, genomic survey sequence.//0.0042:295:62//AQ214623  
R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074  
R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346\_K10, complete sequence.//4.0e-78:498:86//AC006120  
R-PLACE1008625  
R-PLACE1008626//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297  
R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836  
R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826  
R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096  
R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001  
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333  
R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742  
R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406  
R-PLACE1008715//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147  
R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP Homo sapiens clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841  
R-PLACE1008757//Homo sapiens 12q24.2 PAC RPC14-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC005864  
R-PLACE1008790//Rattus norvegicus clonal polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GCA-triplet and GAA-triplet repeats.//0.052:108:68//U00762  
R-PLACE1008798//Homo sapiens full length insert cDNA clone Y286C05.//7.7e-58:285:100//AF086088  
R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 2366014, genomic survey sequence.//3.5e-35:223:89//AQ079210  
R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//AF030933  
R-PLACE1008813//Rattus norvegicus rsect15 mRNA, complete cds.//9.7e-45:394:78//AF032668  
R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581  
R-PLACE1008854//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//8.9e-30:166:97//B93289  
R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//AC005058  
R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-37:585:67//AC004932  
R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494\_G17, complete sequence.//0.0022:409:60//AC005820  
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308  
R-PLACE1008925//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860  
R-PLACE1008934  
R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293\_K20, complete sequence.//9.8e-84:429:92//AC005495  
R-PLACE1008947  
R-PLACE1009020  
R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) EST s, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117  
R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391  
R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117\_B12, complete sequence.//2.9e-06:160:70//AC004707  
R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694  
R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023  
R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074  
R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783  
R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206  
R-PLACE1009099  
R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025  
R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYAC88-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140  
R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//

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【表535】

7.5e-06:426:58//Z98551  
R-PLACE1009150//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929  
R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031  
R-PLACE1009158//Homo sapiens full length insert cDNA clone YP10003.//1.9e-105:539:95//AF085876  
R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180\_P\_8, complete sequence.//2.8e-44:360:71//AC005972  
R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046  
R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//AC004925  
R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//1.9e-46:572:69//Z84480  
R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070  
R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560  
R-PLACE1009200//H. sapiens mRNA for sortilin.//1.0e-31:195:92//X98248  
R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338511), complete sequence.//1.8e-75:364:85//AC005392  
R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818  
R-PLACE1009308  
R-PLACE1009319//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801  
R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346\_K\_10, complete sequence.//3.3e-87:576:85//AC006120  
R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176  
R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140  
R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989  
R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-Met, tRNA-Gln, tRNA-A-Tle and tRNA-Val.//1.1e-08:444:60//X05915  
R-PLACE1009388  
R-PLACE1009398//Homo sapiens BAC clone GS011E15 from Sq31, complete sequence.//0.065:279:61//AC002427  
R-PLACE1009404//Homo sapiens clone NHD486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038  
R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142\_H\_19, complete sequence.//9.8e-112:561:96//AC005919  
R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120  
R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598  
R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151  
R-PLACE1009459  
R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531  
R-PLACE1009477//Homo sapiens, clone hRPK.15\_A\_1, complete sequence.//3.4e-46:284:91//AC006213  
R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321  
R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SECT homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160  
R-PLACE1009539//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427  
R-PLACE1009542//CIT-HSP-2166P10, TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614  
R-PLACE1009571//RPC111-61J16, TK RPC111 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146  
R-PLACE1009581  
R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006  
R-PLACE1009596//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051  
R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230  
R-PLACE1009613//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266  
R-PLACE1009621//Sequence 50 from patent US 5591147.//1.5e-20:235:73//I76222  
R-PLACE1009622//CIT-HSP-2023D13, TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey sequence.//0.72:176:62//B81271  
R-PLACE1009637//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276  
R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project).//0.013:521:58//AL021811  
R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159  
R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075  
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534  
R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011  
R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109  
R-PLACE1009731//Homo sapiens DNA sequence from PAC 434014 on chromosome 10q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398  
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024  
R-PLACE1009794  
R-PLACE1009798//Human DNA sequence from clone 1189824 on chromosome 12q25-26.3. Contains MADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996  
R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172  
R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AC002672  
R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945  
R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//5.3e-91:577:88//AC006116  
R-PLACE1009908  
R-PLACE1009921//Homo sapiens cosmid clone HDAB (15149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005  
R-PLACE1009924//HS\_3151\_B1\_B10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412  
R-PLACE1009925//CIT978SK-A-931F6, TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673  
R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308  
R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483  
R-PLACE1009971//Homo sapiens full length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247  
R-PLACE1009992  
R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367  
R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874  
R-PLACE1010023//HS\_3018\_B1\_H10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513  
R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y6D3D.4 and one similar to (predicted) plant, worm, yeast and arc haea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4

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e-115:581:96//AL031775	R-PLACE1010616//Human BAC clone RG343P13 from Tq31, complete sequence.//3.0e-13:151:75//AC002465
R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692	R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370
R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094	R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79//AF053356
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//4.6e-87:543:88//AF065482	R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE. 21 unordered pieces.//2.3e-97:515:94//AC004846
R-PLACE1010076//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone CD473M13: HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.3e-08:489:58//AC005699	R-PLACE1010629//HS_3003_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493
R-PLACE1010083	R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382
R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.//0.14:400:59//B10583	R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102
R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411	R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089
R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556	R-PLACE1010662//Caenorhabditis elegans cosmid C12CB, complete sequence.//9.4e-09:151:73//Z81467
R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09:510:59//AE001374	R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536
R-PLACE1010106//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54820, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304	R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822
R-PLACE1010134	R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300:95//AF092564
R-PLACE1010148//HS_3128_A1_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790	R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400
R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417	R-PLACE1010743
R-PLACE1010181//Homo sapiens clone DJ0914B06, WORKING DRAFT SEQUENCE. 1 unordered pieces.//3.6e-06:207:66//AC004928	R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294.J.22, complete sequence.//3.0e-103:511:97//AC005921
R-PLACE1010194//HS_2232_B1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425	R-PLACE1010771
R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type I Cytoskeletal 18 (KRT18, CKY18, K18, CK18) pseudogene and an STS, complete sequence.//0.0003:5:383:61//AL031585	R-PLACE1010786
R-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377	R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE. 30 unordered pieces.//1.8e-43:545:71//AC005682
R-PLACE1010261	R-PLACE1010802//Phoebeis sgarithe large subunit ribosomal RNA gene, partial sequence: tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492:59//AF044862
R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, clone 85a6, reverse read cp85a6.r11a.//0.068:171:63//Z63482	R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524
R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280	R-PLACE1010833
R-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464	R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153
R-PLACE1010321	R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//4.9e-85:507:90//AB020868
R-PLACE1010324//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149	R-PLACE1010870//RPC111-59K21.TK RPC111 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697
R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 in IGLC Region, complete sequence.//7.9e-35:328:79//AC000024	R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182
R-PLACE1010341//Homo sapiens clone DJ125K23, WORKING DRAFT SEQUENCE. 21 unordered pieces.//1.3e-31:418:66//AC004971	R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489
R-PLACE1010362	R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505
R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098	R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488
R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.185.H.2, complete sequence.//1.4e-105:543:95//AC004675	R-PLACE1010916//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557
R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137	R-PLACE1010917
R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927	R-PLACE1010925//HS_2027_B2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081	R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126
R-PLACE1010492//HS_3169_B2_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892	R-PLACE1010942//Homo sapiens intersexin short form mRNA, complete cds.//1.9e-80:441:93//AF064243
R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082	R-PLACE1010944
R-PLACE1010547	R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533
R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929	R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077
R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein var1.//1.7e-05:271:65//X02893	R-PLACE1010960//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522
R-PLACE1010580	R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444:84//U52077
R-PLACE1010599	

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【表537】

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.59:345:61//AJ235272  
 R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242  
 R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248  
 R-PLACE1011046//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153  
 R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region on chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483  
 R-PLACE1011056//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985  
 R-PLACE1011057//CIT-HSP-2014F10, TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896  
 R-PLACE1011090//Homo sapiens chromosome 4 clone B200MS map 4q25, complete sequence.//0.12:489:59//AC005509  
 R-PLACE101109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531  
 R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone h11-14).//1.7e-29:179:94//Y16709  
 R-PLACE1011133//HS-1058-B1-H02-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//B44006  
 R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127A4, forward read cpg127A4.ftla.//1.0:127:67//Z56550  
 R-PLACE1011160//Homo sapiens HRHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333  
 R-PLACE1011165//Human Cosmid g5129s232 from Tq31.3, complete sequence.//0.47:355:58//AC003968  
 R-PLACE1011185//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820  
 R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//X00908  
 R-PLACE1011219//HS\_3036\_B1\_F08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587  
 R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659  
 R-PLACE1011229//HS\_3002\_B1\_E10\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626  
 R-PLACE1011263//Homo sapiens BAC clone GS166A23 from Tp21, complete sequence.//1.2e-109:571:94//AC005014  
 R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COX1) gene, complete cds.//0.00027:337:61//M97514  
 R-PLACE1011291  
 R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887  
 R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661  
 R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.0e-10:511:59//AE001398  
 R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344  
 R-PLACE1011340//Human BAC clone RG341D10 from Tpl5-p21, complete sequence.//0.67:290:58//AC002530  
 R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310  
 R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140  
 R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022  
 R-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102  
 R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013  
 R-PLACE1011465  
 R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255  
 R-PLACE1011492//A-837A4, TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085  
 R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171\_1\_10, complete sequence.//0.99:267:60//AC004657  
 R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968  
 R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYACB9 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688  
 R-PLACE1011567//Plasmodium falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551  
 R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973  
 R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477  
 R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463  
 R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205  
 R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620  
 R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535  
 R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477  
 R-PLACE1011664//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905  
 R-PLACE1011675//CIT-HSP-2370M16, TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283  
 R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776  
 R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806  
 R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526  
 R-PLACE1011729//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345  
 R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089  
 R-PLACE1011762//Homo sapiens BAC clone RG067E13 from Tq21, complete sequence.//1.9e-35:538:68//AC002383  
 R-PLACE1011778//CIT-HSP-2326C17, TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782  
 R-PLACE1011783//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090  
 R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321  
 R-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.1e-100:511:95//AC004478  
 R-PLACE1011875  
 R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193  
 R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398  
 R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090  
 R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617  
 R-PLACE1011962//CIT-HSP-2294L24, TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352  
 R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994  
 R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889  
 R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738  
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256  
 R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000  
 R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524:95//AF091080  
 R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191  
 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162\_E\_12, complete sequence.//3.0e-55:299:86//AC006236  
 R-PLACE2000021//CIT-HSP-2343C18, TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey sequence.//4.5e-54:295:94//AQ058140

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## 【表538】

R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (PI form).//6.5e-38:298.82//X69907  
 R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-34:200.79//AC005628  
 R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274.89//AC003083  
 R-PLACE2000047//CIT-HSP-2373C2. TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey sequence.//1.8e-48:389.79//AQ112243  
 R-PLACE2000050//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 117715, WORKING DRAFT SEQUENCE.//0.0027:95.76//AL022315  
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429.72//AB011147  
 R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.9e-40:310.84//AC004832  
 R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550.95//AF027219  
 R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189N2 O, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553.95//AC005910  
 R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285.84//AL031730  
 R-PLACE2000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559.97//AL031848  
 R-PLACE2000111//Rat MLCIV gene encoding alkali myosin ventricular light chain, exon 1.//0.00041:347.61//X16325  
 R-PLACE2000115//Carvus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165.63//U63067  
 R-PLACE2000132  
 R-PLACE2000136//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from contig 3-30, complete sequence.//0.0032:310.61//AL008974  
 R-PLACE2000140//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 11703, WORKING DRAFT SEQUENCE.//1.1e-111:566.96//AL020995  
 R-PLACE2000164  
 R-PLACE2000170//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0024K08: HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390.76//AC005598  
 R-PLACE2000172  
 R-PLACE2000176  
 R-PLACE2000187//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//8.7e-45:298.87//AL008718  
 R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495.92//L02897  
 R-PLACE2000223  
 R-PLACE2000235//HS\_3159\_B1\_806\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3159 Col=11 Row=0, genomic survey sequence.//1.8e-88:454.96//AQ179271  
 R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//9.1e-41:282.86//AC005990  
 R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305.80//Z97181  
 R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325.67//AC002394  
 R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287.85//AC003043  
 R-PLACE2000305//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 16915, WORKING DRAFT SEQUENCE.//1.2e-43:295.85//Z93015  
 R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tsp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the R31 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284.65//Z92542  
 R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334.70//AC006147  
 R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGF1, TH, NAP2 genes.//4.0e-05:254.64//AL021880  
 R-PLACE2000347//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504.88//AL022147  
 R-PLACE2000359//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314.80//AL031963  
 R-PLACE2000366//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389.80//AL031291  
 R-PLACE2000371  
 R-PLACE2000373//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231.61//AL008734  
 R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287.67//AC004917  
 R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG island s, complete sequence.//6.8e-108:553.96//AL031432  
 R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326.73//AC005059  
 R-PLACE2000399  
 R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBML H192), complete sequence.//6.5e-84:434.96//AC005216  
 R-PLACE2000411//P.clarkii mRNA: repeat region (10 2R).//0.47:104.70//Z54273  
 R-PLACE2000419  
 R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447.74//AF003528  
 R-PLACE2000427  
 R-PLACE2000433//Human Chromosome 15 pac pD24m8, complete sequence.//3.5e-40:286.85//AC000379  
 R-PLACE2000435  
 R-PLACE2000438//Homo sapiens full length insert cDNA clone ZE04D01.//2.2e-107:523.98//AF086521  
 R-PLACE2000450  
 4.1e-42:328.79//AC006257  
 R-PLACE2000455  
 R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBML H154), complete sequence.//5.1e-116:570.97//AC005740  
 R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408.75//AC002460  
 R-PLACE2000477//M.musculus tex264 mRNA (3' region).//7.5e-06:117.76//X80427  
 R-PLACE3000004  
 R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308.78//Z82976  
 R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273.81//Y17267  
 R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBML H148), complete sequence.//2.3e-10:181.71//AC004648  
 R-PLACE3000103//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495.74//AL022156  
 R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283.85//AC00026  
 R-PLACE3000124//Homo sapiens chromosome 5, PI clone 793c5 (LBML HS7), complete sequence.//9.2e-23:171.76//AC005200  
 R-PLACE3000135//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171.65//Y09645  
 R-PLACE3000142//HS\_3037\_B2\_802\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=0, genomic survey sequence.//0.88:121.66//AQ097023  
 R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472.66//AB001735  
 R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176.73//Z49237  
 R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597\_M\_12, complete sequence.//6.9e-106:549.94//AC005277  
 R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545.70//AC002383  
 R-PLACE3000157  
 R-PLACE3000158//, complete sequence.//1.4e-33:283.81//AC005500  
 R-PLACE3000160  
 R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229.85//AC006130  
 R-PLACE3000194  
 R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401\_0\_9, complete sequence.//7.2e-61:394.89//AC005291  
 R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.//

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0.23:309:57//US2112  
 R-PLACE3000207//CIT-HSP-384B14. TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//1.1e-15:156:81//B54637  
 R-PLACE3000208//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 591N18, WORKING DRAFT SEQUENCE.//1.3e-16:139:87//AL031594  
 R-PLACE3000218//HS\_3185\_B1\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120:75//AQ155720  
 R-PLACE3000220//Homo sapiens chromosome 17, clone HRP1096F1, complete sequence.//2.4e-44:363:80//AC004167  
 R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF078786  
 R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-69:536:81//U95626  
 R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//J35489  
 R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80169  
 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-20:174:94//AB002307  
 R-PLACE3000271//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 423B22, WORKING DRAFT SEQUENCE.//3.9e-54:492:77//AL034379  
 R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176:69//AC004081  
 R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555:97//AC005328  
 R-PLACE3000310//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 467L1, WORKING DRAFT SEQUENCE.//6.2e-51:314:84//Z98884  
 R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-44:289:90//U93037  
 R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153:88//M21006  
 R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-43:230:84//AC005480  
 R-PLACE3000339  
 R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Rosweil Park Cancer Institute Human PAC Library) complete sequence.//2.5e-111:550:97//AC006055  
 R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.5e-44:314:78//AL022323  
 R-PLACE3000352//HS\_3095\_B1\_E09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356:99//AQ123142  
 R-PLACE3000353//Caenorhabditis elegans DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y22F5, WORKING DRAFT SEQUENCE.//0.21:194:63//Z99712  
 R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360:60//AJ002197  
 R-PLACE3000363  
 R-PLACE3000365//Human BAC clone RG343P13 from Tq31, complete sequence.//4.6e-52:487:76//AC002465  
 R-PLACE3000373//HS\_3202\_B1\_G05\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437:90//AQ252699  
 R-PLACE3000388//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 732E4, WORKING DRAFT SEQUENCE.//6.4e-61:515:81//AL008722  
 R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00098:444:60//AC005231  
 R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506  
 R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//8.0e-47:223:81//AC006023  
 R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003  
 R-PLACE3000405//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//2.4e-44:466:74//AF104455  
 R-PLACE3000406//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718  
 R-PLACE3000413  
 R-PLACE3000416//Homo sapiens \*\*\* SEQUENCING IN PROGRESS \*\*\* from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612  
 R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudogene, ESTs and STS  
 s.//1.1e-41:366:78//AL008627  
 R-PLACE3000455//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284  
 R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43899  
 R-PLACE3000477  
 R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to Heymann nephritis antigen gp330.//6.6e-17:344:68//Z11995  
 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352  
 R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984  
 R-PLACE4000049//Human BAC clone GS165I04 from Tq21, complete sequence.//0.29:313:59//AC002379  
 R-PLACE4000052//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557  
 R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356  
 R-PLACE4000089//RPC111-1511.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-1511, genomic survey sequence.//3.2e-07:284:60//B82414  
 R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506  
 R-PLACE4000100  
 R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010  
 R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.5e-45:284:90//AC003007  
 R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969  
 R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034  
 R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939  
 R-PLACE4000192  
 R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631  
 R-PLACE4000233//Homo sapiens full length insert cDNA YHS9C06.//1.8e-79:414:97//AF074981  
 R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156\_L14, complete sequence.//5.7e-59:558:76//AC005821  
 R-PLACE4000250//CIT-HSP-2335L20. TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381  
 R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700\_H6, complete sequence.//1.5e-39:311:83//AC005920  
 R-PLACE4000261//H. sapiens BF1P-gIH03np gene for immunoglobulin heavy chain variable region.//0.33:197:61//Z80410  
 R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327:68//AC005510  
 R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675  
 R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339  
 R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//8.2e-41:295:85//Z99495  
 R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640  
 R-PLACE4000326  
 R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from Tq33-q35, complete sequence.//0.32:135:68//AC005587  
 R-PLACE4000367//H. sapiens gene encoding RING finger protein.//0.61:146:67//Y07829  
 R-PLACE4000369//HS\_3181\_A1\_B02\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222  
 R-PLACE4000379//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312  
 R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913  
 R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377  
 R-PLACE4000401//Human Chromosome 11 overlapping pacs pD1235k10 and

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pDJ239b22, WORKING DRAFT SEQUENCE. 17 unordered pieces. //2.7e-17:143.83//AC000406  
 R-PLACE4000411  
 R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE. 4 unordered pieces. //0.028:91.78//AC005628  
 R-PLACE4000465//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30A23, WORKING DRAFT SEQUENCE. //1.6e-43:532.71//AL02156  
 R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence. //4.1e-06:357.61//AE001427  
 R-PLACE4000494//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //2.7e-37:416.74//AC005865  
 R-PLACE4000522  
 R-PLACE4000548//Homo sapiens 12p13.3 PAC RPC15-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //0.0020:383.60//AC005342  
 R-PLACE4000558//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence. //2.9e-44:465.75//AC002996  
 R-THYR01000026//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16, WORKING DRAFT SEQUENCE. //2.2e-43:354.82//Z83844  
 R-THYR01000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence. //0.022:327.50//AE001422  
 R-THYR01000035//HS\_3018\_B2\_F10\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence. //2.3e-36:228.91//AQ092318  
 R-THYR01000040//Plasmodium falciparum 307 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE. 9 unordered pieces. //1.0:367.56//AC004157  
 R-THYR01000070//\*\*\*ALU WARNING: Human Alu-Sq subfamily consensus sequence. //1.1e-44:284.89//U14573  
 R-THYR01000072//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence. //6.6e-33:150.83//U14567  
 R-THYR01000085  
 R-THYR01000092//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence. //3.3e-36:301.78//AF104455  
 R-THYR01000107//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 12513, WORKING DRAFT SEQUENCE. //1.4e-35:282.82//AL033528  
 R-THYR01000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence. //4.0e-32:351.65//AC002300  
 R-THYR01000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence. //6.6e-77:507.85//U91318  
 R-THYR01000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE. 1 ordered pieces. //0.66:334.59//AC005840  
 R-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds. //2.3e-88:449.96//AF087142  
 R-THYR01000132//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 212A2, WORKING DRAFT SEQUENCE. //1.1e-40:298.84//Z95114  
 R-THYR01000156//Homo sapiens chromosome 17, clone hRPK.849\_M\_15, complete sequence. //3.4e-37:425.73//AC005703  
 R-THYR01000163//RPC111-1820.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-1820, genomic survey sequence. //8.4e-38:276.84//B63536  
 R-THYR01000173//Human DNA sequence from PAC 32386 on chromosome X contains ESTs CpG island. //1.1e-70:553.81//Z83841  
 R-THYR01000186//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 41018, WORKING DRAFT SEQUENCE. //6.7e-41:345.81//AL031732  
 R-THYR01000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta. //1.3e-43:356.80//U18271  
 R-THYR01000190//Homo sapiens chromosome 17, clone HRPC84389, complete sequence. //2.6e-40:386.77//AC004139  
 R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease. //1.1e-108:535.97//AJ005698  
 R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds. //1.4e-113:559.97//AB014552  
 R-THYR01000206//Rat PMSC-induced ovarian mRNA, 3' sequence, N4. //4.0e-43:318.86//D84482  
 R-THYR01000221//Human DNA from overlapping chromosome 19 cosmid R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence. //2.7e-44:452.76//AC002115  
 R-THYR01000241//Homo sapiens Cosmid Clone p129d11 unknown chromosome location, complete sequence. //4.8e-58:447.81//AC000039  
 R-THYR01000242  
 R-THYR01000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence. //3.4e-56:300.84//Z95152  
 R-THYR01000270  
 R-THYR01000279//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 531H16, WORKING DRAFT SEQUENCE. //4.8e-113:584.96//AL031664  
 R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds. //1.1e-98:566.91//AB016068  
 R-THYR01000320//HS\_2033\_B1\_A07\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=8, genomic survey sequence. //0.97:211.63//AQ233366  
 R-THYR01000327//Sequence 1 from patent US 5541298. //2.8e-52:289.93//I24058  
 R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds. //1.1e-111:559.96//AB018333  
 R-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds. //4.6e-47:317.87//U29091  
 R-THYR01000368//HS\_3049\_A1\_E12\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=1, genomic survey sequence. //7.0e-11:111.83//AQ126777  
 R-THYR01000381  
 R-THYR01000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence. //2.4e-101:545.93//AC006019  
 R-THYR01000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE. 11 unordered pieces. //1.6e-46:233.88//AC006078  
 R-THYR01000395//Mouse MIPP mRNA for a placenta-expressed gene. //2.3e-57:395.85//X58523  
 R-THYR01000401  
 3.3e-111:546.97//AF051907  
 R-THYR01000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE. 6 unordered pieces. //2.7e-44:289.89//AC005231  
 R-THYR01000452//Homo sapiens chromosome 17, clone hRPK.243\_K\_12, complete sequence. //6.7e-27:222.82//AC005668  
 R-THYR01000471//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 102D24, WORKING DRAFT SEQUENCE. //2.4e-36:369.76//AL021391  
 R-THYR01000484//Homo sapiens clone DJ1099N07, complete sequence. //1.6e-43:288.81//AC004962  
 R-THYR01000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. //1.1e-95:512.94//AC005740  
 R-THYR01000501//HS\_2208\_A1\_G11\_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence. //0.0063:189.63//AQ091586  
 R-THYR01000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds. //0.19:468.60//AF000987  
 R-THYR01000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence. //0.20:214.58//AC004798  
 R-THYR01000558  
 R-THYR01000569  
 R-THYR01000570//Homo sapiens full length insert cDNA clone ZD76G10. //4.3e-41:209.100//AF086408  
 R-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds. //8.2e-107:533.97//AF075587  
 R-THYR01000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds. //0.36:170.67//AF006072  
 R-THYR01000602//Homo sapiens DNA for amyloid precursor protein, complete cds. //2.2e-53:289.92//D87675  
 R-THYR01000605  
 R-THYR01000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence. //1.3e-31:261.82//AC005546  
 R-THYR01000637//Human DNA sequence from clone Z43E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence. //4.0e-06:249.63//AL022323  
 R-THYR01000641//P. falciparum glutamic acid-rich protein gnen, complete cds. //3.1e-08:244.68//J03998  
 R-THYR01000658//\*\*\*ALU WARNING: Human Alu-Sp subfamily consensus sequence. //3.9e-49:282.93//U14572  
 R-THYR01000662  
 R-THYR01000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence. //1.9e-20:215.77//AL031005  
 R-THYR01000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence. //1.2e-06:227.64//AC004069  
 R-THYR01000684  
 R-THYR01000699  
 R-THYR01000712  
 R-THYR01000734//Human BAC clone RG191D16, complete sequence. //3.7



【表541】

e-14:468:64//AC002460  
 R-THYR01000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533  
 R-THYR01000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//125660  
 R-THYR01000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558  
 R-THYR01000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey sequence.//1.2e-81:391:99//AQ038226  
 R-THYR01000787//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//9.4e-07:494:58//AC004617  
 R-THYR01000793  
 R-THYR01000796//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014  
 R-THYR01000805//Human Chromosome 11 pac pDJ610:20, WORKING DRAFT SEQUENCE, 18 unordered pieces.//4.7e-40:362:76//AC002555  
 R-THYR01000815//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199  
 R-THYR01000829//Sequence 7 from patent US 5716622.//0.97:362:61//187788  
 R-THYR01000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-57:522:76//AC004738  
 R-THYR01000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849  
 R-THYR01000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592  
 R-THYR01000865//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549  
 R-THYR01000895//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719  
 R-THYR01000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0e-97:554:92//AC006015  
 R-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:566:94//AF079529  
 R-THYR01000934//Homo sapiens full length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378  
 R-THYR01000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//8.9e-61:479:81//AC004229  
 R-THYR01000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639  
 R-THYR01000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//AF047440  
 R-THYR01000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//AC006126  
 R-THYR01000983//Homo sapiens chromosome 17, clone hRPK.271\_K\_11, complete sequence.//0.99:71:78//AC005562  
 R-THYR01000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078  
 R-THYR01000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466  
 R-THYR01001003//HS\_3051\_B1\_H01\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727  
 R-THYR01001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466  
 R-THYR01001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677  
 R-THYR01001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882  
 R-THYR01001093  
 R-THYR01001100//Homo sapiens BAC clone RC152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070  
 R-THYR01001120  
 R-THYR01001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417  
 R-THYR01001133//CIT-HSP-2381110.TR CIT-HSP Homo sapiens genomic clone 2381110, genomic survey sequence.//4.7e-12:237:67//AQ111077  
 R-THYR01001134  
 R-THYR01001142//H. sapiens CpG island DNA genomic MseI fragment, clone 81d1, reverse read cpg81d1.rta.//0.95:214:60//Z56037  
 R-THYR01001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145  
 R-THYR01001177  
 R-THYR01001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973  
 R-THYR01001204  
 R-THYR01001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581  
 R-THYR01001262//Homo sapiens, clone hRPK.16\_A\_1, complete sequence.//8.7e-53:442:79//AC006227  
 R-THYR01001271//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0224P12: HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630  
 R-THYR01001290  
 R-THYR01001313//H. sapiens CpG island DNA genomic MseI fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783  
 R-THYR01001320//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207  
 R-THYR01001321//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558  
 R-THYR01001322  
 R-THYR01001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288  
 R-THYR01001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884  
 R-THYR01001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660  
 R-THYR01001374  
 R-THYR01001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953  
 R-THYR01001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377  
 R-THYR01001405  
 R-THYR01001406//RPC111-69F22.TX RPC111 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297  
 R-THYR01001411//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123  
 R-THYR01001426//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens genomic DNA (PAC 111B:22) from chromosome 11: HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553  
 R-THYR01001434//Microcentus carayae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877  
 R-THYR01001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578  
 R-THYR01001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-99:517:95//AC006001  
 R-THYR01001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085  
 R-THYR01001534//HS\_2242\_B2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326  
 R-THYR01001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876  
 R-THYR01001541//Homo sapiens clone RC228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077  
 R-THYR01001559//Homo sapiens 12q24.2 PAC RPC15-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868  
 R-THYR01001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308  
 R-THYR01001573//M. avium rpsL gene.//0.98:131:66//X80120  
 R-THYR01001584//A. longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653  
 R-THYR01001595//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808  
 R-THYR01001602//Homo sapiens chromosome 17, clone hRPK.142\_H\_9, complete sequence.//4.4e-13:320:67//AC005919  
 R-THYR01001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249  
 R-THYR01001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190  
 R-THYR01001637//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

【表542】

R-THYR01001656//HS\_2201\_B2\_A08\_WF CIT Approved Human Genomic Spem Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=8, genomic survey sequence.//0.096:162:63//AQ293168

R-THYR01001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

R-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089

R-THYR01001673//CIT-HSP-2327D12, TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426

R-THYR01001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

R-THYR01001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYR01001721//, complete sequence.//1.3e-101:571:92//AC005500

R-THYR01001738

R-THYR01001745//Homo sapiens chromosome 5, PAC clone 24713 (LBML H 85), complete sequence.//1.1e-15:193:70//AC004777

R-THYR01001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244

R-THYR01001772//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 30423, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYR01001793

R-THYR01001809//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYR01001854//Homo sapiens chromosome 17, clone hRPK\_74\_E\_22, complete sequence.//5.0e-41:245:87//AC005696

R-THYR01001895//Human Chromosome 11p14.3 PAC clone 6-106123, complete sequence.//4.4e-12:419:61//AC005137

R-THYR01001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b 1 n DCCR Region, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF09368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3, TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000058//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-27 9B10, complete sequence.//6.1e-56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D021079

R-Y79AA1000131//\*\*\* SEQUENCING IN PROGRESS \*\*\* Homo sapiens chromosome 4, BAC clone C0548N01: HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 10q24-25.3 Contains exon from gene similar to 40S ribosomal protein n, first coding exon of dynamin 2 (DYNM1). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2, TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cytoskeleton felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS\_3009\_A1\_H03\_T7 CIT Approved Human Genomic Spem Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=0, genomic survey sequence.//6.4e-52:348:88//AQ090225

R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 2 2. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047

R-Y79AA1000313//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540

R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692

R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, V74 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPC111-16B12, TPB RPC111 Homo sapiens genomic clone RPC111-16B12, genomic survey sequence.//0.10:171:65//B88000

R-Y79AA1000410//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037

R-Y79AA1000469//Homo sapiens clone NHO140K04, complete sequence.//1.8e-86:221:90//AC005033

R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282

R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59//AC006143

R-Y79AA1000540//Z.diploperennis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 2384, complete sequence.//0.96:224:61//AC002325

R-Y79AA1000627//Homo sapiens full length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117

R-Y79AA1000705//RPC111-76G7, TV RPC111 Homo sapiens genomic clone R-76G7, genomic survey sequence.//4.6e-88:429:98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11) b mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24, TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-7:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3' region).//1.1e-06:104:78//X80427

R-Y79AA1000802//CIT-HSP-2295G6, TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30H11, complete sequence.//3.1e-26:423:68//U73642

R-Y79AA1000824//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

R-Y79AA1000962//CIT-HSP-2298N11, TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4, TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey sequence.//3.3e-60:295:100//AQ061422

R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823

R-Y79AA1001023

R-Y79AA1001041

R-Y79AA1001048

R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-42 7H10, complete sequence.//1.2e-60:537:78//AC004626

R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.3e-41:405:77//AC005031

R-Y79AA1001077

R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPC111-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801

R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639.//0.0072:309:63//U40259

R-Y79AA1001145//RPC111-59N12, TK RPC111 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068

R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012

R-Y79AA1001177//Human gene for G13 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048

R-Y79AA1001185

【0843】

【表543】

R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPC111-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-3 2:277:81//AC005912

R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924

R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112

R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110113307 (RZPD Berlin)).//3.4e-109:549:95//AJ005892

R-Y79AA1001281

R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126

R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372

R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355

R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.07 0:209:65//X66594

R-Y79AA1001391//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MALIP2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745

R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R2914, complete sequence.//0.99:241:63//AC004221

R-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924

R-Y79AA1001493

R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.3e-35:207:95//AL034430

R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336

R-Y79AA1001541//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574

R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151

R-Y79AA1001555

R-Y79AA1001585

R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X: contains STS.//6.6e-19:241:76//Z94722

R-Y79AA1001603//H. sapiens CpG island DNA genomic MseI fragment, clone 72f8, forward read cp972f8.f1ta.//3.3e-21:131:96//Z62766

R-Y79AA1001613

R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975

R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008

R-Y79AA1001679//O. cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//W22743

R-Y79AA1001692//RPC111-42M5.TJ RPC111 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792

R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178

R-Y79AA1001705

R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139

R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402

R-Y79AA1001805//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone S10011, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044

R-Y79AA1001827//Dryctolagus cuniculus PIUS mRNA, complete cds.//2.3e-90:557:89//U74297

R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152

R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369

R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K23L20, complete sequence.//0.0089:527:58//AB016874

R-Y79AA1001874

R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577

R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377:81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612

R-Y79AA1002103//CIT-HSP-232B121.TR CIT-HSP Homo sapiens genomic clone 232B121, genomic survey sequence.//1.9e-44:245:96//AQ044502

R-Y79AA1002115//CITBI-EI-2514F10.TF CITBI-EI Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752

R-Y79AA1002125//RPC111-15J6.TV RPC111 Homo sapiens genomic clone RPC111-15J6, genomic survey sequence.//8.5e-21:147:91//B75354

R-Y79AA1002139

R-Y79AA1002204

R-Y79AA1002208//Human ankyrin G (ANK-3) mRNA, complete cds.//0.04 0:319:59//U13616

R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4).//0.99:106:65//X65415

R-Y79AA1002210

R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133

R-Y79AA1002220//Plasmodium falciparum DNA \*\*\* SEQUENCING IN PROGRESS \*\*\* from MAL4P1, WORKING DRAFT SEQUENCE.//5.9e-07:535:57//AL034557

R-Y79AA1002229

R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592

R-Y79AA1002246

R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-9 2:453:97//AB013384

R-Y79AA1002298//HS\_3071\_B2\_E08\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331

R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534

R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173112 map 10q25, complete sequence.//1.1e-07:368:61//AC005887

R-Y79AA1002351

R-Y79AA1002361//H. sapiens CpG island DNA genomic MseI fragment, clone 65b9, reverse read cp965b9.r1ta.//0.57:59:79//Z62206

R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPC.700\_H\_6, complete sequence.//2.0e-98:385:99//AC005920

R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842\_A\_23, complete sequence.//5.4e-59:490:76//AC004662

R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//6.3e-08:103:80//AC004087

R-Y79AA1002431

R-Y79AA1002433//Mouse transcriptional control element.//0.064:84:71//M17284

R-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC30 1323), complete sequence.//1.6e-103:525:96//AC006116

R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPC.474\_M\_24, complete sequence.//9.7e-38:302:83//AC006238

R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

【0844】

5'末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのTitle、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

【0845】

【表544】

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069	F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398
F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:L40157	F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893
F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668	F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:A1032875
F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078	F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590
F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:A1253247	F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853
F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]//0.00019:192:65//Hs.7900:W22411	F-HEMBA1000469
F-HEMBA1000050//EST//0.81:74:72//Hs.156298:A1336759	F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBII) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:A1417910	F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734	F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970
F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:342:61//Hs.14207:U86453	F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:AB018340	F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:D13666
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200	F-HEMBA1000505//Homo sapiens KED4p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093
F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//Hs.135552:A1215187	F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646
F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309	F-HEMBA1000518
F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079	F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:A1281881
F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [H.sapiens]//1.3e-18:111:96//Hs.163863:W28729	F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//2.9e-16:132:84//Hs.155871:AA533783
F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802	F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN P8513 [Mus musculus]//2.1e-25:192:87//Hs.22383:R51067
F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:A1240133	F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:AA455706
F-HEMBA1000201//Human nail mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847	F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080
F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529	F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809
F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984	F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389
F-HEMBA1000227//Human RNA-binding protein CUG-BP/hnab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289	F-HEMBA1000545//Human kni repeat mRNA (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:K00629
F-HEMBA1000231	F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684
F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377	F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729
F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703	F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:AB018303
F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460	F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:A1338977
F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562	F-HEMBA1000568//EST//0.12:270:61//Hs.134833:A1091046
F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568	F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042
F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186	F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681
F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406	F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C.elegans]//7.7e-41:217:96//Hs.55084:AA479162
F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664	F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:AJ007509
F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:A1206095	F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7e-27:463:65//Hs.13794:AA203241
F-HEMBA1000303	F-HEMBA1000594//Human clone 230971 defective mariner transposon Hs mar2 mRNA sequence//4.0e-68:574:79//Hs.159176:U92019
F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946	F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:A1092535
F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:A1124898	F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925
F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965	F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333
F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961	F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//7.4e-22:166:84//Hs.26252:AA643235
F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712	F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:AB014590
F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frame s//0.020:334:59//Hs.23094:M19503	F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174
F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548	F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582
F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802	F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:A1123912
F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087	F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073
F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010	F-HEMBA1000687//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878
F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853	F-HEMBA1000688
F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878	F-HEMBA1000702
F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320	F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309
F-HEMBA1000390//Homo sapiens BAC clone RGT19C02 from Tp15//2.3e-141:712:95//Hs.22900:AC004520	F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:A1039850
F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533	F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:M92630
F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008	F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:A1281881
F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915	F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491
F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:A1079253	F-HEMBA1000747
F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875	F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:A1091568
F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.158897:AB007970	F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:HS2716
F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034	F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239

【0846】

【表545】

F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803  
 F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA35216  
 F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300  
 F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536  
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542  
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367  
 F-HEMBA1000843  
 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962  
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572  
 F-HEMBA1000867  
 F-HEMBA1000869//ESTs//5.1e-33:166:77//Hs.141186:R99609  
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:A1367237  
 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047  
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660  
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:A1203154  
 F-HEMBA1000910//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain L1KE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:298046  
 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537  
 F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142  
 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119  
 F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596  
 F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:AA609476  
 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199  
 F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369  
 F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161  
 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:A1127903  
 F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775  
 F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314  
 F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGK $\iota$ ) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936  
 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.127338:AB007961  
 F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132  
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895  
 F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835  
 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984  
 F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529  
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:AB007937  
 F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:A1239572  
 F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238  
 F-HEMBA1001022  
 F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970  
 F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142  
 F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515  
 F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:A1281881  
 F-HEMBA1001052//EST//0.94:149:67//Hs.131216:A1017971  
 F-HEMBA1001059//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:U06088  
 F-HEMBA1001060//EST//6.8e-14:150:78//Hs.24821:AA044813  
 F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420  
 F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//Hs.147802:R71297  
 F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172  
 F-HEMBA1001085//Human hSAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248  
 F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284  
 F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017  
 F-HEMBA1001099

F-HEMBA1001109//Homo sapiens tapasin (MCS-17) mRNA, complete cds//2.4e-61:341:85//Hs.5247:AF029750  
 F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497  
 F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940  
 F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917  
 F-HEMBA1001133//EST//0.50:222:63//Hs.131018:A1015747  
 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341  
 F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582  
 F-HEMBA1001172//EST//0.77:158:60//Hs.158894:A1378457  
 F-HEMBA1001174//ESTs//1.4e-63:363:92//Hs.132798:AA922226  
 F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499  
 F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:A1183463  
 F-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717  
 F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:A1369694  
 F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748  
 F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:A1084058  
 F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046  
 F-HEMBA1001265  
 F-HEMBA1001281  
 F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155  
 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69 G12//5.1e-30:530:64//Hs.154050:AC004131  
 F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741  
 F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219  
 F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:A1129590  
 F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201  
 F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:M55873  
 F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301  
 F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861  
 F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:A1073427  
 F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013  
 F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569  
 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358  
 F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794  
 F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:A1198074  
 F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:M62156  
 F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353  
 F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848  
 F-HEMBA1001388  
 F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:M41660  
 F-HEMBA1001398  
 F-HEMBA1001405//EST//1.0:135:63//Hs.146833:A1151117  
 F-HEMBA1001407//ESTs//0.53:190:57//Hs.150447:A1017798  
 F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:A1253108  
 F-HEMBA1001413  
 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:A1051605  
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040  
 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:A1025726  
 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053  
 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031  
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:AA573499  
 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIP1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666  
 F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107  
 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412  
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390  
 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144  
 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:A1365451

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F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219	8:60//Hs.6151:D87078
F-HEMBA1001510//H. sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054	F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293
F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frame s//4.5e-105:773:82//Hs.23094:M19503	F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324
F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902	F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:AB014517
F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:A1376869	F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121
F-HEMBA1001526	F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN G LUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:A1141922
F-HEMBA1001533//EST//1.0:75:73//Hs.145360:A1252476	F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036
F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580	F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.158095:AB007953
F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652	F-HEMBA1001896
F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205	F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346
F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814	F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:A1312633
F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP) //7.0e-175:678:99//Hs.159597:AJ012449	F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC 50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302
F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184	F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511
F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:A1357228	F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141
F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988	F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145
F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918	F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:A1377295
F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210	F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221
F-HEMBA1001620//ESTs//1.1e-39:211:98//Hs.131063:A1016400	F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:A1219882
F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:A1361870	F-HEMBA1001945//EST//0.98:142:64//Hs.161540:M85943
F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H. sapiens]//0.038:198:64//Hs.34579:A1338536	F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360
F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899	F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MB02 (MB02) mRNA, complete cds//0.30:85:69//Hs.25674:AF072242
F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204	F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930
F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560	F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708
F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283	F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (pre-sumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178
F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121	F-HEMBA1001979//ESTs//0.85:184:67//Hs.77208:AA044732
F-HEMBA1001661	F-HEMBA1001987//ESTs, Moderately similar to hTAF1168 [H. sapiens]//2.8e-29:151:100//Hs.124106:AA948100
F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MB03 (MB03) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943	F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581
F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.158095:AB007953	F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis: keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487
F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788	F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582
F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060	F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426
F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760	F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907
F-HEMBA1001709//EST//0.85:131:65//Hs.131451:A1023995	F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:A1049827
F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:A1302836	F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057
F-HEMBA1001712//EST//0.26:214:59//Hs.159088:A1383114	F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H. sapiens]//4.5e-26:223:81//Hs.105292:AA504776
F-HEMBA1001714//ESTs, Highly similar to ATPASE IMH1B1TOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//3.0e-30:195:92//Hs.132948:AA194452	F-HEMBA1002084
F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554	F-HEMBA1002092
F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197	F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF 1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832
F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:A1028363	F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:A1190276
F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:A1000415	F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:A1129973
F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:A1052250	F-HEMBA1002119
F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924	F-HEMBA1002125//H. sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802
F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328	F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393
F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens]//0.76:218:60//Hs.135553:M41598	F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:U86980
F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622	F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263
F-HEMBA1001784//Homo sapiens mRNA for KIAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:AB007943	F-HEMBA1002151
F-HEMBA1001791	F-HEMBA1002153//EST//0.014:328:60//Hs.149115:A1244695
F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570	F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976
F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817	F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965
F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.1e-07:439:59//Hs.266:U06233	F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590
F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.5e-175:809:98//Hs.118164:AB007969	F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219
F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305	
F-HEMBA1001815	
F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.158174:U66561	
F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845	
F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:AF064244	
F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:AF071309	
F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:28	

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F-HEMBA1002177/Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245	s.79385:U90905
F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141	F-HEMBA1002569/Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587
F-HEMBA1002189//EST//5.1e-24:193:81//Hs.163161:AA778363	F-HEMBA1002583/Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132
F-HEMBA1002191/Homo sapiens mRNA for KIAA0589 protein, partial cds//0.27:382:59//Hs.21992:AB014589	F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159
F-HEMBA1002199/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.158897:AB007970	F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363
F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696	F-HEMBA1002609/Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169
F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767	F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013
F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281	F-HEMBA1002624/Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351
F-HEMBA1002226/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957	F-HEMBA1002628/Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334
F-HEMBA1002229/Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394	F-HEMBA1002629/Human density enhanced phosphatase-1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886
F-HEMBA1002237//EST//0.044:137:66//Hs.144448:AA812455	F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390
F-HEMBA1002241	F-HEMBA1002651
F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887	F-HEMBA1002659/Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142
F-HEMBA1002257/Homo sapiens diacylglycerol kinase iota (DGKI) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936	F-HEMBA1002661/Human Line-1 repeat mRNA with 2 open reading frame s//1.4e-122:781:85//Hs.23094:M19503
F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420	F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497
F-HEMBA1002267/Homo sapiens GDP-L-fucose pyrophosphorylase (GFPF) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445	F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368
F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404	F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457
F-HEMBA1002321/Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//Hs.77729:AB010710	F-HEMBA1002688/Homo sapiens hyperpolarization-activated channel 1 (H1) mRNA, partial cds//1.8e-11:541:60//Hs.124161:AF065164
F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982	F-HEMBA1002696//Homo sapiens DNA from chromosome 19, cosmid R21944//1.9e-06:345:61//Hs.155647:AC004221
F-HEMBA1002337/Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087	F-HEMBA1002703/Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924
F-HEMBA1002341/Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314	F-HEMBA1002712
F-HEMBA1002348//EST//1.0e-19:285:70//Hs.121860:AA776692	F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800
F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996	F-HEMBA1002728/Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521
F-HEMBA1002363/Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563	F-HEMBA1002730/Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867
F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216	F-HEMBA1002742//EST//0.97:138:60//Hs.160545:AI271596
F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144	F-HEMBA1002746/Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372
F-HEMBA1002417/Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954	F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786
F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141	F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817
F-HEMBA1002430/Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U97289	F-HEMBA1002768/Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126
F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561	F-HEMBA1002770//ESTs, Highly similar to TIPI20 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947
F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B. 6. BK [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490	F-HEMBA1002777/Homo sapiens prostate apoptosis response protein p ar-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809
F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160	F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392
F-HEMBA1002462/Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783	F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N80326
F-HEMBA1002469/Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:O50912	F-HEMBA1002794/Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756
F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508	F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938
F-HEMBA1002477/Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133	F-HEMBA1002810/Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185
F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235	F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744
F-HEMBA1002495	F-HEMBA1002818/Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119
F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161	F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:AI279904
F-HEMBA1002503/H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173	F-HEMBA1002833
F-HEMBA1002508/Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080	F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550
F-HEMBA1002513/Homo sapiens mRNA for Histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972	F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823
F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795	F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEE08.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730
F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951	F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AI279429
F-HEMBA1002542/Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219	F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679
F-HEMBA1002547/Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903	F-HEMBA1002921
F-HEMBA1002552/Human Hep2 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875	F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001
F-HEMBA1002555/Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB021622	F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:M77915
F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205	F-HEMBA1002935/Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148
F-HEMBA1002561/Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905	F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene P C26:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053
	F-HEMBA1002939/H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703
	F-HEMBA1002944/Human putative endothelin receptor type B-like pro

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tein mRNA, complete cds//0.83:326:58//Hs.27747:U87460	0//Hs.154782:X99459
F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.126762:AA913925	F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254
F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099	F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328
F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092	F-HEMBA1003330
F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828	F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-2
F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219	6:256:78//Hs.146395:AB002329
F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosop	F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmid R
hila)-homolog phosphodiesterase E4//1.5e-37:247:89//Hs.188:L20971	31240, R30272 and R28549 containing the EKLF, GCM, CRT, and RAD2
F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCA	3A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092
P-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564	F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159
F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525	F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819
F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:	F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//
81//Hs.155464:AF088219	/Hs.73919:X81637
F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:W26486	F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017
F-HEMBA1003034//Homo sapiens PYRIN (MEFY) mRNA, complete cds//7.4	F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:M95552
e-70:330:78//Hs.113283:AF018080	F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488
F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//H	F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813
s.159425:AJ001454	F-HEMBA1003403//Adducin 2 (beta) (alternative products)//5.0e-05:4
F-HEMBA1003037//EST//0.53:59:74//Hs.148011:AI268003	45:61//Hs.90951:U43959
F-HEMBA1003041//ESTs, Weakly similar to F58C11.6 [C.elegans]//1.7	F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309
e-64:337:95//Hs.105907:AA186514	F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine
F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase be	synthetase), regulatory (30.8kd)//9.5e-05:541:58//Hs.89709:L35546
ta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182	F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962
F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438	F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0
F-HEMBA1003067	e-149:686:99//Hs.25812:AF058696
F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1	F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:2
(IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164	71:60//Hs.47822:AB002378
F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:	F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8
542:62//Hs.48998:AB007865	e-08:775:58//Hs.3847:U59632
F-HEMBA1003078//CYTOCHROME P450 1VF3//2.0e-29:452:67//Hs.106242:AB	F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578
002454	F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cd
F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461	s//0.16:321:60//Hs.13999:AB014600
F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881	F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443
F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721	F-HEMBA1003531//Human mRNA for KIAA0333 gene, partial cds//4.9e-5
F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription fact	1:451:78//Hs.22271:D26067
or [M.musculus]//0.98:216:61//Hs.97865:AA405872	F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811
F-HEMBA1003098//EST//2.9e-29:73:73//Hs.152366:AA486721	F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (isle
F-HEMBA1003117//H. sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U078	t-1)//5.0e-75:736:73//Hs.505:U07559
02	F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311
F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:50	F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cd
7:58//Hs.12432:AF070575	s//3.6e-33:562:64//Hs.81469:U01833
F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cd	F-HEMBA1003556
s//0.038:288:63//Hs.6162:AB018314	F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122
F-HEMBA1003136	F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327
F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279	F-HEMBA1003569//Human metastasis-associated metal mRNA, complete cd
F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:	s//2.0e-58:455:66//Hs.101448:U35113
850:99//Hs.63931:AJ005670	F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972
F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete c	F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546
ds//1.1e-24:171:83//Hs.141874:AB014588	F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6
F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740	e-19:108:99//Hs.18420:AA599232
F-HEMBA1003179//EST, Weakly similar to hypothetical protein in pur	F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-8
B 5' region [E.coli]//4.7e-20:118:97//Hs.118831:AA211895	S:487:92//Hs.57937:W68285
F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523	F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymph
F-HEMBA1003199//SOD-3 PROTEIN//0.00034:383:60//Hs.157429:X71135	ocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405
F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412	F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827
F-HEMBA1003204//Homo sapiens PYRIN (MEFY) mRNA, complete cds//4.6	F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916
e-33:154:85//Hs.113283:AF018080	F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory
F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765	protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782
F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784	F-HEMBA1003617//Homo sapiens mRNA for HRHFB2157, partial cds//7.9
F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310	e-171:501:97//Hs.124956:AB015344
F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012	F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT p
F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//	rotein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF
0.00054:432:58//Hs.132206:AF039694	F077954
F-HEMBA1003250	F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750
F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) m	F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159
RNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292	F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans s
F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991	udo gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF0
F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020	13591
F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864	F-HEMBA1003640//ESTs//1.1e-11:267:66//Hs.34359:AI122791
F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867	F-HEMBA1003645
F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1, 4-galactosyltr	F-HEMBA1003646
ansferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662	F-HEMBA1003656
F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete c	F-HEMBA1003662
ds//1.6e-167:799:98//Hs.12836:AB011009	F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381
F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912	F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906
F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160	F-HEMBA1003680//Human plectin (PLECT) mRNA, complete cds//3.4e-06:
F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.105486:AA521012	464:61//Hs.79706:U53204
F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinas	F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-1
e, complete cds//1.5e-189:865:99//Hs.124224:AB001872	71 [H.sapiens]//1.6e-100:478:98//Hs.118866:AI017072
F-HEMBA1003322//H. sapiens mRNA for sigma 3B protein//4.5e-49:399:8	F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cd

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s//9.5e-74:606:77//Hs.9028:AF039691  
 F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187  
 F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cd  
 s//0.81:254:62//Hs.32316:AB011116  
 F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995  
 F-HEMBA1003715//ESTs//1.3e-11:228:60//Hs.101237:AA708760  
 F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:69  
 2:68//Hs.91916:AF035317  
 F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921  
 F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839  
 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frame  
 s//8.6e-102:753:81//Hs.23094:M19503  
 F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:24  
 2:62//Hs.153325:AC005390  
 F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:A1198946  
 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:43  
 0:69//Hs.8136:U81984  
 F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920  
 F-HEMBA1003783//ESTs, Weakly similar to COIH6.7 [C.elegans]//1.7e-  
 24:224:81//Hs.18171:AA524327  
 F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172  
 F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L3  
 9064  
 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel  
 (KCNH3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815  
 F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239  
 F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.1  
 19537:M88108  
 F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:A1379721  
 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cd  
 s//3.3e-85:586:87//Hs.6051:AB014516  
 F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:A1204220  
 F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC  
 WARNING ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:M74314  
 F-HEMBA1003856//ESTs//8.6e-53:286:95//Hs.116645:A1005167  
 F-HEMBA1003864//Human mRNA for KIAA0359 gene, complete cds//0.11:1  
 44:66//Hs.21355:AB002367  
 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete c  
 ds//4.3e-30:580:63//Hs.27621:U52840  
 F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//  
 Hs.89563:D32002  
 F-HEMBA1003880  
 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cd  
 s//4.2e-18:302:67//Hs.23711:AB018295  
 F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTE  
 IN IN YMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.2e-49:295:92  
 //Hs.114673:M72675  
 F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236  
 F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cd  
 s//0.081:345:58//Hs.78494:AB011097  
 F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:A1032875  
 F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-3  
 8:313:69//Hs.154668:AB002389  
 F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562  
 F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]  
 is//0.0029:222:61//Hs.144236:W52380  
 F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055  
 F-HEMBA1003953//Zinc finger protein 7 (KIX 4, clone HF.16)//0.0001  
 4:271:66//Hs.2076:M29580  
 F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W  
 ARNING ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230  
 F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:M78567  
 F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:A1138965  
 F-HEMBA1003978  
 F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009  
 F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456  
 F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts bi  
 nding protein (FBI1) mRNA, complete cds//0.022:349:58//Hs.104640:A  
 F000561  
 F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468  
 F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493  
 F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573  
 F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:A1379721  
 F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete c  
 ds//5.2e-51:359:84//Hs.15519:AB018315  
 F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:A1239930  
 F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:A1312281  
 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA584160  
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.  
 6101:M60315  
 F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638  
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:45  
 7:58//Hs.82837:L13435  
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferas  
 e, complete cds//1.5e-46:199:80//Hs.46328:D87942  
 F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426  
 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107  
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.7566  
 6:M28713  
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, co  
 mplete cds//4.3e-39:335:79//Hs.46468:U45984  
 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-2  
 4:610:61//Hs.80712:D86957  
 F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064  
 F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:A1419759  
 F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1/  
 /0.00055:343:62//Hs.5923:X82260  
 F-HEMBA1004143  
 F-HEMBA1004146  
 F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:A1186056  
 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete c  
 ds//1.8e-15:591:60//Hs.159277:AB018341  
 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:  
 649:97//Hs.59988:AF067855  
 F-HEMBA1004199  
 F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:A1375427  
 F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1  
 [Zea mays]//1.2e-35:205:94//Hs.10092:A1189282  
 F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040  
 F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748  
 F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514  
 F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.01  
 2:156:67//Hs.163588:A1073878  
 F-HEMBA1004238  
 F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571  
 F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522  
 F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) ge  
 ne, complete cds//1.1e-28:295:72//Hs.56205:U96876  
 F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:55  
 3:60//Hs.83634:U52112  
 F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete c  
 ds//4.9e-73:490:77//Hs.141874:AB014588  
 F-HEMBA1004272  
 F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444  
 F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:11  
 8:65//Hs.155313:AB002331  
 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete c  
 ds//1.0:364:56//Hs.118738:AB018343  
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-  
 1 mRNA, complete cds//6.9e-187:868:99//Hs.101766:AF022795  
 F-HEMBA1004289  
 F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484  
 F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:A1270047  
 F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:A1336314  
 F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:45  
 2:65//Hs.69740:U09367  
 F-HEMBA1004323//EST//0.44:134:64//Hs.145464:A1204532  
 F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete  
 cds//0.017:209:64//Hs.43627:U35612  
 F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062  
 F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888  
 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete c  
 ds//0.49:80:73//Hs.139648:AB014606  
 F-HEMBA1004341  
 F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, compl  
 ete cds//2.7e-39:270:86//Hs.80686:D89667  
 F-HEMBA1004354//Human CHL1 potential helicase (CHL1), complete cd  
 s//1.3e-46:190:92//Hs.27424:U75968  
 F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:6  
 2//Hs.3022:D85376  
 F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse tr  
 ansriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928  
 F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800  
 F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//  
 Hs.112180:AF039019  
 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:M51250  
 F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818  
 F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199  
 F-HEMBA1004408//ESTs, Weakly similar to The hA1539 protein is rela  
 ted to cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:A124642

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【表550】

6	57//Hs.41587:U63139
F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531	F-HEMBA1004771
F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219	F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235
F-HEMBA1004460//Homo sapiens PYRIN (NEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080	F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106
F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606	F-HEMBA1004795
F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984	F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952
F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450	F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971
F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600	F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042
F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431	F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646
F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frame s//9.0e-89:758:76//Hs.23094:M19503	F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481
F-HEMBA1004507//ESTs, Weakly similar to T19810.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492	F-HEMBA1004841//ESTs//2.1e-09:66:98//Hs.158161:AA312511
F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800	F-HEMBA1004850//EST//0.033:253:64//Hs.158782:AI376601
F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416	F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150
F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381	F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987
F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552	F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077
F-HEMBA1004554	F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633
F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331	F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698
F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802	F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304
F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825	F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:M51106
F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF010238	F-HEMBA1004918//EST//0.78:122:61//Hs.145491:AI254348
F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:M41661	F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172
F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:U70370	F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947
F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARRANG ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA174706	F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959
F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198	F-HEMBA1004933//Human pseudautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331
F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178	F-HEMBA1004934
F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416	F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981
F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891	F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813
F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780	F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478
F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522	F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274
F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083	F-HEMBA1004972
F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796	F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914
F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582	F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946
F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141	F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013
F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252	F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750
F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue e//0.64:313:61//Hs.118578:X80821	F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589
F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892	F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026
F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515	F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429
F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019	F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356
F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903	F-HEMBA1005019//Homo sapiens mRNA for KIAA0548 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548
F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909	F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560
F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515	F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:99//Hs.21362:AF039237
F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004	F-HEMBA1005039//Human kni repeat mRNA (cdna clone pcd-kni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627
F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frame s//2.0e-61:663:71//Hs.23094:M19503	F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193
F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813	F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802
F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:M54504	F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462
F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626	F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587
F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.153663:AF011333	F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381
F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082	F-HEMBA1005079//Dihydroliipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785
F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060	F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105
F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120	F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561
F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frame s//4.5e-115:909:78//Hs.23094:M19503	F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916
F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:	F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304
	F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:M51106
	F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875

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【表551】

F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021	76//Hs.155464:AF088219
F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216	F-HEMBA1005528//ESTs. Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471
F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914	F-HEMBA1005530
F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA262197	F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376
F-HEMBA1005202	F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461
F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436	F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13901
F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547	F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257
F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081	F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507
F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302	F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932
F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144	F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873
F-HEMBA1005244//ESTs//2.5e-14:85:100//Hs.128744:AI191922	F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538
F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896	F-HEMBA1005582
F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157	F-HEMBA1005583
F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380	F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381
F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777	F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FOR MS//0.54:439:59//Hs.2137:D49357
F-HEMBA1005293//Homo sapiens clone Z3562 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018	F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002233
F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232	F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609
F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219	F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982
F-HEMBA1005311	F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC, 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280
F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516	F-HEMBA1005621//ESTs. Weakly similar to MITOTIC MAD2 PROTEIN [S. cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845
F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615	F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535
F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117	F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734
F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723	F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199
F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.129361:AJ007581	F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956
F-HEMBA1005353//EST//5.4e-09:222:68//Hs.119508:AA485732	F-HEMBA1005666
F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414	F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142
F-HEMBA1005367//Homo sapiens melanostatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:AF071787	F-HEMBA1005679//Human knpi repeat mRNA (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:X00629
F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905	F-HEMBA1005680
F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452	F-HEMBA1005685
F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI193053	F-HEMBA1005689//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406
F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448	F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678
F-HEMBA1005394//ESTs. Weakly similar to No definition line found [C. elegans]//1.0e-130:620:98//Hs.108990:M25951	F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143
F-HEMBA1005403//ESTs. Weakly similar to No definition line found [C. elegans]//7.7e-151:727:97//Hs.17118:AI033807	F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)//2.6e-20:151:88//Hs.77393:D14697
F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:M24513	F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754
F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347	F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
F-HEMBA1005411	F-HEMBA1005755//Human knpi repeat mRNA (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:X00627
F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248	F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219
F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323	F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
F-HEMBA1005443//Zinc finger protein 157 (HZF2)//9.0e-34:259:72//Hs.89897:U28687	F-HEMBA1005813//ESTs//0.012:209:63//Hs.113365:R77747
F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783	F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346
F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107	F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368	F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frame s//1.4e-88:481:92//Hs.23094:M19503	F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frame s//7.9e-42:690:66//Hs.23094:M19503
F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219	F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:47:0:56//Hs.79706:U53204
F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694	F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
F-HEMBA1005497//Glucocorticoid receptor alpha (alternative product s)//8.7e-41:588:69//Hs.102761:U25029	F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from Tq11.23-q21//1.1e-28:318:73//Hs.159530:AC004957	F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:O13635	F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984
F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911	F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766
F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353	F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
F-HEMBA1005513//ESTs. Weakly similar to males-absent on the first [D. melanogaster]//5.3e-76:378:97//Hs.22767:M99220	F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006
F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693	F-HEMBA1005931//ESTs. Weakly similar to kruppel-related zinc finger protein [H. sapiens]//1.2e-46:228:100//Hs.152178:AI224880
F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575	F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588
F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280	F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883
F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:	F-HEMBA1005963

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F-HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516	ase virus//1.1e-13:346:63//Hs.31257:AA875998
F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:A1127530	F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887: D38081
F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526	F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532
F-HEMBA1006002	F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA868897
F-HEMBA1006005//ESTs, Weakly similar to THI protein [D.melanogaster r]//0.98:197:61//Hs.5184:AA709151	F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.128621:AA910431
F-HEMBA1006031	F-HEMBA1006492
F-HEMBA1006035	F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:A1248625
F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4 e-92:617:84//Hs.113283:AF018080	F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389
F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.141186:R99609	F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072
F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.143321:A1139422	F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cd s//7.3e-141:470:98//Hs.153858:AB014566
F-HEMBA1006081	F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier pr otein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185
F-HEMBA1006090//EST//1.2e-12:340:62//Hs.161195:A1418788	F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002
F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313	F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:A1160081
F-HEMBA1006100//ESTs//7.1e-22:273:73//Hs.144407:AA737799	F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP 1) mRNA, complete cds//4.4e-173:654:98//Hs.21301:AF093419
F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e- 26:273:66//Hs.8763:W30741	F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638
F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968	F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47: 363:79//Hs.21490:AB007898
F-HEMBA1006124//EST//0.047:251:62//Hs.132257:A1027222	F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:A1198425
F-HEMBA1006130//Human H0X4C mRNA for a homeobox protein//1.0:150:6 2//Hs.74061:X59372	F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136
F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734	F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.144372:A1346522
F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:A1281881	F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479
F-HEMBA1006155	F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07: 533:60//Hs.106387:AF029778
F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:NA0575	F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328: 81//Hs.155464:AF088219
F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627	F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cd s//2.6e-38:441:69//Hs.23711:AB018295
F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117	F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862
F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540	F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:A1032875
F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:8 36:98//Hs.109268:AF070557	F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTE IN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97// Hs.40911:A1391502
F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:6 7//Hs.7647:M94046	F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:A1343331
F-HEMBA1006252	F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589
F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:A1140706	F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PRO TEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185
F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete c ds//0.00037:158:69//Hs.159277:AB018341	F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapie ns]//9.7e-05:259:65//Hs.105747:AA505003
F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631	F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, co mplete cds//3.9e-28:108:93//Hs.6196:U40282
F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140	F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615
F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X7677 0	F-HEMBA1006653
F-HEMBA1006283	F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from Tpl2-p14//2. 9e-92:438:98//Hs.8173:AC005189
F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:A1189964	F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:18 0:80//Hs.91916:AF035317
F-HEMBA1006291	F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1. 6e-16:122:90//Hs.5092:Y12065
F-HEMBA1006293	F-HEMBA1006676
F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285	F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575
F-HEMBA1006310//Homo sapiens syntaxin 4 binding protein UNC-18c. (U NC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922	F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145
F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350	F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:A1128198
F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789	F-HEMBA1006708
F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:A1032142	F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545
F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220	F-HEMBA1006717//ESTs//2.6e-31:286:78//Hs.55573:W37226
F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287	F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105
F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//H s.74107:X59244	F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-5 2:360:84//Hs.154326:D42087
F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:A1351026	F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing prot ein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF0355 87
F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POBI) mRN A, complete cds//0.0028:422:59//Hs.80667:AF010233	F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0 e-10:576:56//Hs.149323:AB002325
F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c. (U NC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922	F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720
F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:A1042531	F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:A1252657
F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frame s//2.1e-49:395:80//Hs.23094:M19503	F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250
F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:A1077477	F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:A1369798
F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:A1281881	F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frame s//4.1e-37:781:64//Hs.23094:M19503
F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:7 2//Hs.51048:X68830	F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:6 8//Hs.34054:U79298
F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:A1206835	F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD P ROTEIN TIGH12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//H s.125790:AA287723
F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA983264	F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:A1051551
F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:A1209194	
F-HEMBA1006445	
F-HEMBA1006446//EST//0.14:200:59//Hs.160695:A1282889	
F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//H s.51124:AF019369	
F-HEMBA1006467	
F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:A1091453	
F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna dise	

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F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624	F-HEMBA1007327//ESTs. Weakly similar to HOST CELL FACTOR C1 [H. sapiens]//3.5e-09:144:76//Hs.20597:W58370
F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970	F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130
F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327	F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006
F-HEMBA1006865	F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561
F-HEMBA1006877//ESTs. Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERC7-KMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938	F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568
F-HEMBA1006885//ESTs. Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214	F-HEMBA1000008//H.sapiens mRNA for translin associated protein 1//1.1e-43:370:78//Hs.96247:X95073
F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592	F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.83428:W58603
F-HEMBA1006914//EST//0.065:366:62//Hs.162914:AA666199	F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307
F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:A1376989	F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392
F-HEMBA1006926//Human I kappa B mRNA, complete cds//0.90:545:59//Hs.154764:U16258	F-HEMBA1000030//H.sapiens mRNA for cyclin I1//1.3e-10:525:62//Hs.3232:Z46788
F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539	F-HEMBA1000036
F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W27212	F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:98//Hs.20815:AF084928
F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:A1150382	F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358
F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:AJ010841	F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319
F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633	F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131
F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.14934:AF004828	F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717
F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase//1.9e-79:447:89//Hs.75268:X74570	F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frame s//3.3e-54:259:88//Hs.23094:W19503
F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968	F-HEMBA1000055//ESTs//0.0017:289:62//Hs.125755:AA286923
F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723	F-HEMBA1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304
F-HEMBA1007002	F-HEMBA1000083
F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282	F-HEMBA1000089//EST//0.0016:192:66//Hs.137093:AA917621
F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:70//Hs.43003:AF035812	F-HEMBA1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645
F-HEMBA1007045	F-HEMBA1000103//Human kpn1 repeat mRNA (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:X00627
F-HEMBA1007051//EST//0.85:65:73//Hs.158641:A1370659	F-HEMBA1000113//EST//4.6e-23:221:76//Hs.142065:AA173763
F-HEMBA1007052	F-HEMBA1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521
F-HEMBA1007062	F-HEMBA1000136//ESTs//2.3e-101:507:96//Hs.12659:AA195207
F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212	F-HEMBA1000141//ESTs//2.1e-15:283:69//Hs.126257:A1279044
F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845	F-HEMBA1000144//EST//4.5e-52:298:91//Hs.149580:A1281881
F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:W74002	F-HEMBA1000173//Zinc finger protein 74 (Cos2)//2.4e-63:285:82//Hs.3057:X92715
F-HEMBA1007080	F-HEMBA1000175//EST//1.0:101:65//Hs.162898:AA659646
F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432	F-HEMBA1000198//EST//0.99:179:56//Hs.116880:AA662457
F-HEMBA1007087//Human malonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:57//Hs.3828:U49260	F-HEMBA1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs.101414:AB011129
F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595	F-HEMBA1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277
F-HEMBA1007133//ESTs//0.71:246:62//Hs.96235:AA196354	F-HEMBA1000218//EST//0.11:136:63//Hs.134683:A1092013
F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182	F-HEMBA1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962
F-HEMBA1007129	F-HEMBA1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612
F-HEMBA1007147//ESTs//3.2e-07:235:64//Hs.124813:W46172	F-HEMBA1000244//ESTs//3.2e-15:139:81//Hs.134549:A1078483
F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136	F-HEMBA1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:98//Hs.151411:AF075587
F-HEMBA1007151	F-HEMBA1000258//EST//0.0091:325:60//Hs.97533:AA435884
F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085	F-HEMBA1000264//Human CHL1 potential helicase (CHL1), complete cds//1.4e-33:100:100//Hs.27424:U75968
F-HEMBA1007178//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//4.2e-39:248:90//Hs.157148:AA311921	F-HEMBA1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930
F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965	F-HEMBA1000272//ESTs//1.3e-93:440:99//Hs.109224:W46684
F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:D86987	F-HEMBA1000274//ESTs//0.41:221:65//Hs.71990:AA151796
F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252	F-HEMBA1000284//EST//0.00024:108:73//Hs.100725:F13689
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197:AB018340	F-HEMBA1000307//EST//3.6e-10:149:73//Hs.140415:AA786574
F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.82314:M31642	F-HEMBA1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0092:252:65//Hs.41153:AB018326
F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204	F-HEMBA1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787
F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:64//Hs.12432:AF070575	F-HEMBA1000318//EST//0.014:184:61//Hs.155758:A1311870
F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749:U13695	F-HEMBA1000335//EST//0.99:187:63//Hs.137424:AA243729
F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836	F-HEMBA1000336//EST//1.0:209:63//Hs.150410:A1003611
F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:W06475	F-HEMBA1000337//EST//0.086:133:66//Hs.128207:AA972330
F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529	F-HEMBA1000338//EST//7.1e-07:129:72//Hs.140488:AA767127
F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637	F-HEMBA1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:76//Hs.155464:AF088219
F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:A1300062	F-HEMBA1000341
F-HEMBA1007301//Collagen, type I, alpha 1(I)1.5e-09:406:61//Hs.111913:Z74615	F-HEMBA1000343//EST//0.66:163:63//Hs.150822:A1302729
F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506	F-HEMBA1000354//ESTs//7.1e-61:292:100//Hs.152266:AA926874
F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:W63634	F-HEMBA1000369//ESTs. Highly similar to t-BOP [M.musculus]//0.013:157:64//Hs.129982:A1420970
F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241	F-HEMBA1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934

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n/9.4e-165:762:98//Hs.16184:AJ001642  
 F-HEM8B1000402//EST//0.013:291:59//Hs.149191:A1246155  
 F-HEM8B1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194  
 F-HEM8B1000420//EST//6.3e-52:258:98//Hs.136434:AA557925  
 F-HEM8B1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735:AF010144  
 F-HEM8B1000438//ESTs//0.073:446:58//Hs.134632:A1223429  
 F-HEM8B1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627  
 F-HEM8B1000449//EST//5.5e-21:356:67//Hs.157848:A1362501  
 F-HEM8B1000455//ESTs//0.092:147:65//Hs.106446:N93227  
 F-HEM8B1000472  
 F-HEM8B1000480//EST//0.98:83:71//Hs.146462:A1124898  
 F-HEM8B1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206  
 F-HEM8B1000490//ESTs//2.5e-27:200:79//Hs.56825:A1057560  
 F-HEM8B1000491  
 F-HEM8B1000493//ESTs//0.019:103:69//Hs.138358:T66178  
 F-HEM8B1000510//Glucocorticoid receptor alpha (alternative product s)//1.6e-46:409:77//Hs.102761:U25029  
 F-HEM8B1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413  
 F-HEM8B1000523//ESTs//0.69:332:59//Hs.106845:W19543  
 F-HEM8B1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710  
 F-HEM8B1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-31:554:67//Hs.157142:U85996  
 F-HEM8B1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953  
 F-HEM8B1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:AB018293  
 F-HEM8B1000564  
 F-HEM8B1000573//H.sapiens HCG 11 mRNA//7.5e-27:197:76//Hs.146333:X81001  
 F-HEM8B1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238  
 F-HEM8B1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533  
 F-HEM8B1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091  
 F-HEM8B1000591//ESTs//1.0e-17:370:64//Hs.58156:W1990  
 F-HEM8B1000592//EST//0.0038:51:88//Hs.148022:A1269323  
 F-HEM8B1000593//Homo sapiens chromosome Tq22 sequence//4.7e-109:503:99//Hs.3386:AF053356  
 F-HEM8B1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U65589  
 F-HEM8B1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809  
 F-HEM8B1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864  
 F-HEM8B1000631//ESTs//1.7e-06:247:64//Hs.156864:A1346481  
 F-HEM8B1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349  
 F-HEM8B1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075  
 F-HEM8B1000638//EST//0.0076:92:75//Hs.125496:AA883735  
 F-HEM8B1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830  
 F-HEM8B1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778  
 F-HEM8B1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531  
 F-HEM8B1000665//EST//0.44:152:63//Hs.149534:A1280924  
 F-HEM8B1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503  
 F-HEM8B1000673//ESTs//0.99:177:59//Hs.149864:N80474  
 F-HEM8B1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.73821:M35663  
 F-HEM8B1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723  
 F-HEM8B1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125  
 F-HEM8B1000706//EST//8.6e-14:373:61//Hs.138281:R55703  
 F-HEM8B1000709//EST//0.99:110:65//Hs.162437:AA577510  
 F-HEM8B1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741  
 F-HEM8B1000726//EST//1.3e-43:257:84//Hs.162197:AA535216  
 F-HEM8B1000738//EST//5.9e-13:259:64//Hs.159699:A1417328  
 F-HEM8B1000749//EST//3.1e-42:271:87//Hs.162197:AA535216  
 F-HEM8B1000763  
 F-HEM8B1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830  
 F-HEM8B1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5e-116:580:97//Hs.5009:AA081390  
 F-HEM8B1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876  
 F-HEM8B1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:AB014577  
 F-HEM8B1000790//ESTs//1.2e-52:344:86//Hs.35254:A1133727  
 F-HEM8B1000794//ESTs//0.00098:289:59//Hs.138782:N73572  
 F-HEM8B1000807//ESTs//2.1e-91:434:99//Hs.61334:A1298375  
 F-HEM8B1000810//ESTs//0.038:92:71//Hs.148763:AA668871  
 F-HEM8B1000821//EST//0.94:129:62//Hs.162299:AA555154  
 F-HEM8B1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421  
 F-HEM8B1000826//ESTs//4.8e-13:343:65//Hs.153429:A1283069  
 F-HEM8B1000827  
 F-HEM8B1000831  
 F-HEM8B1000835//EST//4.3e-27:201:85//Hs.141451:N29915  
 F-HEM8B1000840//EST//6.3e-75:380:96//Hs.142557:AA464948  
 F-HEM8B1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:M19503  
 F-HEM8B1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238  
 F-HEM8B1000870//EST//0.00091:246:62//Hs.126502:AA913831  
 F-HEM8B1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351  
 F-HEM8B1000883//ESTs//0.42:107:67//Hs.154173:A1379823  
 F-HEM8B1000887  
 F-HEM8B1000888//ESTs//1.0:137:67//Hs.8121:AA521290  
 F-HEM8B1000890//ESTs//1.0:116:65//Hs.7105:T23433  
 F-HEM8B1000893//EST//0.0079:408:58//Hs.146504:A1129834  
 F-HEM8B1000908//EST//9.2e-21:205:79//Hs.132635:A1032875  
 F-HEM8B1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984  
 F-HEM8B1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049  
 F-HEM8B1000915//ESTs//2.5e-90:423:99//Hs.135254:A1095468  
 F-HEM8B1000917//EST//2.8e-49:241:100//Hs.162216:AA548089  
 F-HEM8B1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593  
 F-HEM8B1000947  
 F-HEM8B1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942  
 F-HEM8B1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938  
 F-HEM8B1000975//ESTs//0.78:180:66//Hs.104789:AA417124  
 F-HEM8B1000981  
 F-HEM8B1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569  
 F-HEM8B1000991//EST//0.12:125:66//Hs.22945:R43713  
 F-HEM8B1000996//ESTs//6.9e-05:273:63//Hs.133116:A1054055  
 F-HEM8B1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565  
 F-HEM8B1001008//EST//4.7e-09:203:65//Hs.105221:AA489025  
 F-HEM8B1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310  
 F-HEM8B1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991  
 F-HEM8B1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247  
 F-HEM8B1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:A1420970  
 F-HEM8B1001037//EST//0.0057:192:66//Hs.149987:A1291177  
 F-HEM8B1001047//ESTs//1.6e-22:360:70//Hs.120734:W50721  
 F-HEM8B1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586  
 F-HEM8B1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518  
 F-HEM8B1001058//Seal inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219  
 F-HEM8B1001060//ESTs//1.6e-62:464:81//Hs.138663:M24942  
 F-HEM8B1001063  
 F-HEM8B1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803  
 F-HEM8B1001096//EST//0.017:154:66//Hs.130403:AA909272  
 F-HEM8B1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293  
 F-HEM8B1001105//Human BRCA2 region, mRNA sequence CG016//0.30:84:75//Hs.112434:U50529  
 F-HEM8B1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800  
 F-HEM8B1001114//EST//6.4e-07:296:62//Hs.128420:AA975062  
 F-HEM8B1001117//EST//1.6e-99:464:99//Hs.130493:AA928139  
 F-HEM8B1001119  
 F-HEM8B1001126  
 F-HEM8B1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073  
 F-HEM8B1001137

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F-HEM8B1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23.340:69//Hs.146395:AB002329	F-HEM8B1001454//ESTs//1.4e-46:279:93//Hs.104866:AA26038
F-HEM8B1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854	F-HEM8B1001458//EST//1.7e-09:106:83//Hs.141422:M20920
F-HEM8B1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716	F-HEM8B1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220
F-HEM8B1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863	F-HEM8B1001464//Homo sapiens Coch-SB2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740
F-HEM8B1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334	F-HEM8B1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303
F-HEM8B1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183	F-HEM8B1001500//ESTs//8.1e-28:312:74//Hs.18498:M52088
F-HEM8B1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129	F-HEM8B1001521//Homo sapiens mRNA for alpha(1,2) fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942
F-HEM8B1001199	F-HEM8B1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
F-HEM8B1001208//ESTs//0.12:120:69//Hs.130093:AA928802	F-HEM8B1001531//ESTs//4.3e-33:403:75//Hs.44862:M38735
F-HEM8B1001209//EST//0.00028:215:65//Hs.118276:W15258	F-HEM8B1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
F-HEM8B1001210//EST//2.9e-05:297:60//Hs.88840:AA281452	F-HEM8B1001536//ESTs//0.0047:120:68//Hs.144858:R67748
F-HEM8B1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157	F-HEM8B1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
F-HEM8B1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.158241:AB007976	F-HEM8B1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315
F-HEM8B1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:A1378790	F-HEM8B1001562//ESTs//0.95:161:61//Hs.145075:A1208240
F-HEM8B1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754	F-HEM8B1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
F-HEM8B1001249//EST//0.26:203:63//Hs.140791:AA935909	F-HEM8B1001565//Homo sapiens PYRIN (MEFY) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080
F-HEM8B1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219	F-HEM8B1001585
F-HEM8B1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977	F-HEM8B1001586//EST//0.84:132:64//Hs.145264:A1218708
F-HEM8B1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828	F-HEM8B1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289
F-HEM8B1001271//ESTs//2.5e-05:686:58//Hs.115423:A1359248	F-HEM8B1001603//ESTs//1.3e-12:84:96//Hs.13380:R50414
F-HEM8B1001282//CA-binding protein transcription factor, beta subunit 2 (47KD)//0.39:531:57//Hs.78915:U13045	F-HEM8B1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
F-HEM8B1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021	F-HEM8B1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
F-HEM8B1001289//ESTs//6.4e-100:467:99//Hs.151720:A1287890	F-HEM8B1001630//EST//1.4e-07:334:62//Hs.145698:A1266713
F-HEM8B1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848	F-HEM8B1001635//ESTs//0.92:282:60//Hs.126980:AA934077
F-HEM8B1001302	F-HEM8B1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172
F-HEM8B1001304//ESTs//0.98:109:68//Hs.138972:AA047725	F-HEM8B1001641//EST//0.11:53:81//Hs.112445:AA594279
F-HEM8B1001314//EST//7.4e-39:285:77//Hs.144749:A1217339	F-HEM8B1001653//EST//0.91:124:64//Hs.144213:T40480
F-HEM8B1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219	F-HEM8B1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407
F-HEM8B1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503	F-HEM8B1001668//ESTs//0.94:83:69//Hs.146202:A1252519
F-HEM8B1001326//EST//0.00030:257:63//Hs.62208:H12380	F-HEM8B1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546
F-HEM8B1001331//ESTs, Weakly similar to DF570 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222	F-HEM8B1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496
F-HEM8B1001335	F-HEM8B1001685//EST//2.2e-05:112:73//Hs.130984:A1015430
F-HEM8B1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135	F-HEM8B1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664
F-HEM8B1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694	F-HEM8B1001704//EST//5.8e-20:295:69//Hs.140231:A1054398
F-HEM8B1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878	F-HEM8B1001706
F-HEM8B1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142	F-HEM8B1001707//EST//0.091:241:60//Hs.136830:AA769219
F-HEM8B1001356//EST//0.32:292:59//Hs.135771:A1005648	F-HEM8B1001717//ESTs//2.9e-06:325:60//Hs.150063:A1298064
F-HEM8B1001364	F-HEM8B1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219
F-HEM8B1001366//EST//7.8e-24:367:69//Hs.138765:N70347	F-HEM8B1001736//ESTs, Weakly similar to E0405.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578
F-HEM8B1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219	F-HEM8B1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244
F-HEM8B1001369//EST//0.17:211:63//Hs.120066:AA707973	F-HEM8B1001749//Homo sapiens neuronal thread protein ADTc-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144
F-HEM8B1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099	F-HEM8B1001753//ESTs//0.00013:35:100//Hs.139643:H06263
F-HEM8B1001384	F-HEM8B1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077
F-HEM8B1001387//ESTs//0.61:215:60//Hs.145915:A1342230	F-HEM8B1001760//ESTs//6.5e-06:503:58//Hs.21766:A1357639
F-HEM8B1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503	F-HEM8B1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976
F-HEM8B1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988	F-HEM8B1001785//EST//0.16:262:60//Hs.162526:AA584102
F-HEM8B1001424//EST//0.20:307:58//Hs.135336:A1049827	F-HEM8B1001797//ESTs//0.37:201:63//Hs.91559:AA806370
F-HEM8B1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174	F-HEM8B1001802//ESTs//1.6e-06:447:58//Hs.134672:A1087951
F-HEM8B1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175	F-HEM8B1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956
F-HEM8B1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345	F-HEM8B1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
F-HEM8B1001443	F-HEM8B1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCPI1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209
F-HEM8B1001449//Homo sapiens sodium bicarbonate cotransporter (NBC-Cl) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216	F-HEM8B1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190
	F-HEM8B1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067
	F-HEM8B1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370
	F-HEM8B1001850//EST//0.0035:204:61//Hs.7311:T23858
	F-HEM8B1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:

【0857】



【表556】

82//Hs.155464:AF088219	F-HEM8B1002249//Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006
F-HEM8B1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752	F-HEM8B1002254//Homo sapiens mRNA for KIAA0594 protein, partial cd s//5.0e-47:437:77//Hs.154872:AB011166
F-HEM8B1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371	F-HEM8B1002255//ESTs//0.017:255:61//Hs.126786:U74314
F-HEM8B1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503	F-HEM8B1002266//Homo sapiens retinoblastoma-associated protein MEC mRNA, complete cds//0.17:511:57//Hs.58169:AF017790
F-HEM8B1001872	F-HEM8B1002280//EST//4.0e-35:182:98//Hs.127701:AA864998
F-HEM8B1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//H s.19923:Y12478	F-HEM8B1002300
F-HEM8B1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dea d box protein)//0.32:346:60//Hs.100555:X98743	F-HEM8B1002306//Human G protein-coupled receptor (STRL22) mRNA, co mplete cds//6.3e-14:228:72//Hs.46468:U45984
F-HEM8B1001880//EST//4.0e-28:171:92//Hs.151194:AI125868	F-HEM8B1002327//EST//4.3e-21:242:75//Hs.72377:AA161083
F-HEM8B1001899//ESTs//0.17:242:62//Hs.136969:AA830918	F-HEM8B1002329//ESTs. Weakly similar to C17G10.1 [C.elegans]//1.7 e-77:399:96//Hs.105837:AA536054
F-HEM8B1001905	F-HEM8B1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M211 88
F-HEM8B1001906//ESTs//5.6e-49:290:92//Hs.127298:M09155	F-HEM8B1002342//Homo sapiens mRNA for putative thioredoxin-like pr otein//1.4e-155:724:98//Hs.42644:AJ010841
F-HEM8B1001908//Human monocytic leukaemia zinc finger protein (MO Z) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742	F-HEM8B1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006: L16991
F-HEM8B1001910//EST. Weakly similar to albumin [H.sapiens]//0.047: 206:62//Hs.159777:Z19955	F-HEM8B1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:U00943
F-HEM8B1001911	F-HEM8B1002364//EST//4.7e-16:201:73//Hs.149925:AI288838
F-HEM8B1001915//ESTs//0.92:136:71//Hs.144465:R68882	F-HEM8B1002371//EST//2.4e-07:319:61//Hs.136459:AA577796
F-HEM8B1001921//EST//2.0e-19:398:67//Hs.44789:N36113	F-HEM8B1002381
F-HEM8B1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245	F-HEM8B1002383//vasoactive intestinal peptide receptor 2//0.98:19 0:63//Hs.2126:L36566
F-HEM8B1001925//ESTs//5.7e-27:329:71//Hs.141071:M16398	F-HEM8B1002387//EST//2.1e-07:253:61//Hs.145993:AI277784
F-HEM8B1001930//EST//0.043:157:63//Hs.161927:AA483904	F-HEM8B1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456
F-HEM8B1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-5 5:444:80//Hs.154326:D42087	F-HEM8B1002415//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0501//2.0e-32:371:73//Hs.159897:AB007970
F-HEM8B1001945//ESTs//1.1e-19:142:88//Hs.7341:M57875	F-HEM8B1002425//Fc fragment of IgA <sub>1</sub> receptor//2.7e-32:156:82// Hs.54486:X54150
F-HEM8B1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-2 1:333:66//Hs.40100:AB002390	F-HEM8B1002442
F-HEM8B1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds// 0.020:384:60//Hs.8546:U97669	F-HEM8B1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-5 3:461:77//Hs.154326:D42087
F-HEM8B1001952//EST//7.0e-13:302:63//Hs.120089:AA708101	F-HEM8B1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101
F-HEM8B1001953//ATL-derived PMA-responsive (APR) peptide//0.97:25 2:60//Hs.96:D90070	F-HEM8B1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274
F-HEM8B1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418	F-HEM8B1002477//Human Grb2-associated binder-1 mRNA, complete cds/ /6.0e-89:493:92//Hs.159605:U43885
F-HEM8B1001962//Cytochrome P450, subfamily I (aromatic compound-in ducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053	F-HEM8B1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//Hs.74304:AF001691
F-HEM8B1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:8 8//Hs.56710:X96969	F-HEM8B1002492//EST//0.24:149:62//Hs.146790:AI149051
F-HEM8B1001973//Myelin oligodendrocyte glycoprotein (alternative p roducts)//2.1e-48:426:78//Hs.53217:Z48051	F-HEM8B1002495//Fc fragment of IgE, high affinity I <sub>1</sub> receptor for: beta polypeptide//1.3e-22:331:71//Hs.30:M89796
F-HEM8B1001983	F-HEM8B1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494
F-HEM8B1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051	F-HEM8B1002509//ESTs//0.017:220:63//Hs.155263:AI273725
F-HEM8B1001990//ESTs//0.25:171:64//Hs.7961:AA401205	F-HEM8B1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354
F-HEM8B1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103	F-HEM8B1002520//Human Line-1 repeat mRNA with 2 open reading frame s//2.4e-50:580:72//Hs.23094:M19503
F-HEM8B1001997//EST//5.3e-33:294:76//Hs.161041:M82636	F-HEM8B1002522//EST//0.010:172:62//Hs.147224:AI205719
F-HEM8B1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964	F-HEM8B1002531
F-HEM8B1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093	F-HEM8B1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258: 88//Hs.155464:AF088219
F-HEM8B1002009//ESTs//0.066:441:58//Hs.125313:AI201685	F-HEM8B1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102
F-HEM8B1002015//EST//2.3e-110:310:68//Hs.145899:AI274951	F-HEM8B1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648
F-HEM8B1002042//CYTOCHROME P450 11B1//2.9e-11:446:62//Hs.687:X1669 9	F-HEM8B1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191
F-HEM8B1002043//ESTs. Weakly similar to T06E6.d [C.elegans]//1.0:2 17:60//Hs.3487:AA425553	F-HEM8B1002579//EST//1.0:77:68//Hs.147935:AI250286
F-HEM8B1002044	F-HEM8B1002582//ESTs//0.00032:178:68//Hs.139163:AA226095
F-HEM8B1002045	F-HEM8B1002590//ESTs//0.64:132:63//Hs.155688:AI003657
F-HEM8B1002049//Homo sapiens mRNA for KIAA0713 protein, partial cd s//0.082:201:61//Hs.88756:AB018256	F-HEM8B1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336
F-HEM8B1002050//Breakpoint cluster region protein BCR//0.84:267:59 //Hs.2557:Y00661	F-HEM8B1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds// 3.0e-152:710:98//Hs.129826:AF089749
F-HEM8B1002058//Homo sapiens mRNA for KIAA0612 protein, partial cd s//8.1e-07:402:61//Hs.112499:AB014512	F-HEM8B1002601//EST//9.6e-13:368:62//Hs.137080:AA894817
F-HEM8B1002069	F-HEM8B1002603//EST//0.10:144:63//Hs.158180:AI367945
F-HEM8B1002092//EST//5.1e-15:180:75//Hs.127928:AA969239	F-HEM8B1002607//ESTs//0.024:345:62//Hs.143304:AI084058
F-HEM8B1002094//EST//2.0e-52:264:98//Hs.71763:AA146625	F-HEM8B1002610//EST//2.1e-14:291:64//Hs.140573:AA826323
F-HEM8B1002115//EST//0.0083:244:64//Hs.125353:AA877080	F-HEM8B1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
F-HEM8B1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027	F-HEM8B1002614//ESTs//0.0048:136:71//Hs.106280:R13901
F-HEM8B1002139//ESTs//0.64:145:71//Hs.157821:AI362013	F-HEM8B1002617//EST//0.034:320:59//Hs.41223:H89127
F-HEM8B1002142//ESTs//0.013:311:59//Hs.150037:AI292214	F-HEM8B1002623//ESTs//0.88:222:60//Hs.129920:AA167217
F-HEM8B1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254	F-HEM8B1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:1 00//Hs.151051:U07620
F-HEM8B1002189//EST//0.26:81:70//Hs.147726:AI220208	F-HEM8B1002664//EST//0.00013:203:61//Hs.117141:AA678811
F-HEM8B1002190//Alcohol dehydrogenase 2 (class I), beta polypeptid e//0.16:608:58//Hs.4:X03350	F-HEM8B1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
F-HEM8B1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179: 100//Hs.301:U18934	F-HEM8B1002683//ESTs//0.23:224:61//Hs.128883:AI026679
F-HEM8B1002217//Homo sapiens mRNA for zinc finger protein 10//3.7 e-25:405:67//Hs.104115:X52332	F-HEM8B1002684//ESTs//7.2e-09:82:87//Hs.140457:M05124
F-HEM8B1002218//EST//0.015:241:61//Hs.105298:AA489813	F-HEM8B1002686//EST//0.25:189:62//Hs.132431:AA809674
F-HEM8B1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365: 71//Hs.155464:AF088219	F-HEM8B1002692//ESTs//0.00020:162:66//Hs.118180:N68504
F-HEM8B1002247	F-HEM8B1002697//EST//7.2e-17:219:74//Hs.100459:T61992

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F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TAC1) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614	s//9.0e-75:498:85//Hs.23094:M19503
F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588	F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-5
F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDM2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:A1242922	0:304:85//Hs.154326:D42087
F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729	F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569
F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990	F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344
F-MAMMA1000019	F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:98//Hs.32170:AB015132
F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750	F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590
F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945	F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frame s//2.4e-58:834:68//Hs.23094:M19503
F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739	F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:117:84//Hs.83916:U53468
F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461	F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:A1200725
F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281	F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092
F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019	F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN IN C09F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111
F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:A1336840	F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532
F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067	F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:AF061573
F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174	F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459
F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705	F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:A1377641
F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792	F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:AF034546
F-MAMMA1000117	F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830
F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508	F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:AB011166
F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402	F-MAMMA1000446
F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:A1248319	F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827
F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:A1383843	F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818
F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585	F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830
F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924	F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080
F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050	F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830
F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695	F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948
F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530	F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482
F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657	F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219
F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763	F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878
F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:A1091739	F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352
F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035	F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497
F-MAMMA1000227//ESTs//0.010:268:60//Hs.116412:AA506926	F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352
F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:A1377913	F-MAMMA1000565
F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873	F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006
F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:A1247587	F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045
F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:A1003543	F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:A1276780
F-MAMMA1000264//EST//0.0e-18:217:75//Hs.152748:W53015	F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622
F-MAMMA1000266//EST//0.14:270:60//Hs.132593:A1031874	F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744
F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087	F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886
F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726	F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519
F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:A1347361	F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494
F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505	F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478
F-MAMMA1000284	F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605
F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087	F-MAMMA1000623
F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641	F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751
F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243	F-MAMMA1000643//Homo sapiens nephrocytin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:AF023674
F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529	F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353
F-MAMMA1000312//EST//0.042:183:63//Hs.158928:A1379519	F-MAMMA1000669//Human kpn1 repeat mRNA (cdna clone pcd-kpn1-4), 3' end//9.0e-30:531:64//Hs.139107:K00629
F-MAMMA1000313	F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:A1244490
F-MAMMA1000331	F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743
F-MAMMA1000339	F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:U13220
F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963	F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627
F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892	
F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.158095:AB007953	
F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frame	

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F-MAMMA1000707/ESTs//1.4e-09:225:65//Hs.138722:N51081	F-MAMMA1000957/ESTs//1.0:177:59//Hs.149854:N80474
F-MAMMA1000713/Acetylcholinesterase (14-ES domain) [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129	F-MAMMA1000962/Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//Hs.129735:AF010144
F-MAMMA1000714/Human clone 23947 mRNA, partial cds//0.97:263:61//Hs.27414:U79275	F-MAMMA1000968/ESTs//9.2e-18:128:89//Hs.163980:AA715814
F-MAMMA1000718/ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648	F-MAMMA1000975/ESTs//3.8e-08:219:66//Hs.110937:AA137096
F-MAMMA1000720/ESTs//1.4e-50:301:83//Hs.138852:AA284247	F-MAMMA1000979/EST//0.00022:155:65//Hs.101379:Z39802
F-MAMMA1000723/ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:AA700024	F-MAMMA1000987/EST//1.1e-48:373:81//Hs.139034:W27062
F-MAMMA1000731/Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513	F-MAMMA1000998/EST//2.0e-07:356:62//Hs.132467:AA922007
F-MAMMA1000732/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.158095:AB007953	F-MAMMA1001003/ESTs//0.47:129:67//Hs.164016:A1003724
F-MAMMA1000733/RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075	F-MAMMA1001008/ESTs//1.9e-17:153:82//Hs.141161:AA210711
F-MAMMA1000734/Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:AF100141	F-MAMMA1001021/Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:Y15718
F-MAMMA1000738/EST//1.0:149:63//Hs.136928:AA812580	F-MAMMA1001024/ESTs//0.97:251:62//Hs.59389:R93968
F-MAMMA1000744/Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:AB011147	F-MAMMA1001030/Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:573:61//Hs.98384:AF062006
F-MAMMA1000746/ESTs//2.3e-42:409:76//Hs.61199:AA024494	F-MAMMA1001035/ESTs//6.9e-28:268:77//Hs.139536:AA180857
F-MAMMA1000752/EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663	F-MAMMA1001038
F-MAMMA1000760/Myelin oligodendrocyte glycoprotein (alternative products)//6.2e-47:341:82//Hs.53217:Z48051	F-MAMMA1001041/ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178
F-MAMMA1000761/ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369	F-MAMMA1001050/EST//1.8e-29:321:74//Hs.161240:A1419882
F-MAMMA1000775/EST//6.9e-32:424:69//Hs.44554:N34288	F-MAMMA1001059/ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719
F-MAMMA1000776/ESTs//5.5e-43:154:84//Hs.141581:AA315361	F-MAMMA1001067/EST//0.30:166:60//Hs.148441:A1198503
F-MAMMA1000778/EST//4.4e-28:226:80//Hs.128952:AA984114	F-MAMMA1001073/ESTs//1.0e-98:476:98//Hs.98321:AA455585
F-MAMMA1000782/ESTs//0.35:270:60//Hs.29153:AA551137	F-MAMMA1001074/ESTs//1.6e-82:396:98//Hs.118923:AA252116
F-MAMMA1000798/Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575	F-MAMMA1001075/Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749
F-MAMMA1000802/ESTs//3.1e-67:340:97//Hs.126081:AA459849	F-MAMMA1001078/Human Line-1 repeat mRNA with 2 open reading frame s//2.7e-99:689:83//Hs.23094:M19503
F-MAMMA1000824/ESTs//0.98:44:90//Hs.42802:N20130	F-MAMMA1001080/IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420
F-MAMMA1000831/ESTs//0.0081:194:60//Hs.150400:A1298089	F-MAMMA1001082/ESTs//6.2e-28:275:77//Hs.152685:AA613896
F-MAMMA1000839/Small inducible cytokine A5 (RANTES)//4.7e-48:241:74//Hs.155464:AF088219	F-MAMMA1001091/Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254
F-MAMMA1000841	F-MAMMA1001092/Human knpi repeat mRNA (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627
F-MAMMA1000842/Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//Hs.82210:U47742	F-MAMMA1001105/Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045
F-MAMMA1000843/EST//0.34:113:68//Hs.58415:W74696	F-MAMMA1001110/Human mRNA for KIAA0125 gene, complete cds//0.94:48:57//Hs.38365:D50915
F-MAMMA1000845/EST//2.9e-06:56:80//Hs.123243:AA804877	F-MAMMA1001126/Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219
F-MAMMA1000851/EST//0.78:103:65//Hs.135656:AA907022	F-MAMMA1001133
F-MAMMA1000855	F-MAMMA1001139
F-MAMMA1000856/Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906	F-MAMMA1001143/ESTs//2.6e-18:121:82//Hs.135117:A1091534
F-MAMMA1000859/SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135	F-MAMMA1001145/ESTs//1.5e-36:442:69//Hs.124712:H90217
F-MAMMA1000862/EST//1.0:92:66//Hs.157599:A1357342	F-MAMMA1001154/EST//0.054:208:61//Hs.162088:AA505741
F-MAMMA1000863/ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172	F-MAMMA1001161/Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147
F-MAMMA1000865/ESTs//0.99:127:66//Hs.125230:AA873812	F-MAMMA1001162/EST//4.7e-16:117:90//Hs.130894:A1014299
F-MAMMA1000867/EST//0.027:236:60//Hs.147156:A1191777	F-MAMMA1001181
F-MAMMA1000875/Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459	F-MAMMA1001186/Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171
F-MAMMA1000876/ESTs//1.5e-39:192:90//Hs.132020:AA704147	F-MAMMA1001191/ESTs//5.8e-34:197:94//Hs.121575:AA758083
F-MAMMA1000877/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894	F-MAMMA1001198
F-MAMMA1000880/EST//0.014:142:66//Hs.137044:AA878812	F-MAMMA1001202/ESTs//1.5e-37:210:83//Hs.79788:AA527348
F-MAMMA1000883/EST//1.0:166:62//Hs.126352:AA894465	F-MAMMA1001203/ESTs//1.2e-29:199:76//Hs.141605:H92974
F-MAMMA1000897/H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:X67055	F-MAMMA1001206/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776
F-MAMMA1000905/Cartilage matrix protein//0.97:190:64//Hs.150366:M55683	F-MAMMA1001215/ESTs//1.9e-06:300:63//Hs.113566:T03200
F-MAMMA1000906/ESTs//3.0e-07:145:72//Hs.133556:AA702506	F-MAMMA1001220/Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087
F-MAMMA1000908/ESTs//1.1e-70:484:84//Hs.142497:AA189081	F-MAMMA1001222/Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534
F-MAMMA1000914/Angiopoietin 1//0.14:450:59//Hs.2463:D13628	F-MAMMA1001243/ESTs//5.2e-19:118:94//Hs.122830:AA765587
F-MAMMA1000921/ESTs//6.8e-96:448:99//Hs.135721:A1125239	F-MAMMA1001244
F-MAMMA1000931/CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.116007:S79267	F-MAMMA1001249/ESTs//1.3e-89:420:99//Hs.147744:A1220476
F-MAMMA1000940/EST//2.9e-42:209:76//Hs.140567:AA825968	F-MAMMA1001256/ESTs//2.1e-34:282:80//Hs.46158:A1160121
F-MAMMA1000941/Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785	F-MAMMA1001259/ESTs//2.9e-07:68:95//Hs.6193:AA045149
F-MAMMA1000942/ESTs//1.9e-19:252:71//Hs.141575:AA211734	F-MAMMA1001260/Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561
F-MAMMA1000943/Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303	F-MAMMA1001268/Human Line-1 repeat mRNA with 2 open reading frame s//1.7e-33:336:74//Hs.23094:M19503
F-MAMMA1000956/Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714	F-MAMMA1001271/Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747
	F-MAMMA1001274/Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522
	F-MAMMA1001280/ESTs//7.3e-14:273:67//Hs.126503:AA913832
	F-MAMMA1001292/Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998

【0860】

【表559】

F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426	complete cds//8.0e-45:323:83//Hs.46468:U45984
F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305	F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548
F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 2	F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926
2q11.2-qter, contains gene for GTPase-activating protein similar to	F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA
rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA rep	A, complete cds//1.5e-111:725:84//Hs.159154:U47634
est//1.9e-58:295:97//Hs.102336:Z83838	F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098
F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087	F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768
F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:	F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245
745:73//Hs.93174:X57147	F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frame
F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806	s//4.7e-67:822:69//Hs.23094:M19503
F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197	F-MAMMA1001751//Homo sapiens two P domain potassium channel subuni
F-MAMMA1001343//EST//0.0024:323:62//Hs.119238:AA476267	t (HCHO1) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632
F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cd	F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822
s//0.94:89:75//Hs.109358:AB018258	F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109
F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.	F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense t
3e-49:273:80//Hs.42674:U61981	ranscript, partial//6.6e-41:309:84//Hs.102576:AJ010230
F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX	F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072
ACID LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826	F-MAMMA1001768//Human transcription factor, forkhead related activ
F-MAMMA1001397//Prostaglandin I2 (prostaglandin) synthase //1.3e-2	ator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF04
6:358:67//Hs.61333:D83402	2832
F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763	F-MAMMA1001769//Homo sapiens PYRIN (NEFY) mRNA, complete cds//1.1
F-MAMMA1001411//Autosomal dominant polycystic kidney disease type	e-85:686:79//Hs.113283:AF018080
I1//1.0:176:64//Hs.82001:U50928	F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete
F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:4	cds//0.00071:392:60//Hs.32981:U38276
09:80//Hs.43681:AL022394	F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940
F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferas	F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549
e, complete cds//0.00042:125:75//Hs.46328:D87942	F-MAMMA1001788//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3'
F-MAMMA1001435//Human HSLIM15 mRNA for HsLim15, complete cds//8.2	end//6.7e-21:212:77//Hs.103948:K00627
e-43:543:71//Hs.37181:D64108	F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:1
F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321	39:72//Hs.5158:AB007869
F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590	F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987
F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040	F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884
F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053	F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:H47096
F-MAMMA1001476//Human mRNA for 5'-terminal region of UBRK, complete	F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582
cds//7.2e-04:273:72//Hs.75939:D78335	F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589
F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapie	F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CL
ns)]//3.2e-25:397:68//Hs.116874:AA524909	F-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293
F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366	F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742
F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete	F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691
cds//0.99:258:61//Hs.154196:U87269	F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315,
F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795	complete cds//2.0e-29:641:62//Hs.56808:D88827
F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506	F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665
F-MAMMA1001547	F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028
F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cd	F-MAMMA1001854
s//7.5e-130:614:98//Hs.129937:AB007931	F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218
F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-1	F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060
71 [H.sapiens]]//0.71:181:62//Hs.118866:AI017072	F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR m
F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150	RNA, complete cds//0.084:672:58//Hs.152455:AF044209
785:M61764	F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687
F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339	F-MAMMA1001878
F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132	F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944
F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375	F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576
F-MAMMA1001606//Human clone 23527 mRNA, complete cds//0.64:336:58/	F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078
/Hs.23642:U79266	F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521
F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152	F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874
F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58	F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529
//Hs.158229:U28727	F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859
F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome	F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:42
Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unk	3:81//Hs.91916:AF035317
nown putative gene, a pseudogene with high similarity to part of a	F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878
ntigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene	F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sa
and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Co	piens]]//7.9e-09:150:72//Hs.118222:N91115
ntains a predicted CpG island, ESTs, STs and GSSs and genomic mar	F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633
kers DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:AL022165	F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826
F-MAMMA1001633//Human zinc finger protein (LDS-1) mRNA, complete c	F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915
ds//3.6e-44:611:67//Hs.57679:U57796	F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159
F-MAMMA1001635	F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcrip
F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524	t KIAA0484//1.2e-54:455:70//Hs.158095:AB007953
F-MAMMA1001654//Homo sapiens retinal rod Na-Ca/K exchanger (NCKX1)	F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580
mRNA, complete cds//0.00069:140:68//Hs.59829:AB014602	F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225
F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete c	F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256
ds//0.015:135:71//Hs.27349:AB007917	F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305
F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sa	F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frame
piens]]//0.064:472:60//Hs.110819:AI027548	s//0.5e-36:382:75//Hs.23094:M19503
F-MAMMA1001671	F-MAMMA1002078
F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317	F-MAMMA1002082
F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889	F-MAMMA1002084//EST//0.37:351:59//Hs.46576:M46012
F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765	F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase,
F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549	partial//0.54:388:57//Hs.99423:AJ010840
F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, co	F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120

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F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932  
 F-MAMMA1002125//Seal inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219  
 F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:A1272963  
 F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:HS2638  
 F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338  
 F-MAMMA1002145//EST//0.12:204:60//Hs.160983:A1392837  
 F-MAMMA1002153  
 F-MAMMA1002155//ESTs. Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385  
 F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:58//Hs.87149:M35999  
 F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196  
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206  
 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400  
 F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548  
 F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362  
 F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120  
 F-MAMMA1002219//ESTs. Weakly similar to coded for by C. elegans CDNA yk52b10.3 [C. elegans]//9.5e-41:202:100//Hs.118849:AA215645  
 F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:A1024063  
 F-MAMMA1002236//ESTs. Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:A1359536  
 F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986  
 F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903  
 F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:A1308841  
 F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172  
 F-MAMMA1002269  
 F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715  
 F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440  
 F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019  
 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M52302  
 F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460  
 F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914  
 F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935  
 F-MAMMA1002308//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41:293:83//Hs.105292:AA504776  
 F-MAMMA1002310//Homo sapiens serine protease-like protease (nesl) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481  
 F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956  
 F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291  
 F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908  
 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536  
 F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515  
 F-MAMMA1002329//Homo sapiens clone 24444 Rap2 interacting protein 8 (RPI8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026  
 F-MAMMA1002332//Human kpn1 repeat mRNA (cdna clone pcd-kpn1-8), 3' end//1.2e-26:342:72//Hs.103948:K00627  
 F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254  
 F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633  
 F-MAMMA1002347//EST. Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591  
 F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907  
 F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:A1247086  
 F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:A1357539  
 F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901  
 F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733  
 F-MAMMA1002359//EST//1.1e-44:254:77//Hs.141095:H23818  
 F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830  
 F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923  
 F-MAMMA1002362//EST//0.25:304:58//Hs.162427:AA576345  
 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677  
 F-MAMMA1002384//ESTs//1.1e-05:220:65//Hs.141388:R52022  
 F-MAMMA1002385//ESTs. Moderately similar to T11C6.8 [C.elegans]//

8.4e-118:578:97//Hs.25516:A1086362  
 F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624  
 F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:A1142632  
 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737  
 F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745  
 F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788  
 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030  
 F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087  
 F-MAMMA1002446  
 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809  
 F-MAMMA1002461//Human diacylglycerol kinase (DGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707  
 F-MAMMA1002470  
 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779  
 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:M67059  
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460  
 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628  
 F-MAMMA1002498//ESTs. Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920  
 F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392  
 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214  
 F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788  
 F-MAMMA1002554  
 F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822  
 F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421  
 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:A1351368  
 F-MAMMA1002573//ESTs//2.1e-48:265:94//Hs.155128:A1224516  
 F-MAMMA1002585  
 F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831  
 F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:A1334107  
 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958  
 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220  
 F-MAMMA1002612//ESTs. Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:65//Hs.60895:AA428463  
 F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357  
 F-MAMMA1002618  
 F-MAMMA1002619  
 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449  
 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:M52300  
 F-MAMMA1002625  
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs.158241:AB007976  
 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400:AB006626  
 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733  
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385  
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190  
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:A1393335  
 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:A1005489  
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336  
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398  
 F-MAMMA1002673  
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363:D86987  
 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:M69915  
 F-MAMMA1002688//ESTs//2.5e-09:190:68//Hs.138292:A1220397  
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085  
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:A1274697  
 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2) fucosyltransferase, complete cds//1.1e-51:307:79//Hs.46328:D87942  
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:M25041  
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692  
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:A1150165  
 F-MAMMA1002728//ESTs. Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccharomyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193502  
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853  
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312

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F-MAMMA1002748	F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518
F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848	F-MAMMA1003056
F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:1	F-MAMMA1003057//ESTs. Moderately similar to hypothetical protein M
51:98//Hs.32168:AB007902	D6 [M. musculus]//1.3e-88:334:97//Hs.96500:A1206781
F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293	F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:A1022618
F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782	F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cd
F-MAMMA1002769	s//4.5e-51:329:71//Hs.75154:AB014531
F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putativ	F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278
e M8504 Met protein (M8504 Met) gene//7.6e-84:417:97//Hs.77705:U0	mRNA, complete cds//8.5e-44:288:88//Hs.81008:AF043045
7563	F-MAMMA1003104//H. sapiens mRNA for ASM-like phosphodiesterase 3a//
F-MAMMA1002780//EST//0.78:210:63//Hs.149413:A1273988	1.0:213:60//Hs.42945:Y08136
F-MAMMA1002782	F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.
F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:A1380710	99:200:64//Hs.32950:X82634
F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919	F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, co
F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:A1378514	mplete cds//5.4e-27:421:66//Hs.5394:AF105424
F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete c	F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786
ds//2.4e-57:286:88//Hs.15731:AB011135	F-MAMMA1003140
F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-5	F-MAMMA1003146//Homo sapiens mRNA for Gait3 protein//7.2e-82:397:9
2:583:72//Hs.22271:D26067	7//Hs.151344:Y15062
F-MAMMA1002835	F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cd
F-MAMMA1002838//ESTs. Weakly similar to NADH-UBIQUINONE OXIDOREDUC	s//0.00019:297:61//Hs.108945:AB011087
TASE CHAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H2995	F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2
1	e-31:487:65//Hs.3847:U59632
F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590	F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:24
F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cd	4:63//Hs.79706:U53204
s//5.4e-137:635:99//Hs.7531:AB018353	F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-6
F-MAMMA1002844//ESTs. Weakly similar to Y53C12A.3 [C.elegans]//1.6	e:385:92//Hs.82510:D31886
e-07:329:58//Hs.107747:A1357868	F-NT2RM1000032
F-MAMMA1002858	F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-11
F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643	0:849:81//Hs.78442:D83782
F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:69	F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cd
6:78//Hs.83987:U09284	s//3.5e-108:542:95//Hs.60103:AB014590
F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423	F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:54
F-MAMMA1002886//EST//2.0e-09:364:59//Hs.145181:A183632	5:57//Hs.79706:U53204
F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, co	F-NT2RM1000055//ESTs. Highly similar to TIP120 [R.norvegicus]//3.2
mplete cds//3.8e-30:680:61//Hs.129732:D45027	e-69:353:96//Hs.154980:AA948067
F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.0007	F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7)
5:504:60//Hs.19944:U04270	mRNA, complete cds//0.029:281:59//Hs.46465:U45285
F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657	F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210
F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666	F-NT2RM1000080//Homo sapiens chromosome 9, Pl clone 11659//2.8e-10
F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265	2:493:97//Hs.3439:AC004472
F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cd	F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete c
s//0.00053:382:57//Hs.61796:U85658	ds//5.8e-116:550:97//Hs.65238:AB014561
F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952	F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.
F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125	42:190:63//Hs.431:L13689
F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730	F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds
F-MAMMA1002937//ESTs. Weakly similar to ZINC FINGER PROTEIN 84 [H.	//0.00086:126:70//Hs.92693:AF007155
sapiens]//7.9e-103:485:99//Hs.102928:A1346344	F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:2
F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete c	48054
ds//1.6e-194:910:98//Hs.31720:AB014598	F-NT2RM1000127
F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:A1423389	F-NT2RM1000131
F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:A1313418	F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56
F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:	subunit mRNA, nuclear gene encoding mitochondrial protein, complete
60//Hs.54697:AB007884	te cds//3.7e-92:448:97//Hs.49767:AF044959
F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400	F-NT2RM1000153//Homo sapiens mRNA for MTC8-related protein MTC16a,
F-MAMMA1002972	complete cds//1.0:545:58//Hs.110099:AB010419
F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932	F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds
F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944	//0.00081:126:70//Hs.92693:AF007155
F-MAMMA1002987//EST//0.044:254:59//Hs.135014:A1095645	F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:A1424382
F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue fac	F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete c
tor)//3.9e-22:185:83//Hs.62192:J02931	ds//0.87:454:59//Hs.47061:AF045458
F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcrip	F-NT2RM1000242
t KIAA0501//1.0e-16:343:61//Hs.159897:AB007970	F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1
F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979	(C-NAP1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105
F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cd	F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190
s//6.2e-51:620:69//Hs.75258:AF054174	F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-
F-MAMMA1003013//Human H0X4C mRNA for a homeobox protein//0.73:347:	13:248:69//Hs.1674:M90516
58//Hs.74061:X59372	F-NT2RM1000257//ESTs. Highly similar to similar to mago nashi [H.s
F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062	sapiens]//2.9e-98:530:93//Hs.104650:A1037879
F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:A1374951	F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-5
F-MAMMA1003026//EST//1.0:136:67//Hs.9123:Y50137	8:460:80//Hs.23106:DS0920
F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549	F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047
F-MAMMA1003035	F-NT2RM1000272
F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391	F-NT2RM1000280//ESTs. Highly similar to VACUOLAR ATP SYNTHASE SUB
F-MAMMA1003040//Homo sapiens tapasin (NCS-17) mRNA, complete cds//	UNIT D [Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144
1.5e-93:339:85//Hs.5247:AF029750	F-NT2RM1000300
F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639	F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-1
F-MAMMA1003047//H. sapiens mRNA for F25B3.3 kinase like protein fro	28:708:92//Hs.5719:D63880
m C. elegans//1.0:209:60//Hs.99491:Y12336	F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds
F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742	//1.8e-35:182:99//Hs.9837:D79205

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F-NT2RM1000341//ESTs//2.3e-72:381.95//Hs.23070:AA631976	s//0.084:386.58//Hs.101474:AB018350
F-NT2RM1000354//EST//5.2e-27:202.84//Hs.151186:AI125798	F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:29
F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7	9:59//Hs.83419:D87440
e-75:387.95//Hs.108619:W28608	F-NT2RM1000978
F-NT2RM1000365//ESTs//1.7e-99:495.97//Hs.103926:AA165691	F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP)
F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase	mRNA, complete cds//1.3e-161:760.98//Hs.58488:U97067
ase [H.sapiens]//7.4e-91:481.95//Hs.163707:AA137181	F-NT2RM1001008//ESTs//1.3e-12:144.75//Hs.133122:AI025200
F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.893	F-NT2RM1001043//EST//0.24:117.64//Hs.161536:N80395
9:X80507	F-NT2RM1001044//ESTs, Weakly similar to C43E11.9 [C.elegans]//3.0
F-NT2RM1000394//HISTONE H3.3//8.5e-91:474.93//Hs.118838:MI1353	e-98:491.96//Hs.102173:AA045270
F-NT2RM1000399	F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:53
F-NT2RM1000421	3:57//Hs.79706:U53204
F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP m	F-NT2RM1001066//ESTs//1.2e-114:538.99//Hs.129020:AI380703
RNA, complete cds//1.2e-85:418.97//Hs.20815:AF084928	F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//
F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapien	0.69:586.56//Hs.62354:M83822
s]//1.6e-38:201.97//Hs.106262:AI052382	F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth facto
F-NT2RM1000539//EST//0.070:145.62//Hs.149711:AI284660	r-like)//0.0019:294.64//Hs.30223:X90846
F-NT2RM1000553//EST//2.2e-48:265.95//Hs.99230:AA49847	F-NT2RM1001082//Archain//3.9e-37:290.81//Hs.33642:X81198
F-NT2RM1000555//ESTs//0.82:193.61//Hs.96944:AI359957	F-NT2RM1001085
F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:	F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770.68//Hs.
58//Hs.79706:U53204	74107:X59244
F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//	F-NT2RM1001102//ESTs//1.2e-35:638.63//Hs.131737:AI343331
0.98:226.61//Hs.17931:AB006625	F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246.63//Hs.75188:
F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER	U10564
5 and other AHPC/TSA proteins [C.elegans]//6.2e-51:254.98//Hs.1320	F-NT2RM1001112//ESTs//8.9e-82:437.93//Hs.6330:M38495
96:AA314601	F-NT2RM1001115
F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA	F-NT2RM1001139//Keratin 9//1.5e-05:518.59//Hs.2783:Z29074
A, complete cds//8.5e-55:276.97//Hs.19122:AF038957	F-NT2RM2000006//ESTs//3.9e-16:96.98//Hs.101117:AA576113
F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60	F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:
//Hs.113936:AB005297	640.59//Hs.148027:X63563
F-NT2RM1000669//ESTs//5.5e-63:481.85//Hs.90527:AI188279	F-NT2RM2000030
F-NT2RM1000672	F-NT2RM2000032//ESTs//7.1e-18:138.68//Hs.114031:AA700958
F-NT2RM1000691//Homo sapiens mRNA for HRHFB2060, partial cds//7.0	F-NT2RM2000042//ESTs//0.0091:241.61//Hs.147895:AI286243
e-121:582.98//Hs.146282:AB015348	F-NT2RM2000092
F-NT2RM1000699//ESTs//1.1e-89:435.97//Hs.28964:AA715101	F-NT2RM2000093//ESTs//2.6e-40:226.94//Hs.163521:H42085
F-NT2RM1000702//ESTs//5.4e-90:429.99//Hs.151001:AA564706	F-NT2RM2000101//ESTs//1.0:235.61//Hs.48860:N27428
F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//	F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//
1.5e-66:435.85//Hs.5038:AJ004832	5.8e-46:287.88//Hs.77271:X07767
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cd	F-NT2RM2000191//Homo sapiens cAMP phosphodiesterase A1 (PDE9A) mRNA
s//2.6e-127:690.92//Hs.147946:AB011139	A, complete cds//3.0e-139:566.97//Hs.18953:AF067223
F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2	F-NT2RM2000192//EST//3.5e-07:168.65//Hs.163122:AA756999
e-68:524.83//Hs.112360:AF027208	F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-
F-NT2RM1000746//ESTs//2.6e-37:231.89//Hs.94446:AA845465	93:489.95//Hs.143499:R72672
F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:	F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete c
321.63//Hs.150390:AB007885	ds//2.8e-176:805.99//Hs.129952:AB011132
F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3)	F-NT2RM2000363//ESTs//1.2e-24:139.96//Hs.48818:N63543
p36 subunit//0.053:271.60//Hs.139745:U39067	F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK
F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frame	7 mRNA, partial cds//3.7e-96:599.86//Hs.75871:U48251
s//6.9e-20:128.94//Hs.23094:M19503	F-NT2RM2000371
F-NT2RM1000781//ESTs//4.4e-60:346.92//Hs.35089:N50845	F-NT2RM2000374//ESTs//3.2e-13:98.91//Hs.65853:AI050866
F-NT2RM1000800	F-NT2RM2000395//Growth arrest-specific 1//0.80:129.67//Hs.65029:LI
F-NT2RM1000802	3698
F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2	F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714.59//Hs.2
e-64:490.84//Hs.112360:AF027208	8757:U81006
F-NT2RM1000826//ESTs//0.82:193.61//Hs.96944:AI359957	F-NT2RM2000407//ESTs//9.4e-92:458.96//Hs.148873:T33582
F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//	F-NT2RM2000420//EST//1.8e-61:296.99//Hs.147186:AI193053
0.92:283.58//Hs.2314:X15422	F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transpor
F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:17	ter, serotonin), member 4//1.5e-06:260.61//Hs.553:L05568
8:67//Hs.1376:U26726	F-NT2RM2000452//ESTs//1.0:132.62//Hs.110004:AI097379
F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequenc	F-NT2RM2000469//ESTs//0.34:249.60//Hs.149575:AI281807
e//3.8e-06:384.59//Hs.90314:L05148	F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cd
F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase,	s//2.4e-16:386.63//Hs.8309:AB018290
partial//3.0e-149:726.97//Hs.99423:AJ010840	F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA
F-NT2RM1000857//ESTs//0.52:274.60//Hs.112095:AA447643	A, complete cds//0.99:272.61//Hs.76669:U08021
F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//	F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complet
5.3e-54:277.96//Hs.11125:AI015619	e cds//1.6e-172:824.97//Hs.4812:AF061243
F-NT2RM1000874//ESTs//0.032:185.64//Hs.97713:AA442239	F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.1
F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2	8:313.60//Hs.129725:AF047487
69730) containing the HFEM1 gene//4.0e-155:750.97//Hs.132898:AC004	F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.el
770	egans]//2.7e-41:231.94//Hs.7049:AI141736
F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA,	F-NT2RM2000556//ESTs//3.1e-33:183.96//Hs.136990:AA769220
complete cds//8.8e-158:762.97//Hs.26285:AF082516	F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751.97//Hs.74369:AF03
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete c	
ds//6.3e-19:310.67//Hs.65238:AB014561	
F-NT2RM1000894	
F-NT2RM1000898	
F-NT2RM1000905//EST//4.8e-07:77.84//Hs.148017:AI268701	
F-NT2RM1000924//HOMEBOX PROTEIN HOX-A5//0.00051:458.59//Hs.37034:	
M26679	
F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cd	

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## 【表563】

- 2108  
F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508  
F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128  
F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETAS E, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993  
F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:D86987  
F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220  
F-NT2RM2000594  
F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:AF040963  
F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313  
F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548  
F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093  
F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258  
F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:AB018272  
F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558  
F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:A1189702  
F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:AB014576  
F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:A1337371  
F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.5321:AF006083  
F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D85984  
F-NT2RM2000718//Homo sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342  
F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244  
F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286  
F-NT2RM2000795//Homo sapiens tapasin (NCS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750  
F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338  
F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:A1346701  
F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580:AB015046  
F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075:A1023761  
F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433  
F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831  
F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs.17035:A1080471  
F-NT2RM2001065  
F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258  
F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153  
F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190  
F-NT2RM2001141  
F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042  
F-NT2RM2001177  
F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:A1286739  
F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959  
F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630  
F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349  
F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:A1004766  
F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928  
F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:AF039694  
F-NT2RM2001256  
F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845  
F-NT2RM2001306//Homo sapiens paroxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601  
F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615  
F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:A1138605  
F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567  
F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706  
F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905  
F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:24:61//Hs.82925:U70322  
F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382  
F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378  
F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:AJ007509  
F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303  
F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903  
F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969  
F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459  
F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262  
F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800  
F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077  
F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902  
F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:A1391729  
F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431  
F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:A1016073  
F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:A1393918  
F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518  
F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:A1276952  
F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725  
F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:A1016073  
F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301  
F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287  
F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195  
F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907  
F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129  
F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:A1365356  
F-NT2RM2001675  
F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305  
F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211  
F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216  
F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937  
F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:A1277415  
F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:A1003817  
F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826  
F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788  
F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:W81650  
F-NT2RM2001718  
F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123  
F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931  
F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132  
F-NT2RM2001743  
F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399  
F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:A1016073  
F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:A1222742  
F-NT2RM2001771//Zinc finger protein 10 (KIX 1)//1.1e-66:569:71//Hs.2479:X78933  
F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698  
F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:A1193595  
F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2

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69730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770	F-NT2RM4000155
F-NT2RM2001797//Human mRNA for KIAA0055 gene, partial cds//6.1e-6	F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
6:481:72//Hs.70617:D31763	F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//Hs.159228:AF041853
F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, c	F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
complete cds//0.49:142:66//Hs.78202:U29175	F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190
F-NT2RM2001803//Homo sapiens I kappa B kinase complex associated pro	F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
tein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195	F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARN1
F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341	NG ENTRY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147
F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068	F-NT2RM4000200
F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:55	F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//
4:60//Hs.74441:X86691	0.0027:424:60//Hs.91400:AB006626
F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//	F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete c
1.2e-132:738:90//Hs.7753:AF013759	ds//4.4e-184:856:98//Hs.111138:AB018255
F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8	F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//
e-58:329:86//Hs.113283:AF018080	0.0013:358:60//Hs.75055:M93651
F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M5	F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete c
7567	ds//0.65:572:60//Hs.47061:AF045458
F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-	F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
28:421:66//Hs.8763:W30741	F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723	F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccha
F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete c	romyces pombe]//1.1e-16:112:92//Hs.93841:AA442297
ds//6.1e-189:866:97//Hs.4198:AB014610	F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferas
F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete codin	e, complete cds//1.8e-48:229:83//Hs.46328:DB7942
g sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLC1101133Q7	F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRN
(RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892	A, complete cds//2.5e-154:609:93//Hs.31305:M99438
F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cd	F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complet
s//9.4e-178:859:97//Hs.129937:AB007931	e cds//0.070:460:59//Hs.5372:AB000712
F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete c	F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707
ds//4.2e-08:481:59//Hs.27621:U52840	F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyc
F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROT	es cerevisiae]//2.7e-83:432:95//Hs.12796:W27884
Ein HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U	F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-5
66588	3:666:68//Hs.155291:D13630
F-NT2RM2001935//Homo sapiens clone 614 unknown mRNA, complete sequ	F-NT2RM4000354//ESTs, Weakly similar to lethal (2)denticleless [D.m
ence//2.2e-139:653:98//Hs.21811:AF091080	elanogaster]//0.0078:55:92//Hs.59075:AI023761
F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392	F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425
F-NT2RM2001982	F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cd
F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, parti	s//5.3e-135:628:99//Hs.8152:AB014542
al cds//1.2e-21:123:98//Hs.6454:AF089816	F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745
F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//H	F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome
s.104135:AJ006778	Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's
F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538	dis disease (lymphoproliferative syndrome) (DSHP), part of a 60S Aci
F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//	dic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DDC4
0.99:271:60//Hs.63888:AA203398	LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022
F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cd	718
s//3.5e-37:509:65//Hs.6214:AB018274	F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)/
F-NT2RM2002014//Homo sapiens mRNA for CRMI protein, complete cds//	0.63:166:65//Hs.946:X73029
0.79:429:58//Hs.79090:D89729	F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete
F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-	cds//4.9e-17:114:94//Hs.137580:AB015046
89:822:73//Hs.1674:M90516	F-NT2RM4000421
F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427	F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cd
F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154	s//1.1e-42:432:74//Hs.154872:AB011166
F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377	F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)
F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//	//0.023:543:58//Hs.2175:M59820
Hs.89631:U48508	F-NT2RM4000457
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase,	F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRN
partial//2.5e-165:776:98//Hs.99423:AJ010840	A, complete cds//0.060:178:63//Hs.66369:U95040
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 prot	F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004
ein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435	F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632
F-NT2RM2002128	F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915
F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274	F-NT2RM4000514
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP m	F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409
RNA, complete cds//1.4e-144:800:92//Hs.20815:AF084928	F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cd	F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4
s//1.7e-165:787:97//Hs.11147:AB007936	[Mus musculus]//1.8e-153:756:96//Hs.125870:AI364967
F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis: keratosis	F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:M78987
palmaris et plantaris) //0.064:291:61//Hs.99936:X14487	F-NT2RM4000534
F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD) //8.0e-10:	F-NT2RM4000585
610:59//Hs.148027:X63563	F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete c
F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074	ds//1.2e-19:593:62//Hs.7764:AB007938
F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464	F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROT
F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674	Ein CO2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:5
F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511	32:96//Hs.6092:T75227
F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product	F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-1
is related to human RNA helicase A. [H.sapiens]//1.6e-30:369:70//H	s:305:68//Hs.40100:AB002390
s.114623:AI204280	F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068
F-NT2RM4000086	F-NT2RM4000616
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF	F-NT2RM4000674
210 (ZNF210) mRNA, complete cds//1.3e-24:345:68//Hs.13128:AF060865	F-NT2RM4000689
F-NT2RM4000139	F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529

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F-NT2RM4000700	9:356:59//Hs.26971:AC003003
F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.42400:AF022789	F-NT2RM4001313//H. sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973
F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163:771:97//Hs.6823:W18181	F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335
F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605	F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016
F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cd s//1.2e-159:743:98//Hs.137168:AB018303	F-NT2RM4001340//EST//0.40:135:70//Hs.161198:A1418988
F-NT2RM4000741	F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714
F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs.112361:R99396	F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANX repe at region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818
F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:M67815	F-NT2RM4001371//EST//0.52:262:59//Hs.145991:A1277656
F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731	F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:AF098799
F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete c ds//1.8e-173:810:98//Hs.18586:AB007920	F-NT2RM4001384
F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186	F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs.25817:AC005306	F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520
F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLSTERASE PR ECURSOR [Homo sapiens]//6.7e-19:160:80//Hs.124902:A1337820	F-NT2RM4001412
F-NT2RM4000796//Human Kt channel subunit gene, complete cds//0.96:292:62//Hs.124212:M64676	F-NT2RM4001414//ESTs, Moderately similar to F18547_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:A1073817
F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301	F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087
F-NT2RM4000813//Homo sapiens sRNA activating protein complex 190k D subunit (SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF 032387	F-NT2RM4001444
F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:M16568	F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658
F-NT2RM4000833	F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914
F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//Hs.7841:AB002322	F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784
F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934	F-NT2RM4001489//Homo sapiens mRNA for KIAA0585 protein, complete c ds//3.9e-157:724:99//Hs.153121:AB014585
F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapiens]//4.4e-29:164:95//Hs.115095:A13929 43	F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619
F-NT2RM4000887	F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.c erevisiae]//1.3e-114:536:99//Hs.88820:AA456247
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosami ne pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011 004	F-NT2RM4001557
F-NT2RM4000950	F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487
F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:A1014546	F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subu nit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453
F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875	F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:A1198859
F-NT2RM4000996//Zinc finger protein 3 (AB-51)//8.7e-34:381:67//Hs.2481:X78926	F-NT2RM4001582
F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cd s//1.6e-171:803:98//Hs.19542:AB018272	F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cd s//1.1e-126:584:99//Hs.15711:AB014539	F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cd s//0.0072:484:60//Hs.129892:AB011094
F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete c ds//4.8e-05:469:58//Hs.5333:AB018254	F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077
F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.muscul us]//7.0e-56:340:92//Hs.87310:A1247543	F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete c ds//1.1e-163:750:99//Hs.23255:AB018334
F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I " A FORM" PRECURSOR//0.79:142:69//Hs.77424:M63835	F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739
F-NT2RM4001084	F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEM BRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:A1147946
F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758	F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339
F-NT2RM4001116	F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320
F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701	F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323
F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730	F-NT2RM4001682//EST//0.027:145:70//Hs.133253:A1052638
F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:A1004145	F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384
F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351	F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957
F-NT2RM4001187	F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:A1332905
F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220	F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M139 03
F-NT2RM4001200//Zinc finger protein 10 (KIX 1)//4.0e-68:799:69//H s.2479:X78933	F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, comp lete cds//1.4e-153:707:99//Hs.14934:AF004828	F-NT2RM4001746//H. sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306
F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205	F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POL YPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719
F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) m RNA, complete cds//7.0e-63:715:70//Hs.104925:AF059611	F-NT2RM4001758//H. sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630
F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homo log [C.elegans]//1.1e-67:208:96//Hs.26676:AA033997	F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cd s//7.4e-175:803:99//Hs.39871:AB018270
F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete c ds//0.0019:435:59//Hs.6360:AB007950	F-NT2RM4001783//ESTs, Weakly similar to T12D8.1 [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677
F-NT2RM4001309//Human Chromosome 16 BAC clone C17987SK-254P9//0.01	F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105
	F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547

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F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712	F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:A1205764
F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens]//2.3e-40:252:90//Hs.119294:A1379442	F-NT2RM4002266//Human kinase Mytl (Mytl) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118
F-NT2RM4001828//Zinc finger protein 157 (ZF22)//1.8e-75:688:72//Hs.89897:U28687	F-NT2RM4002278//EST//0.33:138:63//Hs.144096:A1032180
F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824	F-NT2RM4002281
F-NT2RM4001841//ESTs//0.85:156:67//Hs.146276:A1214204	F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979
F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814	F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457
F-NT2RM4001856	F-NT2RM4002301
F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250	F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:A1343331
F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CA LC//2.3e-150:704:98//Hs.61628:Y17711	F-NT2RM4002339
F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984	F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454
F-NT2RM4001880	F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:AB014549
F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:A1204212	F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263
F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:A1312633	F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:W0293
F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875	F-NT2RM4002390
F-NT2RM4001938	F-NT2RM4002398
F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162	F-NT2RM4002409
F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087	F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C. elegans]//1.1e-55:282:96//Hs.26676:AA033997
F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H. sapiens]//1.8e-65:337:96//Hs.130135:AA905493	F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151
F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:A1312862	F-NT2RM4002452
F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341	F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783
F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082	F-NT2RM4002460//EST//1.0:142:65//Hs.145370:A1252780
F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936	F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.8765:AF083255
F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:A1302271	F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591
F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601	F-NT2RM4002493
F-NT2RM4002034	F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:M99347
F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048	F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219
F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912	F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020
F-NT2RM4002055//Homo sapiens mRNA for KIAA0540 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540	F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075
F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:A126802	F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176
F-NT2RM4002063	F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004
F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309	F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273
F-NT2RM4002067//EST//2.3e-34:455:69//Hs.118273:AA626040	F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C. elegans]//3.3e-88:484:93//Hs.105837:AA536054
F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302	F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase [H. sapiens]//0.059:121:70//Hs.155413:AA429394
F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.12967:AF059569	F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151
F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) [alternative products]//9.2e-34:532:65//Hs.146459:X66975	F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275
F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743	F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402
F-NT2RM4002128//Homo sapiens mRNA for KIAA0542 protein, partial cds//0.93:202:63//Hs.8152:AB014542	F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587
F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877	F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449
F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158	F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907
F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H. sapiens]//1.6e-135:646:97//Hs.104650:A1037879	F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647
F-NT2RM4002161//Homo sapiens laforin (EPN2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535	F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834
F-NT2RM4002174	F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924
F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998	F-NT2RP1000111
F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276	F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699
F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454	F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:A1084025
F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182	F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H. sapiens]//1.4e-71:382:94//Hs.127842:W38901
F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//8.4e-125:588:98//Hs.23900:U82984	F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792
F-NT2RM4002251//EST//1.0:77:74//Hs.155135:AA910966	F-NT2RP1000170//EST//0.68:130:63//Hs.146994:A1184430
	F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535
	F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499
	F-NT2RP1000202//H. sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703
	F-NT2RP1000243
	F-NT2RP1000259

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F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.4214:AF067730  
 F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:NA1661  
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551  
 F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231  
 F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204  
 F-NT2RP1000357  
 F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807  
 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:85//Hs.77864:AB014538  
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594  
 F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031  
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159  
 F-NT2RP1000416//ESTs. Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181  
 F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815  
 F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603  
 F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862  
 F-NT2RP1000460  
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R2709 0, genomic sequence//3.7e-134:665:96//Hs.143187:AC002985  
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634  
 F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102  
 F-NT2RP1000493  
 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977  
 F-NT2RP1000522//Homo sapiens clone DT1PIA11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992  
 F-NT2RP1000547//H. sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098  
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418  
 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213  
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385  
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC C17-HSP-311e8 (BC2 69730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770  
 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475  
 F-NT2RP1000630  
 F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576  
 F-NT2RP1000688//ESTs. Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553  
 F-NT2RP1000695//ESTs. Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736  
 F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148  
 F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612  
 F-NT2RP1000730//ESTs. Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:A1338045  
 F-NT2RP1000733//GI to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644  
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434  
 F-NT2RP1000746  
 F-NT2RP1000767  
 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023  
 F-NT2RP1000796//H. sapiens mRNA for RDX protein//0.17:404:57//Hs.25497:X96401  
 F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 2 2q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat//2.7e-23:147:91//Hs.102336:Z83838  
 F-NT2RP1000833//Homo sapiens cAMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:95//Hs.18953:AF067223  
 F-NT2RP1000834//EST//0.18:280:60//Hs.157215:A1332903  
 F-NT2RP1000836//EST//0.60:103:66//Hs.145708:A1267990  
 F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:A1288838  
 F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875  
 F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023  
 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094  
 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:A1218683  
 F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:A1248847  
 F-NT2RP1000916//ESTs. Weakly similar to coded for by C. elegans CD NA cm04e9 [C.elegans]//2.2e-27:159:94//Hs.122153:AA780270  
 F-NT2RP1000943//Human hSLAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248  
 F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA658400  
 F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds//2.7e-26:185:87//Hs.108332:U93317  
 F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803  
 F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:A1248847  
 F-NT2RP1000959//Ribosomal protein, large, PO//0.36:76:73//Hs.73742:M17885  
 F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858  
 F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:M28866  
 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435  
 F-NT2RP1001011  
 F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:A1089163  
 F-NT2RP1001014  
 F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764  
 F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901  
 F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:A1360531  
 F-NT2RP1001080//Homo sapiens forkhead protein (FKHL1) mRNA, complete cds//0.57:215:64//Hs.14845:AF032886  
 F-NT2RP1001113//ESTs. Weakly similar to coded for by C. elegans CD NA CEESB2F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087  
 F-NT2RP1001173  
 F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174  
 F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524  
 F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:A1022150  
 F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523  
 F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:A1337094  
 F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231  
 F-NT2RP1001286//H. sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724  
 F-NT2RP1001294  
 F-NT2RP1001302  
 F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341  
 F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:M67815  
 F-NT2RP1001313//Homo sapiens chromosome 11, BAC C17-HSP-311e8 (BC2 69730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770  
 F-NT2RP1001361//ESTs. Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853  
 F-NT2RP1001385//EST//0.86:127:65//Hs.156304:A1336859  
 F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673  
 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081  
 F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700  
 F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700  
 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149  
 F-NT2RP1001457//H. sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104  
 F-NT2RP1001466  
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742  
 F-NT2RP1001482  
 F-NT2RP1001494  
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:A1016400  
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277  
 F-NT2RP1001569  
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, parti

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al cds//2.5e-41:496:74//Hs.12956:U90913  
 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420  
 F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequ  
 ence//4.7e-137:685:96//Hs.93677:AF091081  
 F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2  
 e-47:300:89//Hs.6473:AA853955  
 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-1  
 5:241:68//Hs.40100:AB002390  
 F-NT2RP2000008//Human mRNA for KIAA0055 gene, partial cds//1.5e-2  
 9:526:66//Hs.70617:D31763  
 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPT  
 ASE HOMOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359  
 F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:A103867  
 F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cd  
 s//6.1e-78:383:97//Hs.8309:AB018290  
 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56  
 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF0617  
 49  
 F-NT2RP2000054//HOMEBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.  
 74095:L20433  
 F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosph  
 atase epsilon//1.2e-27:146:100//Hs.155991:X54134  
 F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome  
 Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's  
 disease (lymphoproliferative syndrome) (DSHP), part of a 60S Aci  
 dic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DDC4  
 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022  
 718  
 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBML  
 H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609  
 F-NT2RP2000076//H.sapiens mRNA for TFIIA//0.00023:356:62//Hs.12168  
 6:D14887  
 F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRN  
 A, complete cds//6.8e-79:278:97//Hs.54877:AF050078  
 F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:A1279879  
 F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cd  
 s//7.1e-160:752:98//Hs.22926:AB018338  
 F-NT2RP2000091  
 F-NT2RP2000097  
 F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:A1371963  
 F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-1  
 8:200:77//Hs.40100:AB002390  
 F-NT2RP2000114//Homo sapiens mRNA for CM3 synthase, complete cds//  
 1.6e-115:551:97//Hs.17706:AB018356  
 F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTE  
 IN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22  
 670  
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding pro  
 tein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177  
 F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29  
 195  
 F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, co  
 mplete cds//2.2e-18:559:60//Hs.152936:D63475  
 F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complet  
 e cds//0.33:85:70//Hs.256:L10910  
 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291  
 F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:A1188190  
 F-NT2RP2000173  
 F-NT2RP2000175  
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related  
 protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713  
 F-NT2RP2000195//ESTs, Weakly similar to C3TE2.2 [C.elegans]//3.6e-  
 37:233:90//Hs.56750:A1148761  
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050  
 F-NT2RP2000208  
 F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related  
 protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462  
 F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990  
 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//  
 0.17:342:59//Hs.8546:U97669  
 F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:22  
 7:60//Hs.47822:AB002378  
 F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719  
 F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth facto  
 r-like)//0.51:227:60//Hs.30223:X90846  
 F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691  
 F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011  
 F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599  
 F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910  
 F-NT2RP2000288  
 F-NT2RP2000289  
 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRN  
 A, complete cds//4.2e-60:744:70//Hs.37138:U35376  
 F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:A1123467  
 F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PROD  
 H) mRNA, complete cds//4.3e-13:140:80//Hs.58218:U82381  
 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:A1417006  
 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:A1332905  
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:  
 607:66//Hs.101642:X60673  
 F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//  
 0.96:126:69//Hs.153706:AF026547  
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34)  
 mRNA, complete cds//1.2e-130:627:97//Hs.76556:U83981  
 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cd  
 s//0.56:464:57//Hs.12259:AB014530  
 F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047  
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//  
 1.6e-67:375:93//Hs.808:L28010  
 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.  
 sapiens]//3.9e-75:413:92//Hs.36779:AA626790  
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase  
 mRNA, complete cds//6.7e-128:609:96//Hs.5819:AF102265  
 F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381  
 F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:A1393918  
 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.1  
 54655:Z68747  
 F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293  
 F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702  
 F-NT2RP2000510  
 F-NT2RP2000516  
 F-NT2RP2000523//ESTs, Highly similar to APOLIPROTEIN B mRNA EDI  
 TING PROTEIN [Rattus norvegicus]//3.2e-15:167:75//Hs.10984:AA80676  
 8  
 F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cd  
 s//5.6e-38:196:98//Hs.14409:AB011144  
 F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha  
 (cardiomyopathy, hypertrophic 1)//1.0:242:57//Hs.114001:Z20656  
 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cd  
 s//4.2e-151:732:97//Hs.7314:AB014514  
 F-NT2RP2000646//ESTs//0.035:276:60//Hs.43660:N33174  
 F-NT2RP2000656  
 F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA20602  
 F-NT2RP2000668  
 F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:A1093453  
 F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONIN  
 E-PROTEIN KINASE CA1C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis  
 elegans]//2.4e-31:233:78//Hs.114905:AA088442  
 F-NT2RP2000710  
 F-NT2RP2000715  
 F-NT2RP2000731  
 F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242  
 F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN  
 [Saccharomyces cerevisiae]//1.6e-74:445:89//Hs.21421:AA911739  
 F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101  
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.2  
 2:351:58//Hs.159275:AF030880  
 F-NT2RP2000814  
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cd  
 s//1.0:311:61//Hs.118087:AB011182  
 F-NT2RP2000819  
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-2  
 8:390:70//Hs.20695:AB002292  
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA,  
 complete cds//9.5e-29:167:94//Hs.75794:U80811  
 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:A1336850  
 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROT  
 EIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:  
 207:92//Hs.135235:A1081880  
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete c  
 ds//7.7e-142:732:94//Hs.3615:AB018284  
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase k  
 inase kinase 5 [H.sapiens]//0.50:189:65//Hs.46146:AA418097  
 F-NT2RP2000931//MATRIN 3//1.1e-130:610:98//Hs.78825:AB018266  
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from T2p1//5.5e-6  
 6:326:97//Hs.15144:AC005014  
 F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408  
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete c  
 ds//1.9e-113:533:98//Hs.19822:AB018298  
 F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494

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【表569】

F-NT2RP2000970	5:65//Hs.82201:M55268
F-NT2RP2000985//ESTs. Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN S1S2-WT01 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3 e-76:385:96//Hs.21875:AA243700	F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:AB018340
F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944	F-NT2RP2001613
F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292	F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:A1082229
F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117	F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//Hs.58488:U97067
F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.67619:AB007957	F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.159558:AF058718
F-NT2RP2001065	F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328
F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313	F-NT2RP2001675//X-LINKED HELICASE 11//0.040:454:58//Hs.96264:U72936
F-NT2RP2001081	F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314
F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:A1356560	F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621:U52840
F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219	F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091
F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191	F-NT2RP2001720//ESTs. Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:A197870
F-NT2RP2001137//ESTs. Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:A1336362	F-NT2RP2001721
F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582	F-NT2RP2001740//Homo sapiens Rigui (RIGU1) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991
F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:A1091361	F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)//1.2e-19:151:86//Hs.77393:U14697
F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:AB007949	F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//5.2e-34:191:96//Hs.47504:AF091754
F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011	F-NT2RP2001813//EST//0.46:183:57//Hs.144096:A1032180
F-NT2RP2001196	F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:A1052250
F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598	F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610
F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053	F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219
F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367	F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768
F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813	F-NT2RP2001883
F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353	F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE P RECURSOR//3.0e-113:633:90//Hs.142189:M74161
F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277	F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650
F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412	F-NT2RP2001907//ESTs. Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757
F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287	F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:A1393754
F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:A1146387	F-NT2RP2001936
F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783	F-NT2RP2001943
F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522	F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883	F-NT2RP2001947
F-NT2RP2001366//ESTs. Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244	F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
F-NT2RP2001378	F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892
F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:A1377558	F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB011117
F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203a13 (LBML H155), complete sequence//0.28:225:62//Hs.159402:ACD05609	F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196
F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:A1189767	F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299
F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088	F-NT2RP2002032
F-NT2RP2001420	F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:A1003543
F-NT2RP2001423//ESTs. Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018	F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336
F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:A1032875	F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509
F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966	F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:A1284198
F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248	F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284
F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218	F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634
F-NT2RP2001449	F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241
F-NT2RP2001450	F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183
F-NT2RP2001467	F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014
F-NT2RP2001506	F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:A1313156
F-NT2RP2001511//ESTs. Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:A1333779	F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein //3.2e-112:533:97//Hs.155218:AJ007509
F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:Y14494	F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.122755:AF032986
F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134	F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286
F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586	F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:MB3363
F-NT2RP2001560	F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112
F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.67619:AB007957	F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:A1085314
F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389	F-NT2RP2002185//ESTs. Weakly similar to ubiquitin S6 (1) [D.melanog
F-NT2RP2001581//EST//1.0:28:96//Hs.148002:A1264876	
F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:16	

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aster]/6.8e-61:354:91//Hs.109966:C06057  
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Scl) mRNA, complete cds//3.7e-37:194:97//Hs.91728:M58460  
 F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT p  
 rotein PIASx-alpha mRNA, complete cds//6.8e-15:228:67//Hs.111323:A  
 F077954  
 F-NT2RP2002208  
 F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628  
 F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:A1394318  
 F-NT2RP2002235//H.sapiens mRNA for PHAP12b protein//0.86:67:82//H  
 s.84264:U70439  
 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cd  
 s//0.79:264:59//Hs.129748:AB011099  
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, compl  
 ete cds//2.1e-51:315:89//Hs.150595:AF005418  
 F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:34  
 3:71//Hs.92137:M19720  
 F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//  
 1.3e-31:206:88//Hs.4029:278373  
 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079  
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2)  
 mRNA, partial cds//5.0e-95:467:96//Hs.24812:AF069532  
 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445  
 F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11  
 a) mRNA, complete cds//1.3e-124:640:95//Hs.31034:AB015594  
 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:2  
 57:60//Hs.75516:X54637  
 F-NT2RP2002373  
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced var  
 iant mRNA, complete cds//3.1e-139:673:97//Hs.109051:AF038958  
 F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.9  
 0798:U79289  
 F-NT2RP2002408//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.0069:265:65/  
 /Hs.74095:L20433  
 F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:A1269098  
 F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326  
 F-NT2RP2002442//ESTs, Weakly similar to similar to molybdenum bi  
 osynthesis MDEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA9  
 04265  
 F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:A1091436  
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.001  
 3:207:63//Hs.1560:D42045  
 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:A1139929  
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, c  
 omplete cds//7.6e-125:607:96//Hs.125856:AB005289  
 F-NT2RP2002498  
 F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete c  
 ds//2.2e-89:314:87//Hs.102681:U95044  
 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete c  
 ds//3.8e-159:761:97//Hs.23255:AB018334  
 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.  
 107563:M28212  
 F-NT2RP2002537  
 F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096  
 F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979  
 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete c  
 ds//2.9e-33:285:78//Hs.159277:AB018341  
 F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:  
 235309  
 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frame  
 s//6.4e-24:144:95//Hs.23094:M19503  
 F-NT2RP2002609//Human guanine nucleotide regulatory protein (tial)  
 mRNA, complete cds//1.0:120:68//Hs.334:U02082  
 F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, spi  
 ce variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805  
 F-NT2RP2002621  
 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, com  
 plete cds//0.0022:210:64//Hs.155302:U57317  
 F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:M52493  
 F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROT  
 EIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:27  
 8:97//Hs.109857:AA088385  
 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58  
 583  
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete c  
 ds//8.0e-42:631:65//Hs.6336:AB014572  
 F-NT2RP2002727  
 F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217  
 F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:A1150297  
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-3  
 0:628:62//Hs.87435:D89016  
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-2  
 9:285:75//Hs.146395:AB002329  
 F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709  
 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705  
 F-NT2RP2002769//Human pleiotin (PLEC1) mRNA, complete cds//0.017:50  
 7:57//Hs.79706:U53204  
 F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:A1216407  
 F-NT2RP2002800  
 F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763  
 F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:A1382142  
 F-NT2RP2002862  
 F-NT2RP2002880  
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cd  
 s//1.0:237:62//Hs.106487:AB014573  
 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:M22606  
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRN  
 A, complete cds//3.9e-136:623:99//Hs.116674:AF038392  
 F-NT2RP2002929//Homo sapiens ataxin-7 (SCAT7) mRNA, complete cds//  
 0.24:158:65//Hs.108447:AJ000517  
 F-NT2RP2002939  
 F-NT2RP2002954  
 F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH  
 5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317  
 F-NT2RP2002979  
 F-NT2RP2002980  
 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, co  
 mplete cds//7.8e-11:272:61//Hs.122967:AF059569  
 F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:A1004740  
 F-NT2RP2002993  
 F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:  
 81//Hs.155464:AF088219  
 F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741  
 F-NT2RP2003073//Human clone 230971 defective mariner transposon Hs  
 mar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019  
 F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190  
 F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:  
 67//Hs.153704:U11050  
 F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633  
 F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:A1291379  
 F-NT2RP2003125//Serum response factor (c-fos serum response elemen  
 t-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161  
 F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544  
 F-NT2RP2003137  
 F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cd  
 s//0.40:227:61//Hs.105958:AB014520  
 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, comp  
 lete cds//5.7e-113:581:93//Hs.9736:D67025  
 F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:A1424170  
 F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944  
 F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-3  
 9:342:79//Hs.153014:AB002353  
 F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:M91123  
 F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:A1393223  
 F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594  
 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794  
 F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947  
 F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-  
 4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//H  
 s.108966:U48696  
 F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclea  
 r protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153  
 F-NT2RP2003265  
 F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanog  
 aster]//5.8e-57:313:93//Hs.109966:C06057  
 F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cd  
 s//4.9e-147:714:96//Hs.154919:AB014525  
 F-NT2RP2003280  
 F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete c  
 ds//0.0097:243:65//Hs.21862:AB011159  
 F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:A1269334  
 F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 mediating protein,  
 complete cds//2.0e-86:416:97//Hs.7943:AB006572  
 F-NT2RP2003297//EST//0.99:240:60//Hs.133228:A1052312  
 F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752  
 F-NT2RP2003308  
 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROT  
 EIN CD2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:5  
 32:95//Hs.6092:T75227  
 F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:A1346765

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F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963	F-NT2RP2003912//ESTs. Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA ( <i>Emmericella nidulans</i> )//2.2e-113:632:92//Hs.50072:A1378221
F-NT2RP2003367//Human HsLIM15 mRNA for HsLIM15, complete cds//0.9:243:60//Hs.37181:D64108	F-NT2RP2003952//ESTs. Moderately similar to 60S RIBOSOMAL PROTEIN L32 [ <i>H.sapiens</i> ]//1.0:146:67//Hs.156920:AA489296
F-NT2RP2003391	F-NT2RP2003968//Homo sapiens HUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.35085:AB014458
F-NT2RP2003393	F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916
F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023	F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347
F-NT2RP2003401	F-NT2RP2003984
F-NT2RP2003433//ESTs. Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [ <i>Canis familiaris</i> ]//3.7e-33:303:77//Hs.14038:R06800	F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:A1050036
F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893	F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
F-NT2RP2003446//Prostaglandin receptor, epl subtype//0.81:273:61//Hs.159360:L22647	F-NT2RP2004013//ESTs. Highly similar to TRANSCRIPTION FACTOR BTF3 [ <i>Homo sapiens</i> ]//7.0e-104:556:93//Hs.111081:A1380378
F-NT2RP2003456//EST//0.17:95:65//Hs.147190:A1193320	F-NT2RP2004014
F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2 69730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770	F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106	F-NT2RP2004042
F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136	F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573
F-NT2RP2003506	F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:A1217942
F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803	F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828
F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-7:8:403:94//Hs.78482:Y16270	F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (s human sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783	F-NT2RP2004142
F-NT2RP2003522//Zinc finger protein 148 (pH2-52)//1.1e-17:512:60//Hs.112180:AF039019	F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:A1138765	F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666
F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010	F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:A1419966
F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:A1356513	F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:A1343501
F-NT2RP2003564//Sjogren syndrome antigen A1 (SZKD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800	F-NT2RP2004187//ESTs. Moderately similar to zinc finger protein [ <i>H.sapiens</i> ]//1.7e-16:276:67//Hs.36779:AA626790
F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931	F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317
F-NT2RP2003581//EST//1.0:59:76//Hs.158575:A1368947	F-NT2RP2004196
F-NT2RP2003596//ESTs. Weakly similar to No definition line found [ <i>C.elegans</i> ]//1.3e-63:224:95//Hs.34627:AA126463	F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067	F-NT2RP2004226//ESTs. Weakly similar to teg292 protein [ <i>M.musculus</i> ]//1.8e-80:386:98//Hs.68791:AA527270
F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166	F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252	F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006	F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:A1032875	F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247	F-NT2RP2004245//ESTs. Weakly similar to No definition line found [ <i>C.elegans</i> ]//8.2e-51:474:74//Hs.108990:M25951
F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561	F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:49:0:60//Hs.112432:AC005263
F-NT2RP2003704//ESTs. Weakly similar to putative p150 [ <i>H.sapiens</i> ]//5.1e-44:269:91//Hs.139757:M95271	F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4, 5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097	F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416
F-NT2RP2003713	F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:M27735
F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180	F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879	F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme Ubch5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318	F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
F-NT2RP2003751	F-NT2RP2004365
F-NT2RP2003760	F-NT2RP2004366//Homo sapiens mRNA for OFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986
F-NT2RP2003764	F-NT2RP2004373
F-NT2RP2003769	F-NT2RP2004389//ESTs. Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09C8.3 IN CHROMOSOME III [ <i>Caenorhabditis elegans</i> ]//3.3e-97:47:7:98//Hs.30490:AA146916
F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677	F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
F-NT2RP2003777	F-NT2RP2004396//Homo sapiens BAC clone RGI35C18 from 7q21//1.4e-17:4:875:95//Hs.152759:AC005164
F-NT2RP2003781//ESTs. Weakly similar to C47D12.3 [ <i>C.elegans</i> ]//3.7e-63:356:92//Hs.16131:AA568689	F-NT2RP2004399//ESTs. Weakly similar to KOI12.1 [ <i>C.elegans</i> ]//1.2e-92:519:91//Hs.13275:A1341468
F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955	F-NT2RP2004400//EST//0.018:150:65//Hs.158739:A1375367
F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742	F-NT2RP2004412
F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368	F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944
F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425	F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687
F-NT2RP2003859	F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K <sup>+</sup> channel 1 (TASK) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823
F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780	F-NT2RP2004490
F-NT2RP2003885	F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:A1091203
	F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1)

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mRNA, complete cds//1.3e-29:270:79//Hs.73614:U83460	omplete cds//0.22:498:59//Hs.137574:AF055917
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cd	F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838
s//4.6e-139:687:96//Hs.129908:AB01163	F-NT2RP2005116//Homo sapiens mRNA for KIAA0564 protein, partial cd
F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:A1346891	s//6.4e-105:495:98//Hs.22616:AB014564
F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//	F-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dea
8.8e-06:291:61//Hs.132206:AF039694	d box protein)//9.2e-29:157:98//Hs.100555:X98743
F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:	F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
82//Hs.155464:AF088219	F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete c	F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, co
ds//0.98:136:64//Hs.28020:AB018309	mplete cds//8.3e-91:447:96//Hs.132226:AF045583
F-NT2RP2004594//ESTs. Highly similar to MKR2 PROTEIN [Mus musculu	F-NT2RP2005147
s]//1.0:104:68//Hs.125729:N98898	F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:A1357582
F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:	F-NT2RP2005162//ESTs. Weakly similar to Y53C12A.3 [C.elegans]//0.9
60//Hs.24756:U43895	7:80:73//Hs.107747:A1357868
F-NT2RP2004602//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNI	F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein
NG ENTRY !!!! [H. sapiens]//3.0e-59:273:93//Hs.12845:N28835	//4.4e-127:633:96//Hs.155218:AJ007509
F-NT2RP2004614//EST//0.99:103:68//Hs.148738:A1224908	F-NT2RP2005204//H. sapiens ST4 gene for ST4 Oncofetal antigen//0.00
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-1	34:187:66//Hs.82128:AJ012159
04:496:98//Hs.5198:AJ006291	F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from Tpl2-p14//1.
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cd	3e-66:340:95//Hs.8173:AC005189
s//5.2e-155:728:98//Hs.29956:AB007929	F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783
F-NT2RP2004675//EST//0.65:151:62//Hs.130504:A1003839	F-NT2RP2005254//H. sapiens mRNA for PHAP12b protein//1.0:101:71//H
F-NT2RP2004681	s.84264:U70439
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cd	F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete c
s//4.1e-61:327:94//Hs.154919:AB014525	ds//0.56:114:68//Hs.154503:U36341
F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942	F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, co
F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780	mplete cds//1.2e-40:594:65//Hs.81452:AF030555
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete c	F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:A1383932
ds//2.1e-118:582:96//Hs.4236:AB007947	F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRN
F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242	A, complete cds//2.3e-123:604:96//Hs.27007:AF060219
F-NT2RP2004761//EST//1.5e-09:303:65//Hs.148374:AA948183	F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:9
F-NT2RP2004768//ESTs. Highly similar to SERINE/THREONINE-PROTEIN	8//Hs.44766:AJ007590
KINASE PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504	F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833
F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p5	F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cd
4 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451	s//3.6e-97:483:96//Hs.115763:AB014576
F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, com	F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, co
plete cds//0.99:121:64//Hs.2864:L40157	mplete cds//2.6e-23:166:90//Hs.1569:U11701
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase	F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190k
beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF	D subunit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF
058953	032387
F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:W36043	F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cd
F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//	s//2.8e-30:456:66//Hs.44697:AB011138
6.8e-103:495:97//Hs.67052:AF054179	F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958
F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83	F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MB03 (MB0
//Hs.84775:W23161	3) mRNA, complete cds//1.4e-100:489:96//Hs.107254:AC005943
F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:A1290258	F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122
F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:W79111	F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mR
F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.	NA, complete cds//0.87:244:59//Hs.113252:U80761
5e-84:418:95//Hs.25619:AB007144	F-NT2RP2005407
F-NT2RP2004936	F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cd
F-NT2RP2004959	s//0.28:338:57//Hs.6189:AB011133
F-NT2RP2004961//Human mRNA for KIAA0665 gene, partial cds//7.2e-2	F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068
6:456:66//Hs.70617:D31763	F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:A1091164
F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:A1149478	F-NT2RP2005457//ESTs. Highly similar to NADH-UBIQUINONE OXIDOREDU
F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:A1239735	CTASE SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA1668
F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete c	53
ds//1.0:218:61//Hs.7414:AB007927	F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243
F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRN	F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//
A, complete cds//0.13:260:60//Hs.41723:U37426	0.032:176:64//Hs.16:D10656
F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-2	F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:A1378412
2:431:65//Hs.8127:D63478	F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete c
F-NT2RP2004999	ds//9.9e-48:432:77//Hs.15519:AB018315
F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1	F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573
(IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164	F-NT2RP2005491
F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete c	F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:A1084164
ds//1.9e-160:782:97//Hs.155972:AB014515	F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-4
F-NT2RP2005003//H. sapiens Stat50 mRNA//9.9e-44:430:75//Hs.68054:X8	8:621:68//Hs.6833:AB002324
2200	F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, co
F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5	mplete cds//1.6e-63:503:78//Hs.7688:M64930
e-100:501:96//Hs.31575:AF100141	F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//
F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:	0.56:139:66//Hs.8546:U97669
J03600	F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine
F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433	synthetase), regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546
F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3)	F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCA
p36 subunit//0.095:271:60//Hs.139745:U39067	P-E) mRNA, complete cds//1.2e-82:444:92//Hs.119023:AF092563
F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:33	F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete c
8:61//Hs.112743:D67035	ds//2.2e-19:112:99//Hs.6232:AB018307
F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial c	F-NT2RP2005531//ESTs. Weakly similar to erythrocyte membrane prote
ds//0.098:217:50//Hs.58167:D30612	in 4.1 [H. sapiens]//3.5e-50:366:83//Hs.61833:AA036735
F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, c	F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)

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//9.4e-155:747:97//Hs.159597:AJ012449	F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664
F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:AB007963	F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093
F-NT2RP2005549//ESTs. Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407	F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469
F-NT2RP2005555//EST//0.046:308:57//Hs.145962:A1276822	F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:A1337416
F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:A1422839	F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970
F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436	F-NT2RP2006100
F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:A1218627	F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135
F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071	F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349
F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085	F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240
F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702	F-NT2RP2006166
F-NT2RP2005635	F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910
F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905	F-NT2RP2006185//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:AB014554
F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:A1292145	F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:AB018315
F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:A1375440	F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:A1205503
F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.143065:M86917	F-NT2RP2006219//H.sapiens mRNA for DGC6 protein//4.4e-118:618:93//Hs.153910:X96484
F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400:AB006626	F-NT2RP2006237
F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239	F-NT2RP2006238
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98//Hs.25664:AF089814	F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:A1269970
F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702	F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630
F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:M77836	F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:60//Hs.75111:D87258
F-NT2RP2005694	F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262
F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (P2A) mRNA, complete cds//0.15:496:55//Hs.79326:L76703	F-NT2RP2006320//ESTs. Moderately similar to maternal transcript Ma id [M.musculus]//1.9e-29:151:100//Hs.36794:A1038407
F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:AB018342	F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:HD9371
F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:M57527	F-NT2RP2006323//Homo sapiens mRNA for MBPox, complete cds//4.7e-06:170:70//Hs.87202:D82344
F-NT2RP2005722//Zinc finger protein 136 (clone pM2-20)//8.2e-46:415:77//Hs.69740:U09367	F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:AF076974
F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017	F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174
F-NT2RP2005726//EST//3.4e-15:95:95//Hs.156170:A1334191	F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501
F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086	F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341
F-NT2RP2005741//Homo sapiens chondroadherin gene, 5' flanking region and//0.80:362:58//Hs.97220:U96769	F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734
F-NT2RP2005748//H.sapiens ZNF338 gene//0.47:99:65//Hs.72991:X68688	F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:A1221934
F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868	F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:A1360509
F-NT2RP2005753//Homo sapiens l-l receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516	F-NT2RP2006456
F-NT2RP2005763//ELUKARYOTIC INITIATION FACTOR 4A-LIKE NUX-34//2.3e-05:425:56//Hs.79768:D21853	F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//1.1e-149:545:98//Hs.72160:AJ006266
F-NT2RP2005767//Homo log 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895	F-NT2RP2006467
F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836	F-NT2RP2006472
F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z50115	F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048
F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:A1378556	F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134
F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.34853:U28368	F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966
F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820	F-NT2RP2006571//Cytochrome P450, subfamily 11A (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029
F-NT2RP2005812	F-NT2RP2006573
F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:A1193595	F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223
F-NT2RP2005835	F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180
F-NT2RP2005841//Homo sapiens retinal rod Na-Ca/K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//Hs.59829:AB014602	F-NT2RP3000003//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:AJ011972
F-NT2RP2005853	F-NT2RP3000046//Homo sapiens TTF-1 interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560
F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:98//Hs.50758:AF092564	F-NT2RP3000047
F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567	F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376
F-NT2RP2005868	F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961
F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.1216782	F-NT2RP3000068
F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943	F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769
F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360	F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670
F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399	F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608
F-NT2RP2005933//ESTs. Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:AA292186	F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:A1253140
F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770	F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:A1243595
F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339	F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from Tpl2-p14//5.0e-94:438:100//Hs.8173:ACD05189
F-NT2RP2006023	F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:AB011164
F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382	

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F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frame s//4.1e-20:133:94//Hs.23094:M19503  
 F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.127338:AB007961  
 F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779  
 F-NT2RP3000207  
 F-NT2RP3000220  
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.122967:AF059569  
 F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:M26740  
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-11:691:86//Hs.75863:D86972  
 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733  
 F-NT2RP3000252  
 F-NT2RP3000255  
 F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568  
 F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.80261:L43821  
 F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863  
 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153  
 F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:A1091242  
 F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097  
 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390  
 F-NT2RP3000348  
 F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754  
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673  
 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921  
 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymanaea stagnalis]//4.0e-116:596:95//Hs.21094:A1337016  
 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639  
 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873  
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185  
 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frame s//2.7e-33:610:65//Hs.23094:M19503  
 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948  
 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487  
 F-NT2RP3000441  
 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:A1051562  
 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705  
 F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068  
 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:A1289822  
 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:A1084058  
 F-NT2RP3000512//Homo sapiens box 83//3.1e-18:109:97//Hs.49931:X16667  
 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:M21379  
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966  
 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:M08308  
 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412  
 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404  
 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723  
 F-NT2RP3000578  
 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277  
 F-NT2RP3000584  
 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904  
 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914  
 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811  
 F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492  
 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980  
 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:A1421203  
 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683  
 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162  
 F-NT2RP3000628//EST//0.96:221:61//Hs.131161:A1017333  
 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904  
 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219  
 F-NT2RP3000661  
 F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789  
 F-NT2RP3000685  
 F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001  
 F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884  
 F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854  
 F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:A1369426  
 F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765  
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937  
 F-NT2RP3000815  
 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:M45132  
 F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700  
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476  
 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012  
 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase ENK//6.5e-48:593:68//Hs.157199:X97630  
 F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520  
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:85//Hs.155464:AF088219  
 F-NT2RP3000852  
 F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918  
 F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476  
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445  
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204  
 F-NT2RP3000875  
 F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101  
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:A1348374  
 F-NT2RP3000917  
 F-NT2RP3000919//MAP KINASE PHOSPHATASE 1//0.19:340:60//Hs.109895:X68277  
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407  
 F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:A1204212  
 F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411  
 F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:M92198  
 F-NT2RP3001007  
 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707  
 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.30303:A1244662  
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//Hs.27007:AF060219  
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325  
 F-NT2RP3001095//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428:60//Hs.155481:AJ006470  
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969  
 F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:A1337050  
 F-NT2RP3001111  
 F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088  
 F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023  
 F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779  
 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384  
 F-NT2RP3001120//Zinc finger protein 135 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367  
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318  
 F-NT2RP3001133//Homo sapiens box A4//0.00011:484:59//Hs.77637:M74297  
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305  
 F-NT2RP3001147  
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605  
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266  
 F-NT2RP3001176  
 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:A1417859  
 F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:M19981  
 F-NT2RP3001221//ESTs, Weakly similar to WD506.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866  
 F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010  
 F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:A1362756  
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62/

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/Hs.103042:L06237	F-NT2RP3001646
F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132	F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)
F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:29	//1.1e-172:816:98//Hs.159597:AJ012449
3:60//Hs.32934:U27109	F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027
F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete c	F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA
ds//1.2e-48:761:64//Hs.107809:AB018269	[Pseudomonas fluorescens]//9.0e-53:375:85//Hs.41127:AA555184
F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box	F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:3
(KRAB) domain polypeptide) //1.2e-42:454:72//Hs.41728:L75847	21:65//Hs.79077:D87071
F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566	F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROT
F-NT2RP3001274	EIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-111:5
F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811	18:99//Hs.20364:A1420022
F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-4	F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:
8:544:69//Hs.31463:D87457	230:63//Hs.7486:D83198
F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete	F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329
cds//0.72:151:68//Hs.159437:U44060	F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219
F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase	F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTE
(glycogen debranching enzyme, glycogen storage disease type III) //	IN PRECURSOR [D.melanogaster]//1.4e-31:191:94//Hs.131279:AA486291
0.012:522:56//Hs.904:U84010	F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds
F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731	//0.41:259:59//Hs.58435:AF001862
F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-3	F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEI
0:345:73//Hs.79347:D86966	N 1 PRECURSOR [Mus musculus]//7.6e-159:747:98//Hs.6823:W18181
F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete c	F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding pro
ds//6.3e-67:559:80//Hs.18586:AB007920	tein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177
F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1	F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROT
(IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164	EIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.5e-116:5
F-NT2RP3001355//ESTs, Weakly similar to ADP-ATP CARRIER PROTEIN, L	54:98//Hs.144332:AA046836
LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831	F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-10
F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.1	5:811:78//Hs.90998:D50918
5:313:60//Hs.129725:AF047487	F-NT2RP3001739
F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022	F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:8
F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:6	0//Hs.116549:AL009172
5//Hs.30965:AB001451	F-NT2RP3001753//Human putative cerebral cortex transcriptional reg
F-NT2RP3001384//Homo sapiens mRNA for HRHFB2018, partial cds//2.1	ulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.2213
e-158:743:98//Hs.146214:AB015332	8:U49250
F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595	F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete
F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783	cds//2.4e-47:725:64//Hs.41688:U27193
F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box	F-NT2RP3001777//Human eukaryotic translation initiation factor (el
(KRAB) domain polypeptide) //1.0e-05:189:56//Hs.41728:L75847	F3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525
F-NT2RP3001399//Homo sapiens mitochondrial citrate transport prote	F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cd
in (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567	s//9.1e-153:710:98//Hs.28169:AB007928
F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658	F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:6
F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047	9//Hs.79024:L03532
F-NT2RP3001426	F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:A1091361
F-NT2RP3001427	F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.5356
F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.	3:L41162
8e-73:431:91//Hs.85844:X66397	F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-11//0.
F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX	90:379:58//Hs.32950:X82634
WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393	F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729
F-NT2RP3001447	F-NT2RP3001855//Human homeobox-containing protein mRNA, complete c
F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:6	ds//7.8e-35:481:67//Hs.158225:U68727
8//Hs.89631:U48508	F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706
F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212	F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.e
F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323	legans]//2.9e-94:452:98//Hs.54952:AA872675
F-NT2RP3001459	F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin Ia//0.65:245:61
F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA,	//Hs.6139:AL022326
complete cds//4.2e-10:168:70//Hs.32317:AF072836	F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896
F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877	F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185
F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231	F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247
F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T	F-NT2RP3001931
RC8 (TRC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801	F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//
F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B)	0.0022:268:61//Hs.106070:U22398
mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500	F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete c
F-NT2RP3001529//ESTs, Moderately similar to topoisomerase I C-term	ds//5.8e-167:815:96//Hs.15869:AB014575
inal fragment [H.sapiens]//0.28:224:65//Hs.105912:A1431328	F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:A1339335
F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:A1198074	F-NT2RP3001969
F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//	F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:A1032180
Hs.147918:U38291	F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:
F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9	83//Hs.155464:AF088219
e-06:426:59//Hs.162:X16302	F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//H
F-NT2RP3001587//Guanine nucleotide binding protein (G protein), al	s.75087:X86779
pha 11 (Gq class)//0.049:185:65//Hs.1686:W69013	F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946
F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.	F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821
4)//9.6e-51:345:82//Hs.144563:AF057280	F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:1
F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688	75:67//Hs.147189:D88153
F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:A1091349	F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [H.musculus]
F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435	//3.8e-48:353:81//Hs.127507:AA993745
F-NT2RP3001629	F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0
F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4	e-25:212:83//Hs.71622:AA195155
e-62:276:97//Hs.9899:AF099149	F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PR
F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173	OTEIN I [Homo sapiens]//4.2e-82:407:97//Hs.131888:A1091806

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F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frame s//3.7a-21:168:85//Hs.23094:M19503	F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//Hs.41086:A1337400
F-NT2RP3002062//EST//0.46:198:62//Hs.157711:A1359710	F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:A1421991
F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779	F-NT2RP3002682//ESTs, Weakly similar to FITC11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:A1367584
F-NT2RP3002081	F-NT2RP3002687
F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.073:297:61//Hs.102732:U88153	F-NT2RP3002688//EST//1.0:312:58//Hs.156800:A1352200
F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256	F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:A1393657
F-NT2RP3002108	F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:A1279514
F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018	F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291
F-NT2RP3002146//H. sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260	F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//Hs.129736:AF040753
F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse Hm1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009	F-NT2RP3002785
F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644	F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713
F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985	F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H. sapiens]//1.4e-76:423:93//Hs.41068:AAB44350
F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNCP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140	F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:AF004715
F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046	F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070
F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915	F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582
F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA306435	F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895
F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656	F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040
F-NT2RP3002248	F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314
F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261	F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:A1138765
F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.110637:AC004080	F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//Hs.3826:U69560
F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139	F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:AB011160
F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386	F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262
F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910	F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870
F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871	F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997
F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383	F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:A1287703
F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:588:75//Hs.154672:X16396	F-NT2RP3002985//Human TFIIB related factor hBRF (hBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838
F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (7-17A) gene//4.2e-166:770:98//Hs.6483:Y16355	F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:A1218308
F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200	F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083
F-NT2RP3002399	F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446
F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274	F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749
F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:AB014578	F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609
F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:A1291310	F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108	F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935	F-NT2RP3003078
F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.57738:U35246	F-NT2RP3003101
F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:AB018272	F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC W ARMING ENTRY !!!! [H. sapiens]//0.98:88:68//Hs.99715:AA292700
F-NT2RP3002549//ESTs, Weakly similar to POLYPOIS LOCUS PROTEIN 1 [H. sapiens]//1.3e-42:510:70//Hs.96759:AA469984	F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:A1090740
F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706	F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054	F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:A1187919	F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944
F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508	F-NT2RP3003150
F-NT2RP3002603	F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376
F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888	F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093
F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900	F-NT2RP3003193//Zinc finger protein 10 (KIX 1)//2.4e-74:737:71//Hs.2479:X78933
F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:AJ006470	F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.151518:U38847	F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308	F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
	F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
	F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
	F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:O44497
	F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460
	F-NT2RP3003251//H. sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200
	F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M99225
	F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924

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F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2 e-133.694:93//Hs.11702:L36983  
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953  
 F-NT2RP3003301//EST//1.0:58:74//Hs.158575:A1368947  
 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frame s//3.1e-91:681:80//Hs.23094:M19503  
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947  
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:A1084058  
 F-NT2RP3003327//H.sapiens Stat50 mRNA//8.0e-31:253:67//Hs.68054:X82200  
 F-NT2RP3003330  
 F-NT2RP3003344  
 F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-red uctase//1.2e-42:644:66//Hs.2638:Z28339  
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833  
 F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542  
 F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791  
 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363  
 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850  
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653  
 F-NT2RP3003411//Human metallothionein-1e gene (hMT-1e)//0.99:116:62//Hs.74170:M10942  
 F-NT2RP3003421//ESTs//0.24:447:61//Hs.160907:A1422830  
 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425  
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.14934:AF004828  
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:AB018268  
 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330  
 F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302  
 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:AF038169  
 F-NT2RP3003552  
 F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:A1418322  
 F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365  
 F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311  
 F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247  
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741  
 F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104:D14012  
 F-NT2RP3003625  
 F-NT2RP3003656  
 F-NT2RP3003659  
 F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586  
 F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:W76184  
 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:63//Hs.44585:U58334  
 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF050000  
 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:A1249848  
 F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865  
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513:AB018300  
 F-NT2RP3003746  
 F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230  
 F-NT2RP3003799  
 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422:M19722  
 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656  
 F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF042832  
 F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.102877:U41315  
 F-NT2RP3003825  
 F-NT2RP3003826//ESTs//2.1e-12:434:61//Hs.156864:A1346481  
 F-NT2RP3003831  
 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:AF070611  
 F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:W73780  
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268  
 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:AB018343  
 F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576  
 F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN C LUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659  
 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358  
 F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396  
 F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:A1359006  
 F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.93909:AF042498  
 F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs.142151:AA984061  
 F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.155302:U57317  
 F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234  
 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317  
 F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:A1032875  
 F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.100007:X76091  
 F-NT2RP3004093  
 F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258  
 F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390  
 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:A1096509  
 F-NT2RP3004145  
 F-NT2RP3004148  
 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900  
 F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706  
 F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640  
 F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523  
 F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:A1221835  
 F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361  
 F-NT2RP3004242  
 F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240  
 F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:A1149140  
 F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067  
 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982  
 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871  
 F-NT2RP3004332  
 F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285  
 F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426  
 F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999  
 F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915  
 F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain I(V) chain [C.elegans]//4.3e-125:608:98//Hs.128781:AA160707  
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804:90//Hs.123122:X97249  
 F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113  
 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403  
 F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016  
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:AB007917  
 F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564  
 F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219  
 F-NT2RP3004472  
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925  
 F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735

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【表578】

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851  
 F-NT2RP3004498//ESTs. Moderately similar to ROSA26AS [M.musculus]/3.5e-89:425:99//Hs.126082:A1077718  
 F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256  
 F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948  
 F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046  
 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110  
 F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:A1031571  
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:AB014532  
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:AB011126  
 F-NT2RP3004566//ESTs. Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.125870:A1364967  
 F-NT2RP3004569  
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete cds//3.3e-181:860:97//Hs.122752:AF026445  
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:AB007923  
 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266  
 F-NT2RP3004617//ESTs. Weakly similar to estrogen-responsive finger protein, etp [H.sapiens]//6.4e-13:356:64//Hs.124138:A1266336  
 F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232  
 F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204  
 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436  
 F-NT2RP4000008//ESTs. Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//0.0e-177:827:98//Hs.118991:AA675919  
 F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668  
 F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495  
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761  
 F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:AJ006470  
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:AJ012449  
 F-NT2RP4000102//ESTs//0.8e-33:184:82//Hs.93054:H47743  
 F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538  
 F-NT2RP4000111  
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952  
 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069  
 F-NT2RP4000150  
 F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356  
 F-NT2RP4000159  
 F-NT2RP4000167  
 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946  
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600  
 F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006  
 F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731  
 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984  
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:AJ006470  
 F-NT2RP4000246//ESTs. Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298  
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092  
 F-NT2RP4000263  
 F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580  
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481  
 F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732  
 F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112  
 F-NT2RP4000355  
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281  
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195  
 F-NT2RP4000370//ESTs. Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:A1382073  
 F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678  
 F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965  
 F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368  
 F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688  
 F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds//0.014:178:66//Hs.125315:AF027156  
 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984  
 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087  
 F-NT2RP4000449//EST//0.84:113:65//Hs.145274:A1249468  
 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853  
 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499  
 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535  
 F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742  
 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995  
 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293  
 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594  
 F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904  
 F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840  
 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372  
 F-NT2RP4000524  
 F-NT2RP4000528  
 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:A1348154  
 F-NT2RP4000556//ESTs. Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026  
 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351  
 F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053  
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730  
 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513  
 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396  
 F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907  
 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848  
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783  
 F-NT2RP4000724//ESTs. Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622  
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178  
 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440  
 F-NT2RP4000739//DESMOPLAKIN 1 AND 11//0.99:192:63//Hs.74316:AL031058  
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162  
 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123  
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939  
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189  
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833  
 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:M27603  
 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278  
 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367  
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:A1206803  
 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843  
 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-5

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【表579】

2:933:61//Hs.3781:AC004142  
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901  
 F-NT2RP4000918  
 F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865  
 F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503  
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532  
 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371  
 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:DB3542  
 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888  
 F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058  
 F-NT2RP4000979  
 F-NT2RP4000984  
 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913  
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068  
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204  
 F-NT2RP4001004  
 F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718  
 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.113287:AF009204  
 F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494  
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:L40157  
 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157  
 F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:AJ006470  
 F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497  
 F-NT2RP4001079//Homo sapiens mRNA for putative Ca<sup>2+</sup>-transporting ATPase, partial//1.4e-131:634:98//Hs.106778:AJ010953  
 F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) [alternative products]//0.025:166:66//Hs.146459:X66975  
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164  
 F-NT2RP4001095  
 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054  
 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEG61 ALPHA SUBUNIT [Canis familiaris]//2.2e-26:171:92//Hs.14038:R06800  
 F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:DB4142  
 F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:100//Hs.126925:AA931237  
 F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.143382:AA476266  
 F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261  
 F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207  
 F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171  
 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734  
 F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324  
 F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264  
 F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324  
 F-NT2RP4001207  
 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636  
 F-NT2RP4001213//KRAB zinc finger protein [alternative products]//1.1e-45:187:74//Hs.22556:U37251  
 F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262  
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.122967:AF059569  
 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778  
 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:DB7463  
 F-NT2RP4001260//Synrophin, alpha (dystrophin-associated protein A 1, 59kD, acidic component)//0.015:246:62//Hs.31121:U40571  
 F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578  
 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U00736  
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250  
 F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917  
 F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110  
 F-NT2RP4001339  
 F-NT2RP4001343  
 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625  
 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445  
 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356  
 F-NT2RP4001372  
 F-NT2RP4001373//Homo sapiens clone DtlP1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194  
 F-NT2RP4001375  
 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190  
 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918  
 F-NT2RP4001407//Homo sapiens mRNA for RGSS, complete cds//0.93:218:58//Hs.24950:AB008109  
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957  
 F-NT2RP4001433//Zinc finger protein 10 (KIX 1)//1.1e-88:839:73//Hs.2479:X78933  
 F-NT2RP4001442  
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326  
 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.26676:AA033997  
 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523  
 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.63220:AA522707  
 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:M40395  
 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260  
 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863  
 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494  
 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:U13220  
 F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534  
 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174  
 F-NT2RP4001567  
 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBRS INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836  
 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410  
 F-NT2RP4001574  
 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228  
 F-NT2RP4001592  
 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903  
 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952  
 F-NT2RP4001634  
 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKHI-STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436  
 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409  
 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629  
 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376  
 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080  
 F-NT2RP4001696  
 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927  
 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302  
 F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198  
 F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878  
 F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656  
 F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from Tq22-q31.1//9.1e-34:400:68//Hs.154212:AC004522  
 F-NT2RP4001803//Human high conductance inward rectifier potassium



【表580】

channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L3 6069	[H.sapiens]//6.7e-60:305:97//Hs.31696:H50008
F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131	F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798
F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690	F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543
F-NT2RP4001828	F-OVARC1000085
F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-5 5:555:73//Hs.78398:D31888	F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442
F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749	F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete cds//0.00017: 414:59//Hs.106387:AF029778
F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete c ds//5.6e-57:813:65//Hs.6336:AB014572	F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600
F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARMING ENTRY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170	F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e- 73:406:92//Hs.109463:AI205174
F-NT2RP4001889	F-OVARC1000109
F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-10 8:535:97//Hs.15144:AC005014	F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250
F-NT2RP4001896	F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete c ds//3.4e-43:532:72//Hs.118401:AB011134
F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848	F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010
F-NT2RP4001927	F-OVARC1000139
F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens]//2.8e-54:375:84//Hs.119294:AI379442	F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293
F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894	F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA510063	F-OVARC1000151
F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868	F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acid Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022 718	F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.1 0:504:59//Hs.154083:U70136
F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, co mplete cds//0.0019:279:65//Hs.159439:AF092047	F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131
F-NT2RP4002018//ESTs, Highly similar to RING CAMAL PROTEIN [Droso phila melanogaster]//0.58:463:55//Hs.3826:U69560	F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139	F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
F-NT2RP4002052	F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379
F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873	F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:46 6:68//Hs.8136:U81984
F-NT2RP4002071//Homo sapiens TTACGG repeat binding factor 2 (hTRF 2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999	F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.0 0084:170:65//Hs.107747:AI357868
F-NT2RP4002075	F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [ H.sapiens]//1.0e-38:243:90//Hs.139115:AA325104	F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M 55654	F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]//0.51:193:66//Hs.6194:AI3 78579
F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.00 15:152:70//Hs.25180:M96684	F-OVARC1000321
F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cd s//8.0e-10:401:59//Hs.89616:M55284	F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subuni t mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946
F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204	F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
F-NT2RP4002888	F-OVARC1000347
F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960	F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-0 6:353:62//Hs.121895:AF001450
F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35: 193:96//Hs.74456:U34995	F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:2 31:64//Hs.156016:D50930
F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071	F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067	F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
F-NT2RP5003492	F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:2 31:58//Hs.156016:D50930
F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotrans ferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179	F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7 e-25:190:84//Hs.139513:AA259082
F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT9875K-A-69 G12//5.1e-14:348:62//Hs.154050:AC004131	F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cd s//0.94:202:63//Hs.8152:AB014542	F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93:281:60 //Hs.76279:X53416
F-NT2RP5003522	F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:11 6:99//Hs.83987:U09284
F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943	F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423
F-NT2RP5003534	F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete c ds//3.2e-140:566:99//Hs.12334:AB014583
F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cd s//4.0e-69:373:94//Hs.108258:AB007934	F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524
F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729	F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58 //Hs.108112:AF070640
F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina mosc hata]//4.4e-75:355:99//Hs.36727:AI051983	F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854
F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304	F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926
F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e- 171:815:98//Hs.81449:AF058922	F-OVARC1000479
F-OVARC1000017//Homo sapiens mRNA for NTAk, complete cds//0.50:48 2:58//Hs.113264:AB005060	F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036
F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2 e-37:238:89//Hs.69469:AF064603	F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327
F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549	F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e- 115:539:99//Hs.111285:AF051850
F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor	F-OVARC1000526//ESTs//2.9e-08:368:61//Hs.42771:N26740
	F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492
	F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475
	F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667
	F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410
	F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:66//Hs.85302:U76421
	F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358

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【表581】

F-OVARC1000576//ESTs//9.4e-22:124.98//Hs.24220:W22200	F-OVARC1001040//ESTs//2.2e-38:204.96//Hs.128927:A1168074
F-OVARC1000578//EST//4.7e-31:335.74//Hs.162881:AA652729	F-OVARC1001044//EST//0.036:304.61//Hs.137342:AA017385
F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263.63//Hs.3080:U29725	F-OVARC1001051
F-OVARC1000605//EST//1.0:148.62//Hs.163346:AA883722	F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381.81//Hs.154968:U02020
F-OVARC1000622//EST//4.3e-50:313.88//Hs.149580:A1281881	F-OVARC1001062//ESTs//0.020:265.60//Hs.146226:A1312873
F-OVARC1000640//ESTs//2.6e-55:441.80//Hs.105319:AA470097	F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183.84//Hs.46680:AA809451
F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424.93//Hs.86859:D43772	F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620.98//Hs.3426:AF082657
F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536.94//Hs.111862:AB011162	F-OVARC1001072//ESTs//1.1e-24:289.74//Hs.139614:AA709013
F-OVARC1000678//EST//1.3e-08:131.77//Hs.145970:A1277106	F-OVARC1001074//ESTs//0.059:198.63//Hs.59974:AA001937
F-OVARC1000679//ESTs//0.66:223.61//Hs.134782:H74279	F-OVARC1001085//H. sapiens mRNA for sortilin//0.99:142.67//Hs.104247:X98248
F-OVARC1000681//EST//0.017:315.61//Hs.147799:A1221639	F-OVARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (clone IMAGE 53337, LLNLC110F1857Q7 (RZPD Berlin) and LLNLC110G0913Q7 (RZPD Berlin))//1.3e-75:289.95//Hs.21753:AJ005897
F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549.99//Hs.125315:AF027156	F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913
F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306	F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710.98//Hs.26584:AF051782
F-OVARC1000700	F-OVARC1001117//ESTs//3.8e-73:347.99//Hs.116029:AA813102
F-OVARC1000703//ESTs//0.41:100.68//Hs.160699:A1284320	F-OVARC1001118
F-OVARC1000722//Homo sapiens chromosome 1q21-lq23 beta-1.4-galactosyltransferase mRNA, complete cds//1.2e-110:451.91//Hs.13476:AF038561	F-OVARC1001129
F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318.91//Hs.7049:A1141736	F-OVARC1001154//Granulin//2.4e-94:686.83//Hs.75451:AF055008
F-OVARC1000746//ESTs//3.2e-123:570.99//Hs.127295:AA918411	F-OVARC1001161//ESTs//2.2e-40:208.97//Hs.113006:AA621725
F-OVARC1000769//ESTs//0.072:177.67//Hs.142573:AA601196	F-OVARC1001162
F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RA B-2 [H.sapiens]//1.2e-38:194.99//Hs.157059:W28130	F-OVARC1001167
F-OVARC1000781//ESTs//4.0e-14:113.89//Hs.41972:AA626793	F-OVARC1001169//ESTs//0.81:158.63//Hs.48527:A1078279
F-OVARC1000787//EST//0.92:91.64//Hs.163258:AA828835	F-OVARC1001170//ESTs//9.0e-87:412.99//Hs.116550:AA813287
F-OVARC1000800//ESTs//1.6e-44:193.81//Hs.163971:N27584	F-OVARC1001171//ESTs//4.9e-26:167.79//Hs.139158:AA226159
F-OVARC1000802//ESTs//4.6e-43:395.80//Hs.115401:AA400032	F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapiens]//1.8e-11:192.69//Hs.130020:AA887581
F-OVARC1000834//ESTs//1.9e-91:431.99//Hs.154450:AA069390	F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551
F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432.100//Hs.155995:AB014543	F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199.71//Hs.109966:C06057
F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584	F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN YMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324.90//Hs.114673:W72675
F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183.93//Hs.108620:AA418155	F-OVARC1001200//ESTs//3.9e-16:104.94//Hs.125520:AA883889
F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133.69//Hs.159234:U89995	F-OVARC1001232//Cyclin A//0.95:124.67//Hs.85137:X51688
F-OVARC1000883//ESTs//0.44:154.63//Hs.98183:AA471143	F-OVARC1001240//EST//0.017:351.60//Hs.120655:AA745676
F-OVARC1000885//EST//0.91:152.63//Hs.160765:A1313323	F-OVARC1001243//ESTs//0.78:291.59//Hs.132458:A1424825
F-OVARC1000886//ESTs//4.6e-08:375.61//Hs.131653:A1025777	F-OVARC1001244//RINGS PROTEIN//2.8e-19:118.95//Hs.75243:D42040
F-OVARC1000890	F-OVARC1001261//EST//1.9e-42:225.96//Hs.158854:A1377837
F-OVARC1000891	F-OVARC1001268//ESTs//0.66:239.61//Hs.132525:AA576821
F-OVARC1000897//ESTs//1.1e-07:145.69//Hs.119878:AA706818	F-OVARC1001270//ESTs//0.99:204.60//Hs.144647:AA625224
F-OVARC1000912//EST//3.6e-08:376.61//Hs.158782:A1376601	F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644.96//Hs.155995:AB014543
F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419.97//Hs.9028:AF039691	F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355.60//Hs.108812:AA044835
F-OVARC1000924//ESTs//3.6e-113:540.98//Hs.66058:AA424456	F-OVARC1001296//ESTs//1.1e-46:237.98//Hs.33746:N78172
F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623.72//Hs.114440:M11119	F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188.64//Hs.152455:AF044209
F-OVARC1000937//EST//2.4e-39:170.96//Hs.129138:AA988078	F-OVARC1001329//ESTs//1.4e-97:486.97//Hs.125886:AA884264
F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157.97//Hs.136243:AA307843	F-OVARC1001330
F-OVARC1000948	F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)//0.021:232.62//Hs.79410:U62531
F-OVARC1000959//EST//0.65:293.55//Hs.134725:A1088986	F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363.99//Hs.105837:AA536054
F-OVARC1000960//Ley L-L//1.4e-41:425.72//Hs.37062:AC005952	F-OVARC1001342//EST//0.98:97.65//Hs.148210:AA897493
F-OVARC1000964//ESTs//1.4e-95:486.96//Hs.57079:D45288	F-OVARC1001344//EST//5.3e-10:241.64//Hs.138777:N67251
F-OVARC1000971//ESTs//0.19:198.62//Hs.153429:A1283069	F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198.61//Hs.105940:AF004715
F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365.56//Hs.2557:Y00661	F-OVARC1001360//ESTs//4.9e-87:429.97//Hs.130145:A1264633
F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312.65//Hs.155302:U57317	F-OVARC1001369//ESTs//6.3e-07:371.62//Hs.131653:A1025777
F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209.62//Hs.10458:AF088219	F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533.74//Hs.109299:AB014554
F-OVARC1001000//EST//4.2e-24:242.77//Hs.128952:AA984114	F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365.73//Hs.129735:AF010144
F-OVARC1001004	F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683.99//Hs.151428:AJ224819
F-OVARC1001010	F-OVARC1001391//Homo sapiens methyl-CpG binding protein MB02 (MBD2) mRNA, complete cds//0.097:235.65//Hs.25674:AF072242
F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234.99//Hs.110327:AA205866	F-OVARC1001399//ESTs//1.1e-35:264.83//Hs.59379:W28225
F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2//0.0076:624.57//Hs.75063:AL023584	F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651
F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578.89//Hs.111974:A1050735	F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-
F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733.97//Hs.9899:AF099149	

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【表582】

49:586:69//Hs.74597:U52426  
 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651  
 F-OVARC1001436  
 F-OVARC1001442  
 F-OVARC1001453  
 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:A1041823  
 F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568  
 F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343  
 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507  
 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243  
 F-OVARC1001525  
 F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786  
 F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595  
 F-OVARC1001555  
 F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:AF031166  
 F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:A1144299  
 F-OVARC1001610//ESTs, Weakly similar to F2Z10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:A1038398  
 F-OVARC1001611  
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500  
 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144  
 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867  
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229  
 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858  
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807  
 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863  
 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825  
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:A1148588  
 F-OVARC1001762  
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.4e-150:708:98//Hs.155377:U97670  
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575  
 F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:A1218697  
 F-OVARC1001791  
 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830  
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:A1005102  
 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287  
 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172  
 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825  
 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453  
 F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567  
 F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537  
 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973  
 F-OVARC1001861  
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611  
 F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709  
 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127  
 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953  
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749  
 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:A1263834  
 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261  
 F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263  
 F-OVARC1001928  
 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204  
 F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN IN ZK652.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794

F-OVARC1001949//KRAB zinc finger protein (alternative products)//1.8e-17:294:67//Hs.22556:U37251  
 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:A1051228  
 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639  
 F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776  
 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417  
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:AB007934  
 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:A1375865  
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063  
 F-OVARC1002107  
 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174  
 F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913  
 F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022  
 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795  
 F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097  
 F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:A1357868  
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568  
 F-OVARC1002182//Homo sapiens ataxin-7 (SCAT7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517  
 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230  
 F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:A1378928  
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789  
 F-PLACE1000014  
 F-PLACE1000031  
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088  
 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494  
 F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:A1076755  
 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499  
 F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans CDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:A1356771  
 F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366  
 F-PLACE1000081//Human transporter protein (glr) mRNA, complete cds//0.30:324:60//Hs.76460:U49082  
 F-PLACE1000094  
 F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:A1380378  
 F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135  
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291  
 F-PLACE1000185  
 F-PLACE1000213  
 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:A1167255  
 F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226  
 F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022  
 F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:A1278202  
 F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294  
 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047  
 F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675  
 F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197  
 F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153  
 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:569:67//Hs.75302:U46024  
 F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516  
 F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260  
 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174  
 F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053  
 F-PLACE1000424  
 F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590  
 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:N35531  
 F-PLACE1000453//Human mRNA for MTC8a protein, complete cds//0.026:

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【表583】

240:60//Hs.31551:043638  
 F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:164878  
 F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:3  
 02:60//Hs.153014:AB002353  
 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573  
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, c  
 omplete cds//0.0046:223:65//Hs.75578:M55289  
 F-PLACE1000562  
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538  
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:52  
 5:72//Hs.21838:AF038179  
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible,  
 67kD//2.3e-85:503:88//Hs.62661:M55542  
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)  
 //1.2e-165:798:97//Hs.159597:AJ012449  
 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751  
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cd  
 s//0.98:215:60//Hs.8152:AB014542  
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986  
 F-PLACE1000636  
 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase  
 mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265  
 F-PLACE1000656//Homo sapiens mRNA for JIM4 protein, complete CDS (c  
 lone IMAGE 546750 and LNC110F1857Q7 (RZPD Berlin))//7.5e-158:77  
 5:97//Hs.25955:AJ005896  
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1  
 (TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353  
 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949  
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-3  
 8:426:70//Hs.47313:D87447  
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288  
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//  
 0.72:331:57//Hs.37110:U10694  
 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858  
 F-PLACE1000769  
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cd  
 s//1.1e-139:663:98//Hs.31921:AB014548  
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-05:3  
 62:59//Hs.44782:D82215  
 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:M56079  
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189  
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180  
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:  
 63//Hs.110826:U00736  
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000  
 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA77428  
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455  
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201  
 F-PLACE1000948  
 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRN  
 A, complete cds//7.9e-10:294:66//Hs.80261:L43821  
 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cD  
 NA yk28h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789  
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:6  
 2//Hs.8597:L11672  
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete c  
 ds//2.6e-141:694:96//Hs.158497:AB018267  
 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913  
 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//  
 0.050:338:61//Hs.1974:M92432  
 F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80  
 //Hs.6940:Z48633  
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876  
 F-PLACE1001024  
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741  
 F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:28  
 4:59//Hs.79705:U53204  
 F-PLACE1001062  
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859  
 F-PLACE1001088  
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//  
 1.0e-96:489:96//Hs.95448:AF065485  
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817  
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP3  
 7) mRNA, complete cds//8.2e-66:676:71//Hs.150406:AF022158  
 F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//  
 1.5e-16:122:91//Hs.1257:M30704  
 F-PLACE1001168  
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135  
 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-  
 28:421:66//Hs.8763:M30741  
 F-PLACE1001238  
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494  
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929  
 F-PLACE1001272//COATOMER BETA SUBUNIT//0.012:50:96//Hs.75724:X704  
 76  
 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:M51283  
 F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1  
 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164  
 F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target su  
 bunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930  
 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6  
 e-08:370:60//Hs.42672:AF016052  
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385  
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591  
 F-PLACE1001351  
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cd  
 s//2.8e-26:155:95//Hs.61638:AB018342  
 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//  
 3.4e-44:393:79//Hs.152005:AF009615  
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748  
 F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP  
 1) mRNA, complete cds//2.6e-09:117:84//Hs.21301:AF093419  
 F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RE  
 CEPTOR KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:  
 N30646  
 F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransfera  
 se, complete CDS//0.0038:496:57//Hs.97681:AJ223333  
 F-PLACE1001399//Human melanoma antigen recognized by T-cells (MAR  
 T-1) mRNA//7.0e-45:456:75//Hs.154069:U06452  
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequ  
 ence//6.5e-71:365:96//Hs.110404:AF091087  
 F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232  
 F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:HI8987  
 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510  
 F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455  
 F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716  
 F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529  
 F-PLACE1001503  
 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914  
 F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753  
 F-PLACE1001545  
 F-PLACE1001551  
 F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835  
 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete c  
 ds//0.013:159:66//Hs.266:U06233  
 F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds  
 //1.1e-10:133:77//Hs.146406:AF069987  
 F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230  
 F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005  
 F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete  
 cds//0.96:141:66//Hs.1572:U11690  
 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete c  
 ds//3.4e-76:702:75//Hs.159277:AB018341  
 F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198  
 F-PLACE1001640  
 F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927  
 F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein  
 (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250  
 F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHAS  
 E THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//  
 Hs.24309:AI125696  
 F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, com  
 plete cds//6.0e-30:347:76//Hs.101555:U93869  
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-6  
 9:369:73//Hs.12413:D83776  
 F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686  
 F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cd  
 s//0.0084:484:60//Hs.129892:AB011094  
 F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:6  
 4//Hs.1480:M60052  
 F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159  
 F-PLACE1001745  
 F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361  
 F-PLACE1001748//Homo sapiens metalloprotease 1 (MPI) mRNA, complet  
 e cds//2.8e-160:773:97//Hs.4812:AF061243  
 F-PLACE1001756//Homo sapiens tapasin (NCS-17) mRNA, complete cds//  
 2.7e-35:269:83//Hs.5247:AF029750  
 F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283  
 F-PLACE1001771//Human putative calcium influx channel (htrp3) mRN

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【表584】

A. complete cds//3.4e-52:548:72//Hs.150981:U47050	F-PLACE1002625
F-PLACE1001781	F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412
F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115	F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138	F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180
F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953	F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903
F-PLACE1001821	F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971
F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494	F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214	F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906	F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:A1049827
F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:A1343257	F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516
F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220	F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:A1368926
F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936	F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
F-PLACE1001928//H. sapiens HMM9 mRNA//0.063:196:66//Hs.2750:X74837	F-PLACE1002815
F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778	F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
F-PLACE1001989	F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:A1089163
F-PLACE1002004	F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:A1334167
F-PLACE1002046	F-PLACE1002851//EST//0.0034:102:72//Hs.129630:A1000405
F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108	F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555	F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707	F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:A1040029
F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178	F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056
F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765	F-PLACE1002962
F-PLACE1002115//EST//0.18:215:62//Hs.135747:A1002637	F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:A1041815
F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831	F-PLACE1002991
F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747	F-PLACE1002993
F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631	F-PLACE1002996//ESTs, Weakly similar to T2003.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959
F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390	F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979
F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:A1366891	F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:AB011088
F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627	F-PLACE1003044//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567
F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674	F-PLACE1003045
F-PLACE1002205//Human clone Z3695 mRNA sequence//0.00080:472:60//Hs.90798:U79289	F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989	F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875
F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:A1024442	F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419
F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935	F-PLACE1003136
F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frame s//2.3e-75:434:83//Hs.23094:M19503	F-PLACE1003145
F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675	F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590
F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279	F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:M01997
F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291	F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797
F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710	F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:221:60//Hs.139756:U59209
F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067	F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532
F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.40993:AF000148	F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:A1208770
F-PLACE1002438//EST//1.4e-48:77//Hs.158575:A1368947	F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208
F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158	F-PLACE1003249//Insulin-like growth factor 1 (somatomedin C)//0.99:175:62//Hs.85112:X57025
F-PLACE1002465	F-PLACE1003256
F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:A1007581	F-PLACE1003258//H. sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802
F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523	F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106
F-PLACE1002493	F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376
F-PLACE1002499	F-PLACE1003334
F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010	F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:A1023308
F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482	F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568
F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:AB018256	F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715
F-PLACE1002532//Homo sapiens BAC clone RG300E22 from Tq21-q31.1//3.1e-115:566:96//Hs.99348:AC004774	F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277
F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369	F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575
F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866	F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858
F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627	F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:A1343009
F-PLACE1002583//EST//0.0028:348:61//Hs.160396:A1393725	F-PLACE1003375//EST//0.75:119:68//Hs.160270:A1149069
F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497	F-PLACE1003383
F-PLACE1002598//EST//0.011:209:62//Hs.131470:A1024187	F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-1
F-PLACE1002604//EST//0.47:220:61//Hs.145434:A1198915	

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【表585】

4 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546	F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178	F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.10223:X90846	F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene sp1//0.85:164:64//Hs.153045:X52056
F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912	F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:X04526
F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874	F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779
F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635	F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
F-PLACE1003516//Human knp1 repeat mRNA (cdna clone pcd-knp1-8), 3' end//3.4e-85:357:86//Hs.103948:X00627	F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785
F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145	F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633	F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248	F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493
F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428	F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
F-PLACE1003553	F-PLACE1004256//EST//0.019:364:58//Hs.123395:AA789273
F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780	F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367	F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.31718:N29128
F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932	F-PLACE1004270//Homo sapiens CACF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736
F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194	F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914
F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARN! NG ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620	F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830
F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965	F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884
F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961	F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576
F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200	F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677
F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104	F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588
F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896	F-PLACE1004336
F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frame s//1.3e-122:737:87//Hs.23094:M19503	F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153
F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105	F-PLACE1004376//ESTs, Weakly similar to F2704.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552
F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762	F-PLACE1004384//Human HsLim15 mRNA for HsLim15, complete cds//2.0e-49:466:76//Hs.37181:D64108
F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413	F-PLACE1004388
F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299	F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871
F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.88558:AF053305	F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579
F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101	F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190
F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adapt or protein//8.5e-09:393:60//Hs.103527:AJ000553	F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283
F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344	F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867
F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648	F-PLACE1004460
F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983	F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363
F-PLACE1003768//Human knp1 repeat mRNA (cdna clone pcd-knp1-4), 3' end//2.7e-40:608:68//Hs.139107:X00629	F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085
F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944	F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416
F-PLACE1003783	F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163
F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cd s//1.0:457:57//Hs.62318:AB018308	F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680
F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169	F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF15 0) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445
F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786	F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150
F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165	F-PLACE1004518
F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124	F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359	F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854
F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257	F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770	F-PLACE1004629//Centromere protein B (80kd)//0.0015:242:64//Hs.85004:X05299
F-PLACE1003886	F-PLACE1004645
F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:O42108	F-PLACE1004646//Retinal pigment epithelium-specific protein (65kd)//1.4e-12:386:63//Hs.2133:U18991
F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050	F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944	F-PLACE1004664
F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142	F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563
F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069	F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606
F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585	F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589
F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537	F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561
F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536	F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131
F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412	F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845
F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812	

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F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542	F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891	F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:AB011182
F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148	F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680	F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:X60673
F-PLACE1004743	F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534
F-PLACE1004751//ESTs. Highly similar to CMP-N-ACETYLNEURAMINATE-8 ETA-1, 4-GALACTOSIDE ALPHA-2, 3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470	F-PLACE1005313
F-PLACE1004773//Homo sapiens invasin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367	F-PLACE1005327//ESTs. Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:R51650
F-PLACE1004777//Human myosin-1XB mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391	F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794
F-PLACE1004793	F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297
F-PLACE1004804	F-PLACE1005373
F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340	F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348
F-PLACE1004814//ESTs. Weakly similar to UI SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284	F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362	F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047	F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433
F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943	F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925
F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97659	F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frame s//3.5e-126:744:87//Hs.23094:M19503
F-PLACE1004838	F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323
F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910	F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973
F-PLACE1004858	F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772	F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
F-PLACE1004900	F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382	F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929	F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130	F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385
F-PLACE1004930//Homo sapiens TNF-induced protein GC2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936	F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592	F-PLACE1005557//ESTs. Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261
F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851	F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278
F-PLACE1004969	F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436
F-PLACE1004972//Human retinoic acid- and interferon-inducible SBK protein R158 mRNA, complete cds//0.031:235:60//Hs.27610:U34605	F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147	F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520	F-PLACE1005611//ESTs. Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057
F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831	F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234
F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459	F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:HI5159	F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943	F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255
F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594	F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148	F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917
F-PLACE1005066//Homo sapiens actin binding protein MAYEN mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569	F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
F-PLACE1005077//EST//0.79:283:59//Hs.89276:AA283899	F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740	F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944
F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147	F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258
F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401	F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302
F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FB11) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561	F-PLACE1005763//ESTs. Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696
F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366	F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227	F-PLACE1005802
F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661	F-PLACE1005803
F-PLACE1005146//ESTs. Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:HI1741	F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156
F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087	F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482
F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:AB014541	F-PLACE1005828//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARMING ENTRY !!!! [H.sapiens]//4.1e-42:327:81//Hs.138404:R70986
F-PLACE1005181//ESTs. Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:AI138605	F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma) //0.038:436:58//Hs.75770:L41870
F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.142465:N70417	F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497
F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009	F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905
F-PLACE1005232//ESTs. Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//Hs.47334:W72370	F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242
F-PLACE1005243	F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487
F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941	F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552

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F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300  
 F-PLACE1005898  
 F-PLACE1005921  
 F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504  
 F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:A1288274  
 F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:M18391  
 F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142  
 F-PLACE1005936//DNA excision repair protein ERCCS//1.0:144:63//Hs.48576:X69978  
 F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357  
 F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468  
 F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:A1357868  
 F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:U13948  
 F-PLACE1005968  
 F-PLACE1005990  
 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981  
 F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256  
 F-PLACE1006011  
 F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743  
 F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:AB018332  
 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906  
 F-PLACE1006076//EST//0.29:92:64//Hs.161536:M80395  
 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:AF039023  
 F-PLACE1006129  
 F-PLACE1006139  
 F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353  
 F-PLACE1006157//ESTs, Weakly similar to ETX1 (alternatively splice d) [H.sapiens]//2.9e-12:119:84//Hs.23153:R92857  
 F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868  
 F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721  
 F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239  
 F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:A1074005  
 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433  
 F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:M49608  
 F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-11 homolog//3.5e-59:369:88//Hs.135623:AA134719  
 F-PLACE1006205  
 F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:A1279486  
 F-PLACE1006225  
 F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668  
 F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185  
 F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:A1085802  
 F-PLACE1006248//Homo sapiens mRNA for KIAA0548 protein, partial cds//7.3e-168:791:98//Hs.31921:AB014548  
 F-PLACE1006262  
 F-PLACE1006288//Homo sapiens mRNA for Pax3 protein//4.8e-37:186:100//Hs.7277:AJ001625  
 F-PLACE1006318  
 F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:A1246503  
 F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:A1361492  
 F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249  
 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481  
 F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581  
 F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715  
 F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693  
 F-PLACE1006385//Homo sapiens epsilon 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085  
 F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296  
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735  
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129  
 F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866  
 F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470  
 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194  
 F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511  
 F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493  
 F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584  
 F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542  
 F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358  
 F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:A1356219  
 F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784  
 F-PLACE1006552//Human (clone M5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529  
 F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280  
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97870  
 F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088  
 F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858  
 F-PLACE1006629//Homo sapiens (clone s22171) mRNA fragment//0.097:29:63//Hs.26956:L40396  
 F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:A1131473  
 F-PLACE1006673//ESTs, Weakly similar to T1484.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917  
 F-PLACE1006678  
 F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403  
 F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612  
 F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354  
 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152  
 F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252  
 F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:A1075783  
 F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:A1051228  
 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.123642:M83941  
 F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:A1422017  
 F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892  
 F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518  
 F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:87//Hs.23094:M19503  
 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876  
 F-PLACE1006860//EST//0.0062:206:65//Hs.158793:A1376773  
 F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273  
 F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254  
 F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601  
 F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:A1089187  
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443  
 F-PLACE1006917  
 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:A1423913  
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211  
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565  
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.12712723  
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67:98//Hs.21806:AA630312  
 F-PLACE1006962//H.sapiens iriB mRNA//2.3e-16:202:71//Hs.135202:X63417  
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922  
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753  
 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102  
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971  
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503  
 F-PLACE1007053//Homo sapiens mRNA for ARND3 protein//0.35:63:82//Hs.129811:AJ223957  
 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243  
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987  
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase

【0889】



【表588】

(glycogen debranching enzyme, glycogen storage disease type III) // 0.18:268:63//Hs.904:U84010  
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:A1223385  
 F-PLACE1007112  
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:A1160121  
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601  
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965  
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669  
 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204  
 F-PLACE1007239//Human mRNA for transcription elongation factor S-I l, hS-II-Tl, complete cds//2.0e-58:405:87//Hs.80598:D50495  
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141  
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467  
 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909  
 F-PLACE1007274  
 F-PLACE1007276//ATPase, Cut+ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:L06133  
 F-PLACE1007282  
 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:A1091436  
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:HS2412  
 F-PLACE1007317//Homo sapiens oxysterol 1alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//Hs.144877:AF029403  
 F-PLACE1007342  
 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EB BP) mRNA, complete cds//1.7e-121:567:98//Hs.76596:AF096870  
 F-PLACE1007367//H. sapiens mRNA for NACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173  
 F-PLACE1007375  
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:A1248642  
 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:A1041287  
 F-PLACE1007409//Homo sapiens mitoxanthrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//Hs.14387:AF093771  
 F-PLACE1007416  
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:A1024436  
 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:A1090359  
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391  
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714  
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103  
 F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975  
 F-PLACE1007488  
 F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385  
 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503  
 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296  
 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979  
 F-PLACE1007537//Homo sapiens PYRIN (MEFY) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080  
 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:A1076755  
 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:AB014561  
 F-PLACE1007557//EST//0.58:80:72//Hs.130267:A1001863  
 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257  
 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:A1089163  
 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533  
 F-PLACE1007621  
 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867  
 F-PLACE1007645  
 F-PLACE1007649  
 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266  
 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:A1027055  
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:A1348503  
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812  
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953  
 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:AF061243  
 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:AA476815  
 F-PLACE1007729//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:64//Hs.104129:AA923278  
 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:AB014585  
 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424  
 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030  
 F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:A1089469  
 F-PLACE1007791//EST//0.39:261:62//Hs.145991:A1277656  
 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504  
 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107  
 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841  
 F-PLACE1007843//EST//0.020:307:59//Hs.145535:A1261635  
 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503  
 F-PLACE1007852  
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:AB018309  
 F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:A1038387  
 F-PLACE1007877  
 F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943  
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.92381:AB007956  
 F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002  
 F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538  
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.5671:AF084530  
 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:739:98//Hs.78106:AF079529  
 F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222:W28567  
 F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:A1097043  
 F-PLACE1008006//Homo sapiens vcl1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693  
 F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031  
 F-PLACE1008044  
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382  
 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060  
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:U60975  
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197  
 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769  
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874  
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:A1218683  
 F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:A1263135  
 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427  
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524  
 F-PLACE1008201  
 F-PLACE1008209  
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:A1001856  
 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:24:7:61//Hs.77318:L13385  
 F-PLACE1008273  
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:A1275113  
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970  
 F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287  
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071  
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129  
 F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362  
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579  
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569  
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911  
 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:A1289171  
 F-PLACE1008398  
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242  
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326  
 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943  
 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Amino-peptidase P (EC 3.4.11.9, XAA-Pro-X-Pro/Proline/Aminoacylproline Amino-peptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653  
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499  
 F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [Hum

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【表589】

an, epidermoid carcinoma cell line A431. mRNA. 3 genes. 1718 nt// 0.019:530:58//Hs.72248:S72487	F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:A1040890
F-PLACE1008437	F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788
F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335	F-PLACE1009113//Homo sapiens X-ray repair cross-complementing prot ein 3 (XRCC3) mRNA. complete cds//1.1e-139:671:97//Hs.99742:AF0355 86
F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901	F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-2 4:718:59//Hs.35804:D25215
F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084: 210:63//Hs.27590:AB002381	F-PLACE1009150//Human HsLIM15 mRNA for HsLIM15, complete cds//1.7 e-50:440:78//Hs.37181:D64108
F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complet e cds//6.8e-07:469:60//Hs.1177:U10886	F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0484//4.0e-46:440:69//Hs.158095:AB007953
F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K <sup>+</sup> channe l (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823	F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRN A, complete cds//0.28:245:61//Hs.92614:M62302
F-PLACE1008531//EST//1.1e-17:190:76//Hs.156041:A1274697	F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887: D38081	F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770
F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter/ /1.1e-45:507:71//Hs.8003:AC004997	F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:A1282621
F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete c ds//1.0:95:71//Hs.117546:U31767	F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:A1283069	F-PLACE1009186//ESTs. Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396
F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete c ds//3.9e-175:812:98//Hs.23255:AB018334	F-PLACE1009190//EST//0.046:95:70//Hs.131646:A1025689
F-PLACE1008621//ESTs. Weakly similar to reverse transcriptase [H.s apiens]//1.2e-15:350:66//Hs.151087:AA649326	F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794	F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77 //Hs.146403:M29540
F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560	F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
F-PLACE1008627//ESTs//3.0e-62:302:93//Hs.120766:M82458	F-PLACE1009298//ESTs. Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735
F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211	F-PLACE1009308//SERUM PROTEIN M5E55//0.44:195:62//Hs.148101:M88338
F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394	F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD 95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192
F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D3 8535	F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frame s//2.3e-91:594:86//Hs.23094:M19503
F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333	F-PLACE1009335//EST//0.037:169:63//Hs.148875:A1240767
F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728	F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473
F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA enc oding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.9044 3:AF038406	F-PLACE1009368
F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs. 119534:AJ224741	F-PLACE1009375
F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080	F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:3 17:81//Hs.43681:AL022394
F-PLACE1008757//ESTs. Weakly similar to unknown protein [R.norvegi cus]//4.3e-17:285:69//Hs.35460:H65503	F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs. 9450:M27878
F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, compie te cds//1.4e-121:503:97//Hs.6458:AF060543	F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61// Hs.101174:AF047863
F-PLACE1008798//ESTs. Weakly similar to putative p150 [H.sapiens]/ /0.30:127:68//Hs.111380:AA258772	F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4 e-27:210:86//Hs.3404:AF035262
F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542	F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-4 5:599:68//Hs.155291:D13630
F-PLACE1008808//Homo sapiens putative checkpoint control protein H RAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905	F-PLACE1009443//H.sapiens ST4 gene for ST4 Oncofetal antigen//0.1 1:350:58//Hs.82128:AJ012159
F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318: 61//Hs.75668:M81883	F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:9 3//Hs.76987:AF012872
F-PLACE1008851//ESTs. Highly similar to CELL DIVISION CONTROL PRO TEIN 2 HOMOLOG [Plasmodium falciparum (isolate KI / thailand)]//0. 73:354:59//Hs.26322:AA156858	F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60 //Hs.151641:Z24680
F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:A1052728	F-PLACE1009468//1-PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE PHOSPHODI ESTERASE BETA 2//0.00039:347:60//Hs.994:M95678
F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:A1221563	F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT9875K-A-67 A1//4.1e-91:464:96//Hs.155049:AC004531
F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frame s//5.5e-51:701:68//Hs.23094:M19503	F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:A1308839
F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323	F-PLACE1009493//Homo sapiens mRNA for LAX-4p, complete cds//1.6e-3 0:608:63//Hs.16165:AB002405
F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cd s//2.1e-159:753:98//Hs.62318:AB018308	F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-6 8:526:78//Hs.8517:U70728
F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:M84771	F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417
F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:A1394026	F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:A1416956
F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937	F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866
F-PLACE1008947//Human TBP-associated factor (hTAF11130) mRNA, part ial cds//2.4e-13:625:58//Hs.24644:U75308	F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs. 147918:U38291
F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:A1024950	F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806
F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:9 6//Hs.34780:AJ003112	F-PLACE1009596//ESTs. Weakly similar to LIS-1 protein [H.sapiens]/ /4.1e-16:281:66//Hs.13889:A1341394
F-PLACE1009039//EST//0.76:111:63//Hs.160997:M55762	F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9 e-52:313:79//Hs.113283:AF018080
F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689	F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:A1074011
F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e- 16:93:100//Hs.119689:S70585	F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:A1094085
F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:A1239698	F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773
F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:A1090525	F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087
F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800	F-PLACE1009639
F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:A1093091	F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete c ds//4.4e-173:816:98//Hs.21862:AB011159
F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:A1337031	F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494
F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X6 8011	F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1 e-149:701:98//Hs.109590:AF062534

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【表590】

F-PLACE1009708//ESTs. Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S. cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926	F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986
F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650	F-PLACE1010401
F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789	F-PLACE1010481//Human BLU protein (BLU) mRNA, complete cds//0.94:254:61//Hs.125257:U70824
F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024	F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:AF039081
F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989	F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500
F-PLACE1009798//Human DNA sequence from clone 1189824 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, C1-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996	F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100
F-PLACE1009845	F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:64//Hs.159273:AF054177
F-PLACE1009861	F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021	F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979
F-PLACE1009886	F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148
F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889	F-PLACE1010580//ESTs. Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661
F-PLACE1009908	F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717	F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379	F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
F-PLACE1009925	F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778
F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153	F-PLACE1010628//EST. Weakly similar to line-1 protein ORF2 [H. sapiens]//0.012:258:62//Hs.144375:AA484200
F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446	F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345	F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114	F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102
F-PLACE1009995//ESTs. Weakly similar to C01A2.4 [C. elegans]//3.3e-24:174:88//Hs.11449:AI201540	F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076
F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529	F-PLACE1010662
F-PLACE1010023	F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376
F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878	F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027
F-PLACE1010053//ESTs. Moderately similar to M-phase phosphoprotein 4 [H. sapiens]//5.2e-63:312:98//Hs.142151:AA984061	F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564
F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596	F-PLACE1010739//Homo sapiens mRNA for Sec24A protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244
F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482	F-PLACE1010743//Human myosin-1Xb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391
F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424	F-PLACE1010761//ESTs. Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925	F-PLACE1010771//ESTs. Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNPG [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140
F-PLACE1010089//ESTs. Highly similar to PROBABLE UBQUITIN CARBOXY-TERMINAL HYDROLASE [Mus musculus]//1.8e-38:212:95//Hs.98067:AA236822	F-PLACE1010786
F-PLACE1010096//ESTs. Highly similar to hypothetical protein, 100K [R. norvegicus]//1.8e-08:100:89//Hs.11469:U69567	F-PLACE1010800
F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761	F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157
F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569	F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085
F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682	F-PLACE1010833//ESTs. Weakly similar to allograft inflammatory factor-1 [H. sapiens]//2.9e-28:245:79//Hs.132736:AA583494
F-PLACE1010134//H. sapiens hbrn mRNA//1.2e-14:380:64//Hs.77590:X7289	F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048
F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740	F-PLACE1010857//ESTs. Weakly similar to KIAA0157 gene product is novel. [H. sapiens]//5.8e-67:336:97//Hs.130135:AA905493
F-PLACE1010152	F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244
F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792	F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182
F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582	F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
F-PLACE1010202//ESTs. Weakly similar to No definition line found [C. elegans]//2.3e-72:391:94//Hs.35225:M69637	F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169
F-PLACE1010231	F-PLACE1010900
F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917	F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981
F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590	F-PLACE1010917
F-PLACE1010274//ESTs. Weakly similar to C01A2.4 [C. elegans]//6.8e-25:149:93//Hs.11449:AI201540	F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537
F-PLACE1010293//EST//4.5e-35:358:74//Hs.162398:AA572813	F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:AB011126
F-PLACE1010310//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433	F-PLACE1010942//Homo sapiens intersection short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:AF064244
F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248	F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985
F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875	F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154
F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659	F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:44:59//Hs.585:X04506
F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117	F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632
F-PLACE1010362//EST//1.9e-41:246:92//Hs.128771:AA236855	F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721
F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648	F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931
	F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032
	F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:U10886
	F-PLACE1011046//1-PHOSPHATIDYL INOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//Hs.994:M95678

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【表591】

F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1/ 6.1e-35:310:78//Hs.2407:249194	F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protei n//8.9e-05:477:59//Hs.37035:U07664
F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//Hs.153640:U56998	F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775
F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320	F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cd s//5.3e-110:526:98//Hs.22572:AB011152
F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663	F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913
F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037	F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4 e-09:478:56//Hs.107747:A1357868
F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:A1214317	F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817
F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:A1370857	F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617
F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949	F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763
F-PLACE1011160	F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514
F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443	F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:A1261591
F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114	F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514
F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1, 4-galactosyl t ransferase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664	F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cd s//4.0e-148:690:98//Hs.88756:AB018256
F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7 e-101:469:99//Hs.8241:AA283057	F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript t KIAA0487//6.5e-54:290:81//Hs.92381:AB007956
F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cD NA CEEL70F [C.elegans]//2.6e-62:221:88//Hs.101821:W27452	F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:A1205503
F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751	F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330
F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cd s//1.4e-147:675:99//Hs.23168:AB011101	F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:W57627
F-PLACE1011263//Homo sapiens BAC clone GS166A23 from Tp21//5.9e-7 1:350:98//Hs.15144:AC005014	F-PLACE2000014//EST//0.10:214:61//Hs.160247:A1138831
F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803	F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:W57627
F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds //3.4e-09:191:65//Hs.140950:AF070637	F-PLACE2000017
F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915	F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP- ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082 557
F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160	F-PLACE2000030
F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310	F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cd s//0.85:234:66//Hs.11342:U91512
F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265	F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cd s//0.058:348:62//Hs.94653:AB011179
F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript t KIAA0501//1.5e-20:120:81//Hs.159897:AB007970	F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:4 73:59//Hs.79706:U53204
F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D3 8535	F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
F-PLACE1011375//ESTs, Moderately similar to potassium channel prot ein Raw3 [R.norvegicus]//6.7e-68:325:99//Hs.107245:AA627053	F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868	F-PLACE2000061
F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552	F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9 e-114:662:86//Hs.23759:W98457
F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cd s//1.5e-158:743:98//Hs.10801:AB011102	F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219
F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frame s//1.9e-53:557:72//Hs.23094:W19503	F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:A1034333
F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:A1025204	F-PLACE2000100
F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete c ds//1.5e-152:703:99//Hs.111138:AB018255	F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:A1219219
F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482	F-PLACE2000111//H.sapiens mRNA for 1-acylglycerol-3-phosphate O-ac yltransferase//0.76:215:65//Hs.6587:U56417
F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264	F-PLACE2000115
F-PLACE1011503//EST//0.67:149:65//Hs.149774:A1285997	F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-4 9:400:79//Hs.153014:AB002353
F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319	F-PLACE2000132
F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476	F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:AA718911
F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:3 25:84//Hs.153563:AF011333	F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.8383 3:U54645
F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180	F-PLACE2000164
F-PLACE1011586//Homo sapiens hLR105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462	F-PLACE2000170
F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029: 585:57//Hs.106387:AF029778	F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:A1219179
F-PLACE1011641	F-PLACE2000176
F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds// 0.00058:499:58//Hs.12784:AB006631	F-PLACE2000187
F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757651	F-PLACE2000216
F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086	F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745	F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-3 8:792:63//Hs.21560:AB002296
F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs. 56045:D86640	F-PLACE2000245//Homo sapiens mRNA for KIAA0795 protein, partial cd s//1.5e-74:367:98//Hs.22926:AB018338
F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78 234	F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete c ds//2.0e-29:366:73//Hs.119387:AB007958
F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:M23366	F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23: 650:62//Hs.144672:AJ000522
F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:3 65:60//Hs.17262:AB002350	F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560
F-PLACE1011725	F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869
F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853	F-PLACE2000317
F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891	F-PLACE2000335//Fc fragment of IgE, high affinity I. receptor for: beta polypeptide//6.1e-24:295:76//Hs.30:M89796
F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:A1208240	F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds// 6.8e-21:593:61//Hs.103983:U66088
F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:A1393693	F-PLACE2000342//Centromere protein B (80kd)//1.4e-06:326:61//Hs.85 004:X05299
F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660	F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//

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3.7e-16:139:82//Hs.28209:A1073817  
 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645  
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045  
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:A1358861  
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:A1131032  
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638  
 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953  
 F-PLACE2000398  
 F-PLACE2000399  
 F-PLACE2000404  
 F-PLACE2000411  
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080  
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966  
 F-PLACE2000427  
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719  
 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257  
 F-PLACE2000438//Hs.sapiens mRNA for UDP-GalNAc:polypeptide N-acetyl galactosaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019  
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080  
 F-PLACE2000455//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082  
 F-PLACE2000458//Hs.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241  
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381  
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-58:520:81//Hs.113283:AF018080  
 F-PLACE2000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262  
 F-PLACE2000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384  
 F-PLACE2000020//Prostaglandin I2 (prostaglandin) receptor (IP)//0.0001:500:61//Hs.393:D38128  
 F-PLACE2000029  
 F-PLACE2000059//ESTs//0.0026:49:100//Hs.42913:A1082248  
 F-PLACE2000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842  
 F-PLACE2000103//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete cds//1.0:186:62//Hs.122752:AF026445  
 F-PLACE2000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295  
 F-PLACE2000121  
 F-PLACE2000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:038081  
 F-PLACE2000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603  
 F-PLACE2000142//EST//0.41:179:59//Hs.137438:AA282243  
 F-PLACE2000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016  
 F-PLACE2000147//EST//5.0e-43:285:86//Hs.160895:A1365871  
 F-PLACE2000148  
 F-PLACE2000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572  
 F-PLACE2000156//ESTs//0.00015:277:62//Hs.156834:A1336023  
 F-PLACE2000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666  
 F-PLACE2000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147  
 F-PLACE2000160  
 F-PLACE2000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219  
 F-PLACE2000194  
 F-PLACE2000197  
 F-PLACE2000199//EST//1.0:108:68//Hs.98488:AA426546  
 F-PLACE2000207//EST//1.0e-32:184:75//Hs.160146:A1049975  
 F-PLACE2000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744  
 F-PLACE2000218//EST//1.3e-46:317:84//Hs.162197:AA535216  
 F-PLACE2000220//EST//9.3e-95:443:99//Hs.112702:AA609377  
 F-PLACE2000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (OFF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019  
 F-PLACE2000226  
 F-PLACE2000230//EST//6.1e-16:173:72//Hs.148578:A1201568  
 F-PLACE2000242//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046  
 F-PLACE2000244

F-PLACE2000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858  
 F-PLACE2000271//ESTs//1.6e-25:195:72//Hs.108452:H78650  
 F-PLACE2000276//ESTs//1.0e-13:274:66//Hs.28589:A1004944  
 F-PLACE2000304//EST//0.043:210:61//Hs.132378:A1026770  
 F-PLACE2000310  
 F-PLACE2000320//EST//1.2e-12:188:70//Hs.145771:A1269586  
 F-PLACE2000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219  
 F-PLACE2000331  
 F-PLACE2000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545  
 F-PLACE2000341//EST//1.8e-05:394:58//Hs.112894:AA620741  
 F-PLACE2000350//ESTs. Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355  
 F-PLACE2000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194  
 F-PLACE2000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetyl galactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514  
 F-PLACE2000362//EST//6.5e-25:302:73//Hs.140504:AA810441  
 F-PLACE2000363  
 F-PLACE2000365//ESTs//0.81:200:60//Hs.141556:N49928  
 F-PLACE2000373//ESTs//0.0071:82:73//Hs.136310:AA442641  
 F-PLACE2000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432  
 F-PLACE2000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637  
 F-PLACE2000400//ESTs//0.53:162:66//Hs.49303:AA810785  
 F-PLACE2000401//EST//2.3e-35:178:100//Hs.162851:AA632270  
 F-PLACE2000402//ESTs//2.4e-84:425:96//Hs.148962:A1219715  
 F-PLACE2000405//EST//2.1e-39:452:73//Hs.140414:AA778541  
 F-PLACE2000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263  
 F-PLACE2000413//ESTs. Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:M61502  
 F-PLACE2000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:AB018344  
 F-PLACE2000425//EST//3.8e-34:286:79//Hs.135301:A1039161  
 F-PLACE2000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202  
 F-PLACE2000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874  
 F-PLACE2000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888  
 F-PLACE2000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190  
 F-PLACE2000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.5e-118:331:100//Hs.105399:AB018352  
 F-PLACE2000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69 G12//1.1e-06:244:63//Hs.154050:AC004131  
 F-PLACE2000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533  
 F-PLACE2000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.40993:AF000148  
 F-PLACE2000063  
 F-PLACE2000089//ESTs//2.2e-10:121:85//Hs.49391:W00713  
 F-PLACE2000093//ESTs//0.0053:273:60//Hs.136952:AA825819  
 F-PLACE2000100//ESTs//8.0e-21:246:73//Hs.140207:N32058  
 F-PLACE2000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931  
 F-PLACE2000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751  
 F-PLACE2000129  
 F-PLACE2000131//ESTs//2.4e-13:194:72//Hs.41418:H90627  
 F-PLACE2000147//ESTs//0.0060:324:60//Hs.85640:AA535856  
 F-PLACE2000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367  
 F-PLACE2000192  
 F-PLACE2000211  
 F-PLACE2000222//EST//1.9e-15:317:66//Hs.149206:A1246594  
 F-PLACE2000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329  
 F-PLACE2000233//ESTs//4.4e-38:240:80//Hs.114605:A1304317  
 F-PLACE2000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250  
 F-PLACE2000250//ESTs//3.8e-72:377:94//Hs.124234:T89609  
 F-PLACE2000252//ESTs//1.0:196:64//Hs.144869:AA493886  
 F-PLACE2000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//5.2e-27:191:87//Hs.2397:Z70200  
 F-PLACE2000261  
 F-PLACE2000269//ESTs. Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645

【表593】

F-PLACE4000270  
 F-PLACE4000300  
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//  
 /Hs.155952:U88966  
 F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365  
 F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798  
 F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:A1147292  
 F-PLACE4000367  
 F-PLACE4000369  
 F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256  
 F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:A1379823  
 F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046  
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cd  
 s//3.1e-47:605:71//Hs.153026:AB014540  
 F-PLACE4000411//ESTs. Moderately similar to plakophilin 2b [H.sapi  
 ens]//4.7e-33:159:81//Hs.154257:A1275982  
 F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cd  
 s//1.3e-45:263:92//Hs.2397:270200  
 F-PLACE4000445  
 F-PLACE4000450  
 F-PLACE4000455//ESTs//1.5e-11:273:65//Hs.145783:AA081874  
 F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:1  
 89:71//Hs.80738:X52075  
 F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951  
 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:A1126289  
 F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731  
 F-PLACE4000522//ESTs. Highly similar to NEUROGENIC LOCUS NOTCH PR  
 OTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:  
 AA767022  
 F-PLACE4000548  
 F-PLACE4000558//Homo sapiens mRNA for OFFRY protein, abundant tran  
 script//0.0035:510:59//Hs.39163:AF000986  
 F-PLACE4000581  
 F-PLACE4000590//ESTs. Highly similar to POL POLYPROTEIN [Friend m  
 urine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:A103  
 4080  
 F-PLACE4000593//ESTs. Weakly similar to F25D7.1 [C.elegans]//5.2e-  
 28:239:79//Hs.109084:A1004675  
 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074  
 F-PLACE4000638//Homo sapiens mRNA from chromosome Sq21-22, clone:s  
 F2//3.5e-47:562:69//Hs.129685:AB002446  
 F-PLACE4000650  
 F-PLACE4000654  
 F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:A1028132  
 F-SKNC1000011//Centromere protein B (80kd)//0.0013:243:62//Hs.850  
 04:X05299  
 F-SKNC1000013//ESTs. Highly similar to MULTIDRUG RESISTANCE PROT  
 EIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.11863  
 4:U66688  
 F-SKNC1000045//Homo sapiens mRNA for KIAA0654 protein, partial cd  
 s//2.5e-148:706:98//Hs.109299:AB014554  
 F-SKNC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.  
 76288:M23254  
 F-SKNC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877  
 F-THYR01000011//Human mRNA for KIAA0315 gene, partial cds//1.0:31  
 0:60//Hs.3989:AB002313  
 F-THYR01000026//H.sapiens OBF-1 mRNA for octamer binding factor 1/  
 /2.9e-35:299:81//Hs.2407:Z49194  
 F-THYR01000034  
 F-THYR01000035//ESTs//4.1e-37:317:79//Hs.141254:A1334099  
 F-THYR01000040//ESTs//0.30:331:59//Hs.87176:A1148326  
 F-THYR01000070//Human mRNA for KIAA0347 gene, complete cds//0.069:  
 278:63//Hs.101996:AB002345  
 F-THYR01000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:72  
 2:77//Hs.6654:AB014557  
 F-THYR01000085  
 F-THYR01000092//ESTs//3.1e-100:469:99//Hs.132207:A1148065  
 F-THYR01000107  
 F-THYR01000111//Human Line-1 repeat mRNA with 2 open reading frame  
 s//6.8e-106:690:86//Hs.23094:M19503  
 F-THYR01000121  
 F-THYR01000124//Human mRNA for alanine aminotransferase//0.0026:42  
 0:58//Hs.103502:U70732  
 F-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds/  
 /2.8e-155:732:98//Hs.87619:AF087142  
 F-THYR01000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203  
 F-THYR01000156//EST//0.32:102:68//Hs.139634:AA478416  
 F-THYR01000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:  
 85//Hs.155464:AF088219  
 F-THYR01000173//Human clathrin assembly protein 50 (AP50) mRNA, co  
 mplete cds//1.1e-05:261:61//Hs.152936:063475  
 F-THYR01000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7  
 e-41:270:87//Hs.101238:Y11312  
 F-THYR01000187//EST//0.11:227:62//Hs.101773:H23270  
 F-THYR01000190//ESTs//0.82:194:63//Hs.128818:AA976883  
 F-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonucleas  
 e//2.4e-175:805:99//Hs.43445:AJ005698  
 F-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete c  
 ds//4.0e-88:616:84//Hs.79672:AB014552  
 F-THYR01000206//EST//0.96:291:61//Hs.104962:AA443848  
 F-THYR01000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.  
 11506:U78297  
 F-THYR01000241//EST//0.48:102:69//Hs.160764:A1313322  
 F-THYR01000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.  
 9450:M27878  
 F-THYR01000253//Homo sapiens mRNA for KIAA0690 protein, partial cd  
 s//0.61:211:64//Hs.60103:AB014590  
 F-THYR01000270  
 F-THYR01000279//ESTs//0.0020:104:72//Hs.121476:A1215500  
 F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3  
 e-180:848:98//Hs.25846:AB016068  
 F-THYR01000320//ESTs. Weakly similar to Similar to glutamate decar  
 boxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803  
 F-THYR01000327//Autocrine motility factor receptor//2.8e-52:290:93  
 //Hs.80731:M63175  
 F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cd  
 s//7.2e-164:763:98//Hs.12002:AB018333  
 F-THYR01000358//Human selenium-binding protein (hSBP) mRNA, comple  
 te cds//6.9e-34:177:84//Hs.7833:U29091  
 F-THYR01000368//ESTs//0.0011:55:96//Hs.34994:AA252919  
 F-THYR01000381//Homo sapiens mRNA for KIAA0562 protein, complete c  
 ds//0.081:240:62//Hs.118401:AB011134  
 F-THYR01000387//EST//3.6e-14:197:71//Hs.139399:AA416855  
 F-THYR01000394//ESTs. Weakly similar to No definition line found  
 [C.elegans]//5.8e-39:245:91//Hs.119095:T79413  
 F-THYR01000395//EST//5.8e-69:333:99//Hs.156524:AA724572  
 F-THYR01000401//ESTs//1.8e-24:132:98//Hs.54852:W26238  
 F-THYR01000438//EST//1.9e-05:217:63//Hs.115930:AA579773  
 F-THYR01000452//B cell lymphoma protein 6 (zinc finger protein 51)  
 //0.096:306:60//Hs.155024:U00115  
 F-THYR01000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.299  
 9:X52520  
 F-THYR01000484//EST. Weakly similar to putative p150 [H.sapiens]//  
 8.9e-22:248:76//Hs.162011:AA513663  
 F-THYR01000488  
 F-THYR01000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X8  
 2200  
 F-THYR01000502//ESTs//1.0:350:57//Hs.119749:AA689298  
 F-THYR01000505//Interleukin 13//0.95:245:60//Hs.845:U31120  
 F-THYR01000558//EST//1.3e-24:351:64//Hs.142326:AA351877  
 F-THYR01000569//Homo sapiens mRNA for dihydropyrimidinase related  
 protein 4, complete cds//0.28:229:61//Hs.100058:AB006713  
 F-THYR01000570//EST//0.80:171:61//Hs.112790:AA609949  
 F-THYR01000585//Homo sapiens protein associated with Myc mRNA, com  
 plete cds//2.4e-168:808:97//Hs.151411:AF075587  
 F-THYR01000596//EST//9.5e-94:461:96//Hs.135397:A1056322  
 F-THYR01000602//EST//4.9e-06:80:80//Hs.162135:AA526331  
 F-THYR01000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62  
 //Hs.2685:Z50053  
 F-THYR01000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:  
 D38081  
 F-THYR01000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941  
 F-THYR01000641//ESTs//0.00017:375:58//Hs.32703:AA054125  
 F-THYR01000658//CD4 receptor (exons 1 and 2) [human, T-lymphocyte,  
 mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267  
 F-THYR01000662  
 F-THYR01000666//ESTs//1.9e-28:149:99//Hs.105187:A1394157  
 F-THYR01000676//CD4 receptor (exons 1 and 2) [human, T-lymphocyte,  
 mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267  
 F-THYR01000684//ESTs. Weakly similar to band-6-protein [H.sapiens]  
 //0.46:368:57//Hs.26557:AA480380  
 F-THYR01000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452  
 F-THYR01000712//ESTs//3.3e-42:211:99//Hs.69330:A1056324  
 F-THYR01000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:  
 631:59//Hs.79706:U53204  
 F-THYR01000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085  
 F-THYR01000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:  
 339:74//Hs.7977:AB007871  
 F-THYR01000756//Homo sapiens protocadherin (PCDH8) mRNA, complete  
 cds//1.0:209:62//Hs.19492:AF061573

【0895】

【表594】

F-THYR01000777//Human mRNA for KIAA0147 gene, partial cds//0.0006 9:636:57//Hs.158132:D63481	F-THYR01001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
F-THYR01000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084	F-THYR01001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//Hs.102877:U41315
F-THYR01000787	F-THYR01001434//ESTs//1.1e-07:274:60//Hs.151093:A1224099
F-THYR01000793	F-THYR01001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:6 53:71//Hs.44782:Z82215
F-THYR01000796	F-THYR01001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:7 8//Hs.51048:X68830
F-THYR01000805//Homo sapiens mRNA from chromosome 5q21-22, clone:s F2//9.4e-36:561:68//Hs.129685:AB002446	F-THYR01001487//EST//1.0:88:71//Hs.160760:A1311943
F-THYR01000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-4 5:465:75//Hs.154326:D42087	F-THYR01001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
F-THYR01000829//ESTs//1.7e-66:361:95//Hs.7906:HI6339	F-THYR01001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
F-THYR01000843	F-THYR01001541//EST//1.4e-10:158:65//Hs.145159:A1150211
F-THYR01000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788	F-THYR01001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
F-THYR01000855//ESTs//0.049:159:64//Hs.163532:A1424170	F-THYR01001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
F-THYR01000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARM1 NG ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103	F-THYR01001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:54 6:95//Hs.25306:AF070572
F-THYR01000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531	F-THYR01001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.822 94:U27655
F-THYR01000916//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0487//1.8e-43:318:79//Hs.92381:AB007956	F-THYR01001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165: 84//Hs.75551:L12535
F-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (P DEBB) mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529	F-THYR01001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
F-THYR01000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63/ /Hs.79217:M77836	F-THYR01001605//EST//0.11:426:57//Hs.151206:A1126071
F-THYR01000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662: 56//Hs.112432:AC005263	F-THYR01001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
F-THYR01000952//Human mRNA for KIAA0208 gene, complete cds//0.98:1 77:65//Hs.83558:D86963	F-THYR01001637//ESTs, Weakly similar to anion exchanger [H.sapien s]//5.2e-13:108:86//Hs.141045:AA191659
F-THYR01000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial prot ein, complete cds//2.7e-15:123:90//Hs.106469:AF042169	F-THYR01001656//Solute carrier family 2 (facilitated glucose trans porter), member 4//0.099:540:55//Hs.95958:M91463
F-THYR01000975//EST//0.45:172:62//Hs.105449:AA513907	F-THYR01001661//ESTs//0.12:53:92//Hs.151586:W45568
F-THYR01000983	F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthet ase 59 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089
F-THYR01000984//EST//0.0075:119:65//Hs.150347:AA984646	F-THYR01001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.781 60:AF010238
F-THYR01000988//ESTs//0.056:99:71//Hs.153409:A1224307	F-THYR01001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:5 7//Hs.122908:AF070552
F-THYR01001003	F-THYR01001706//ESTs//1.8e-24:142:95//Hs.112536:A1147691
F-THYR01001031//Thiopurine S-methyltransferase//3.8e-44:568:71//H s.51124:AF019369	F-THYR01001721//ESTs, Highly similar to RING CANAL PROTEIN [Droso phila melanogaster]//2.5e-51:296:92//Hs.3826:U69560
F-THYR01001033//H.sapiens mRNA for cyclin I1//0.0061:287:60//Hs.3 232:Z46788	F-THYR01001738//EST//6.9e-30:180:94//Hs.58641:W81229
F-THYR01001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:7 9//Hs.51048:X68830	F-THYR01001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
F-THYR01001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-3 3:421:72//Hs.153014:AB002353	F-THYR01001746//EST//0.96:119:63//Hs.144107:A1053590
F-THYR01001100//Human DNA-binding protein mRNA, 3' end//2.1e-74:74 1:74//Hs.159249:Z99130	F-THYR01001772//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARM1 NG ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725
F-THYR01001120//Homo sapiens deltaex (Dx) mRNA, complete cds//4.5e- 18:447:62//Hs.124024:AF053700	F-THYR01001793//ESTs//1.9e-93:439:99//Hs.150116:A1299324
F-THYR01001121//ESTs//0.92:257:61//Hs.118246:N95416	F-THYR01001809//Human mRNA for KIAA0297 gene, partial cds//0.47:16 8:67//Hs.11711:AB002295
F-THYR01001133//EST//1.1e-38:367:75//Hs.144175:H70425	F-THYR01001828
F-THYR01001134//ESTs//1.4e-28:186:91//Hs.109468:W52074	F-THYR01001854//EST//0.038:128:67//Hs.160649:A1241823
F-THYR01001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788	F-THYR01001895//Intercellular adhesion molecule 1 (CD54), human rh inovirus receptor//9.6e-13:288:65//Hs.51061:M24283
F-THYR01001173	F-THYR01001907//EST//1.9e-12:126:80//Hs.139296:AA350198
F-THYR01001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385	F-VESEN1000122
F-THYR01001189//ESTs//2.1e-36:323:76//Hs.120206:A1089163	F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
F-THYR01001204	F-Y79AA1000033
F-THYR01001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256: 81//Hs.155464:AF088219	F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7. 8e-21:230:66//Hs.431:L13689
F-THYR01001262//ESTs//7.9e-44:279:87//Hs.138856:H47461	F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, compl ete cds//7.3e-40:629:64//Hs.75305:U78521
F-THYR01001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:6 0//Hs.6467:AJ002309	F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680
F-THYR01001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, comple te cds//0.014:178:66//Hs.125315:AF027156	F-Y79AA10000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:5 8//Hs.2685:Z50053
F-THYR01001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836	F-Y79AA10000181//Fatty acid synthase (3' region) [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U293 44
F-THYR01001313//ESTs//1.0:244:61//Hs.127488:AA528182	F-Y79AA10000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860
F-THYR01001320//ESTs//0.062:126:67//Hs.133296:A1311872	F-Y79AA10000214//Homo sapiens histone H2A.F/2 variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192
F-THYR01001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:5 60:68//Hs.153563:AF011333	F-Y79AA10000230//Polymeric immunoglobulin receptor//0.98:335:59//H s.842:Z73079
F-THYR01001322//ESTs//0.12:238:61//Hs.29169:N66545	F-Y79AA10000231//ESTs//0.11:209:66//Hs.132184:A1278623
F-THYR01001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207	F-Y79AA10000258//Homo sapiens metase (MET-1) mRNA, complete cds//0. 30:444:61//Hs.99941:L23134
F-THYR01001363//ESTs//1.0e-16:178:78//Hs.163954:N57939	F-Y79AA10000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-1 1:300:64//Hs.23311:AB002365
F-THYR01001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18: 187:79//Hs.12385:AB007877	F-Y79AA10000313//Human mRNA for KIAA0129 gene, complete cds//0.89:7 44:56//Hs.44361:D50919
F-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cd s//7.4e-157:740:97//Hs.138488:AB014607	F-Y79AA10000328
F-THYR01001401//EST//4.6e-14:171:76//Hs.157587:A1356993	F-Y79AA10000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309
F-THYR01001403//ESTs//2.2e-50:464:79//Hs.118046:N49946	F-Y79AA10000346
F-THYR01001405//ESTs//1.7e-44:226:98//Hs.156667:A1347694	F-Y79AA10000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//H
F-THYR01001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20: 459:62//Hs.477:U05659	

【0896】

【表595】

s.123022:J03853	F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60// /Hs.85279:U34879
F-Y79AA1000355	F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110113307 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897	F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229: 83//Hs.155464:AF088219	F-Y79AA1001299//Human Inil mRNA, complete cds//2.2e-116:323:93//H s.155626:U04847
F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018	F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
F-Y79AA1000469//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.28285:AF082516	F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
F-Y79AA1000480	F-Y79AA1001384
F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871	F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70// Hs.66731:U81599
F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521	F-Y79AA1001394//ESTs. Weakly similar to F5483.3 [C.elegans]//1.5e- 90:424:96//Hs.154221:H23167
F-Y79AA1000540//Homo sapiens chromosome Taz2 sequence//0.70:133:69 //Hs.151555:AF053356	F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489
F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706	F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61// Hs.83484:X70683
F-Y79AA1000574//Human mRNA for GC box binding protein, complete cds //0.95:258:62//Hs.150557:031716	F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequ ence//2.8e-154:755:97//Hs.21811:AF091080	F-Y79AA1001533//ESTs. Highly similar to RETROVIRUS-RELATED POL PO LYPROTEIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447
F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, co mplete cds//1.7e-136:644:98//Hs.60580:AF060503	F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:5 9//Hs.22670:AF006513	F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11 b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670	F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969	F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)// 2.5e-05:272:64//Hs.106070:U22398
F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377	F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067	F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468	F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds/ //1.1e-178:847:97//Hs.5151:AF098799	F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete c ds//0.00078:520:57//Hs.12334:AB014583
F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61/ /Hs.79295:U07231	F-Y79AA1001647//ESTs. Weakly similar to ZK1058.5 [C.elegans]//9.4 e-79:421:94//Hs.107039:W27244
F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds// 0.12:244:60//Hs.12307:AF056085	F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.11 0802:X04385
F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, co mplete cds//0.87:466:59//Hs.122967:AF059569	F-Y79AA1001679//Guanine nucleotide binding protein (G protein), be ta polypeptide 1//0.88:243:61//Hs.3620:X04526
F-Y79AA1000805	F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9 e-06:426:59//Hs.162:X16302
F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568	F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
F-Y79AA1000827//Fatty acid synthase (3' region) [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U293 44	F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kin ase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X 06956	F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620
F-Y79AA1000850//ESTs. Weakly similar to T22C1.7 [C.elegans]//6.0e- 77:368:99//Hs.86660:AA398644	F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:18 3:66//Hs.113082:AB007903
F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:D16815	F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699	F-Y79AA1001827//ESTs. Weakly similar to Similar to S.cerevisiae YD 935.03c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213
F-Y79AA1000968//ESTs. Moderately similar to initiation factor eIF- 2B gamma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536	F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533
F-Y79AA1000969//LYMPHOTKIN-BETA RECEPTOR PRECURSOR//1.0:150:64//H s.1116:L04270	F-Y79AA1001848//ESTs. Weakly similar to KIAA0390 [H.sapiens]//1.6 e-19:142:90//Hs.103349:AI141124
F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.7380 9:M23892	F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1 e-09:215:67//Hs.104115:X52332
F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:38 5:58//Hs.79705:U53204	F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06: 412:62//Hs.106387:AF029778
F-Y79AA1001023	F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173
F-Y79AA1001041//Human myt1 homolog (hMYH) gene, complete cds//0.9 9:37:100//Hs.78489:U63329	F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720
F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8. 7e-30:772:60//Hs.82208:L46590	F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382
F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381	F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611
F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511	F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943
F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047	F-Y79AA1002089//ESTs. Weakly similar to putative p150 [H.sapiens]/ /8.3e-53:348:88//Hs.18122:AI338045
F-Y79AA1001078	F-Y79AA1002093
F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, comp lete cds//6.5e-11:247:66//Hs.55967:AF022654	F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865
F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381	F-Y79AA1002115
F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete c ds//1.0:155:63//Hs.5444:AB018293	F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:W40395
F-Y79AA1001177//Human hSIAM2 mRNA, complete cds//6.5e-09:299:65//H s.20191:U76248	F-Y79AA1002139//ESTs. Weakly similar to 80035.14 [C.elegans]//1.2 e-24:165:90//Hs.6473:AA853955
F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646	F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cd s//9.5e-05:393:62//Hs.77864:AB014538
F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965	F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515
F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z 48054	F-Y79AA1002209//ESTs. Weakly similar to TYROSYL-TRNA SYNTHETASE [B acillus caldotenax]//2.3e-113:568:96//Hs.111637:AA305890
F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.5 4472:U48436	F-Y79AA1002210//ESTs. Weakly similar to D2045.8 [C.elegans]//8.6e- 33:338:73//Hs.26662:U55984
	F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477
	F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508
	F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.004 1:203:63//Hs.1560:042045

【0897】



## 【表596】

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:AB014592  
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903  
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:AB014555  
 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489  
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:AB014534  
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999  
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:587:58//Hs.2363:L36069  
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377  
 F-Y79AA1002399  
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569  
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142  
 F-Y79AA1002431  
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318  
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973  
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:A1160765  
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302

## 【0898】

3'末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのTitle、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

## 【0899】

【表597】

R-HEMBA1000005//ESTs. Highly similar to HYPOTHETICAL 31.6 KD PROT E1N FS4F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:50 1:93//Hs.13015:AA628434

R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233

R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198

R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-5 2:528:72//Hs.154326:D42087

R-HEMBA1000050//EST//0.043:155:63//Hs.149031:A1243340

R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329

R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.145811:AA410788

R-HEMBA1000129//ESTs. Weakly similar to contains similarity to hel icases [C. elegans]//4.4e-90:502:90//Hs.55918:AA151667

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cd s//2.1e-100:514:94//Hs.27197:AB018340

R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cd s//3.1e-45:435:77//Hs.153026:AB014540

R-HEMBA1000156//ESTs. Moderately similar to The KIAA0138 gene prod uct is novel. [H. sapiens]//7.7e-92:428:100//Hs.126925:AA931237

R-HEMBA1000158

R-HEMBA1000168//ESTs. Weakly similar to F13B12.1 [C. elegans]//1.3 e-05:58:91//Hs.5570:A1377863

R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545

R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366

R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927

R-HEMBA1000201//Human Inil mRNA, complete cds//3.0e-25:137:99//Hs. 155626:U04847

R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311

R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532

R-HEMBA1000227//EST//2.2e-100:498:96//Hs.161570:W80404

R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:2 87:70//Hs.127649:AB007874

R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete c ds//1.3e-23:276:75//Hs.5737:AB007944

R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019

R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:A1243808

R-HEMBA1000264//ESTs//3.8e-72:487:96//Hs.29258:W37424

R-HEMBA1000280//ESTs. Moderately similar to ovarian-specific prote in [R. norvegicus]//4.9e-14:208:73//Hs.93332:AA811920

R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485

R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962

R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409

R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cd s//1.0:122:67//Hs.129748:AB011099

R-HEMBA1000303//ESTs//7.4e-76:386:97//Hs.22276:AA191323

R-HEMBA1000304//Human Ca<sup>2+</sup>-dependent activator protein for secreti on mRNA, complete cds//8.8e-30:160:98//Hs.151301:U36448

R-HEMBA1000307//ESTs. Highly similar to 8A-2V protein [M. musculus] //1.1e-103:489:99//Hs.108881:A1018024

R-HEMBA1000333//ESTs//9.3e-99:472:98//Hs.163512:AA903238

R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:A1302560

R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460

R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:A1422243

R-HEMBA1000357//Human kpni repeat wna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:X00629

R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857

R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938

R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-4 4:388:77//Hs.3610:D86960

R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460

R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878

R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:A1340248

R-HEMBA1000396//ESTs. Weakly similar to line-1 protein ORF2 [H. sap iens]//1.1e-44:447:75//Hs.42849:N31920

R-HEMBA1000411//ESTs. Weakly similar to ankyrin 3, long form [H. sa piens]//6.1e-92:373:99//Hs.48675:A1005282

R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:A1270700

R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140

R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535: 87//Hs.158122:AJ001189

R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:X38143

R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:A1218014

R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349

R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:A1246316

R-HEMBA1000460

R-HEMBA1000464//EST//0.082:87:70//Hs.147977:A1262370

R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494: 81//Hs.155464:AF088219

R-HEMBA1000488//ESTs. Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H. sapie ns]//1.1e-31:181:94//Hs.61454:AA312449

R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528

R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087

R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:A1077571

R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318

R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531

R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885

R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414

R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280

R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:U15782

R-HEMBA1000531//ESTs. Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H. sapiens]//1.3e-117:550:99//Hs.99722:A1422277

R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809

R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:54 9:80//Hs.91916:AF035317

R-HEMBA1000555//ESTs//2.3e-66:342:97//Hs.71916:AA219699

R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:A1281881

R-HEMBA1000561//ESTs. Moderately similar to zinc finger protein [ R. norvegicus]//1.8e-108:550:96//Hs.26799:W74481

R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196

R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:HO7128

R-HEMBA1000569

R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.145811:AA410788

R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein //3.9e-113:591:94//Hs.155218:AJ007509

R-HEMBA1000592//TYROSINE-PROTEIN KINASE-1TK/TSK//0.024:309:61//Hs. 89519:L10717

R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:A1168041

R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, com plete cds//1.5e-19:129:93//Hs.158334:U86136

R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424

R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438

R-HEMBA1000636//ESTs. Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E. coli]//1.4e-86:422:97//Hs.26252:AA643235

R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cd s//3.7e-99:443:97//Hs.60103:AB014590

R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-5 0:426:79//Hs.40100:AB002390

R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929

R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136

R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:A1123922

R-HEMBA1000682//ESTs. Weakly similar to putative p150 [H. sapiens]// 3.5e-114:553:97//Hs.111730:AA604403

R-HEMBA1000686//ESTs. Weakly similar to C27F2.7 gene product [C. el egans]//6.8e-18:137:86//Hs.7049:A1141736

R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16. 4)//7.4e-52:345:84//Hs.144563:AF057280

R-HEMBA1000705//EST//0.21:139:63//Hs.132687:A1033672

R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213

R-HEMBA1000722//ESTs. Weakly similar to similar to enoyl-CoA hydra tases/isomerases [C. elegans]//7.2e-113:572:95//Hs.28644:A1018612

R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8 e-40:449:75//Hs.74478:U33931

R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777

R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110

R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286: 82//Hs.155464:AF088219

R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131

R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, com plete cds//1.6e-32:309:75//Hs.10458:AF088219

R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612

R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostat e; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclo nal and antibody 1A4))//1.3e-48:284:90//Hs.103458:X53795

R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-4 5:291:87//Hs.154326:D42087

R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939

R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protei n (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977

R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e- 46:410:77//Hs.154103:AF061258

R-HEMBA1000851

R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrog enase)//3.7e-33:284:80//Hs.159608:U46689

R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:A1265794

【0900】

【表598】

R-HEMBA1000869/ESTs//3.1e-16:237.71/Hs.116518:AA653202	R-HEMBA1001294/ESTs//1.0:140:65/Hs.149638:AI298324
R-HEMBA1000870/ESTs//1.6e-43:222.98/Hs.69564:AA203608	R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84/Hs.155464:AF088219
R-HEMBA1000872/ESTs//1.9e-93:453.98/Hs.152622:AA594951	R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68/Hs.20912:AB012162
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79/Hs.155464:AF088219	R-HEMBA1001303/EST//0.00053:271:60/Hs.156148:AI333214
R-HEMBA1000908/ESTs//1.6e-51:291.92/Hs.12247:AI203154	R-HEMBA1001310/ESTs//1.4e-91:486.93/Hs.86228:AA206019
R-HEMBA1000910/EST//0.98:139:64/Hs.132687:AI033672	R-HEMBA1001319/ESTs//0.051:228:61/Hs.99404:AA953977
R-HEMBA1000918/EST//9.6e-30:152.84/Hs.162136:AA526508	R-HEMBA1001323/ESTs//6.2e-83:401.98/Hs.47343:AI282950
R-HEMBA1000919	R-HEMBA1001326/ESTs. Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN IN FABI-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92/Hs.9398:NA1838
R-HEMBA1000934/ESTs//4.1e-38:254.89/Hs.87784:AA460597	R-HEMBA1001327/ESTs//0.60:251:58/Hs.117162:AA701259
R-HEMBA1000942/ESTs//3.5e-20:172.69/Hs.160065:AI018619	R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78/Hs.113283:AF018080
R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78/Hs.33187:AB018291	R-HEMBA1001351/ESTs//0.13:230:57/Hs.138510:R94816
R-HEMBA1000946/ESTs//1.6e-68:352.96/Hs.21331:H93074	R-HEMBA1001361/ESTs//3.5e-107:570.94/Hs.7727:AA142837
R-HEMBA1000960//Homo sapiens tapasin (NCS-17) mRNA, complete cds//4.0e-61:347:81/Hs.5247:AF029750	R-HEMBA1001375/ESTs//1.1e-96:454.99/Hs.59584:AA587334
R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362.84/Hs.159187:AB007977	R-HEMBA1001377/ESTs//8.5e-91:459.95/Hs.61859:AA628550
R-HEMBA1000971/ESTs//2.8e-41:246.91/Hs.104287:AI363498	R-HEMBA1001383/ESTs//0.077:381:58/Hs.163093:AA745458
R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81/Hs.44766:AJ007590	R-HEMBA1001387/ESTs//2.0e-85:405.99/Hs.152127:AI246482
R-HEMBA1000974/ESTs//1.4e-32:166.100/Hs.149274:AI018170	R-HEMBA1001388/ESTs//1.5e-83:395.99/Hs.105191:AA133439
R-HEMBA1000975//Oxytocin receptor//7.7e-46:563.73/Hs.2820:K64878	R-HEMBA1001391/ESTs//7.7e-90:455.96/Hs.120905:R22204
R-HEMBA1000985/ESTs//4.4e-05:125.69/Hs.147434:AI214464	R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89/Hs.89887:D38081
R-HEMBA1000986/ESTs//7.8e-44:266.84/Hs.163784:NA4902	R-HEMBA1001405/ESTs//1.2e-98:485.97/Hs.73287:W16714
R-HEMBA1000991/EST//1.4e-42:162.86/Hs.149580:AI281881	R-HEMBA1001407/ESTs//2.2e-76:365.99/Hs.110128:AA584364
R-HEMBA1001007	R-HEMBA1001411/ESTs//1.2e-102:476.100/Hs.143162:AI380343
R-HEMBA1001008/ESTs//2.3e-82:463.92/Hs.10339:AA058764	R-HEMBA1001413/ESTs//3.7e-66:321.98/Hs.152472:AA041199
R-HEMBA1001009/ESTs. Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280.100/Hs.128738:AA970836	R-HEMBA1001415
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587.95/Hs.158287:AB007937	R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82/Hs.42674:U61981
R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95/Hs.58393:X05360	R-HEMBA1001433/ESTs//1.4e-34:240.77/Hs.95611:U51704
R-HEMBA1001020/ESTs//0.52:86.72/Hs.69683:AA115292	R-HEMBA1001435/ESTs//5.6e-23:292.70/Hs.116315:AA629263
R-HEMBA1001022/ESTs//3.4e-18:102.100/Hs.63243:AI123912	R-HEMBA1001442/ESTs//0.76:414:58/Hs.156189:AI419982
R-HEMBA1001024/ESTs//1.9e-07:262.61/Hs.124399:AA832336	R-HEMBA1001446/ESTs//2.2e-95:447.99/Hs.154091:AA767546
R-HEMBA1001026/ESTs//0.0017:142.67/Hs.144109:AI345543	R-HEMBA1001450/ESTs//1.0e-93:491.94/Hs.16130:AI195077
R-HEMBA1001043//Ankyrin G//0.23:244:60/Hs.75893:U13616	R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frame s//1.7e-47:304.88/Hs.23094:M19503
R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186.79/Hs.132942:AB014521	R-HEMBA1001455/ESTs//7.1e-103:482.99/Hs.97407:AI417220
R-HEMBA1001052/ESTs//5.4e-107:497.99/Hs.121773:AI357886	R-HEMBA1001463
R-HEMBA1001060/ESTs//1.1e-31:298.80/Hs.24821:AA044813	R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66/Hs.36232:D80008
R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179.98/Hs.119571:X14420	R-HEMBA1001478
R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417.64/Hs.127338:AB007961	R-HEMBA1001497
R-HEMBA1001080	R-HEMBA1001510/ESTs//3.3e-44:381.78/Hs.139882:AA854426
R-HEMBA1001085/ESTs//1.9e-47:385.79/Hs.146811:AA410788	R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frame s//5.9e-79:528.84/Hs.23094:M19503
R-HEMBA1001088/ESTs//8.1e-102:546.93/Hs.127273:AA522674	R-HEMBA1001517/ESTs//5.8e-32:272.81/Hs.119512:AA487269
R-HEMBA1001094	R-HEMBA1001522/ESTs//1.7e-84:364.95/Hs.117858:AA702493
R-HEMBA1001099/ESTs//0.24:41.97/Hs.18612:T99245	R-HEMBA1001526/ESTs//1.8e-93:527.93/Hs.10624:N64723
R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396.80/Hs.155464:AF088219	R-HEMBA1001533/ESTs//1.9e-42:211.100/Hs.55830:AA580270
R-HEMBA1001121/ESTs//1.7e-15:216.71/Hs.141605:H92974	R-HEMBA1001557/ESTs//4.2e-83:413.97/Hs.47546:AI181348
R-HEMBA1001122/ESTs//2.0e-90:474.94/Hs.107884:AA131320	R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304.88/Hs.155464:AF088219
R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319.84/Hs.99879:M15530	R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62/Hs.2229:X82324
R-HEMBA1001133/ESTs//1.2e-92:443.99/Hs.99626:AA632341	R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456.77/Hs.159275:AF030880
R-HEMBA1001137/ESTs//2.0e-86:426.97/Hs.157103:W60265	R-HEMBA1001579/ESTs//0.11:299.60/Hs.106090:AA457030
R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323.83/Hs.155464:AF088219	R-HEMBA1001581/ESTs//0.016:350.61/Hs.124664:AI015652
R-HEMBA1001172/ESTs. Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.1e-39:309.82/Hs.96337:AA225358	R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63/Hs.146395:AB002329
R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238.60/Hs.127338:AB007961	R-HEMBA1001589
R-HEMBA1001197/ESTs//0.010:388.61/Hs.14881:R91896	R-HEMBA1001595/ESTs. Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431.88/Hs.26625:W25874
R-HEMBA1001208/ESTs. Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305.62/Hs.100238:U69194	R-HEMBA1001608//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//1.3e-73:533.82/Hs.103948:K00627
R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333.81/Hs.113283:AF018080	R-HEMBA1001620/ESTs. Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537.90/Hs.20218:AA628530
R-HEMBA1001235/EST//2.3e-07:42.92/Hs.141620:N63316	R-HEMBA1001635//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362.60/Hs.132206:AF039694
R-HEMBA1001247/ESTs. Weakly similar to WWP2 [H.sapiens]//2.9e-20:160.87/Hs.103102:W55932	R-HEMBA1001636/ESTs//4.9e-53:267.97/Hs.47459:AA700158
R-HEMBA1001257/ESTs//3.3e-112:544.97/Hs.128749:AA779728	R-HEMBA1001640/ESTs//2.9e-27:299.72/Hs.65236:AA927623
R-HEMBA1001265/ESTs//8.7e-116:564.98/Hs.155150:AI061435	R-HEMBA1001651/ESTs. Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442.95/Hs.63888:AA203398
R-HEMBA1001281/ESTs. Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239.87/Hs.103919:AA159181	R-HEMBA1001655/ESTs//1.5e-101:516.95/Hs.86541:AA214554
R-HEMBA1001286/ESTs//1.4e-97:507.95/Hs.26244:AI352674	R-HEMBA1001658
R-HEMBA1001289/ESTs//8.2e-44:122.96/Hs.76267:AA877534	R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427.61/Hs.106511:AF029343

## 【表599】

R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943  
R-HEMBA1001675  
R-HEMBA1001678//Homo sapiens voltage dependent anion channel prote in mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962  
R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424  
R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916  
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete c ds//6.3e-98:483:96//Hs.31720:AB014598  
R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960  
R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095  
R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHO NDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA 194452  
R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166: 88//Hs.155464:AF088219  
R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPE ATS CONTAINING PROTEIN IN S1S1-MRPL2 INTERGENIC REGION [Saccharomy ces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105  
R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712  
R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-3 9:366:77//Hs.153014:AB002353  
R-HEMBA1001744  
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623  
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162  
R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145  
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306  
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721  
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053  
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243  
R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823  
R-HEMBA1001804//Zinc finger protein 148 (pH2-52)//0.78:232:57//Hs. 112180:AF039019  
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0500//9.0e-114:548:98//Hs.118164:AB007969  
R-HEMBA1001809//ESTs//3.8e-63:292:89//Hs.158591:AI369334  
R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.1357 2:AF068179  
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.1554 70:X07290  
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707  
R-HEMBA1001822//ESTs//2.2e-101:480:99//Hs.159940:AA971578  
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2 e-27:147:97//Hs.23476:AA401210  
R-HEMBA1001835//EST//0.79:216:64//Hs.47437:MS2250  
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513  
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446  
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete c ds//1.1e-109:553:96//Hs.78946:AB014517  
R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853  
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein (alternative p roducts)//1.9e-37:357:76//Hs.53217:Z48051  
R-HEMBA1001869//ESTs, Weakly similar to trithorax homolog HTX, ver sion 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R84329  
R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:7 8//Hs.66710:X96969  
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:HD3128  
R-HEMBA1001910  
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNI NG ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438  
R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomy ces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685  
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706  
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125  
R-HEMBA1001921//Homo sapiens germinal center kinase related protei n kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145  
R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470  
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-4 5:336:82//Hs.40100:AB002390  
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668  
R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452  
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866  
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421  
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048  
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825<sup>1</sup>  
R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (pre sumptive isolat of a Rat gene) and a novel alternatively spliced g ene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:9 7//Hs.11050:AL031178  
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932  
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717  
R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-4 7:303:88//Hs.153014:AB002353  
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (bat a)//1.6e-91:448:97//Hs.5687:AJ005801  
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930  
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837  
R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:19 6:63//Hs.1189:D38550  
R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538  
R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.6 8:256:64//Hs.101238:Y11312  
R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete c ds//2.4e-51:254:85//Hs.15731:AB011135  
R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764  
R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996  
R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354  
R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//H s.11214:AF019369  
R-HEMBA1002113//Prostaglandin I2 (prostacyclin) synthase //1.4e-7 6:280:90//Hs.61333:DB3402  
R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence //1.4e-87:362:94//Hs.103443:AF065854  
R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7 e-16:94:100//Hs.107747:AI357868  
R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.8387 0:X83957  
R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734  
R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199  
R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642  
R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337  
R-HEMBA1002160//Homo sapiens nephrocytin (NPH1) mRNA, partial cd s//1.4e-36:400:75//Hs.75474:AFD23674  
R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9 e-33:294:77//Hs.26929:AF008915  
R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:W64043  
R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887: D38081  
R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457  
R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associa ted molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.15952 3:AF001622  
R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete c ds//1.4e-29:244:72//Hs.119387:AB007958  
R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357  
R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frame s//4.3e-84:557:84//Hs.23094:M19503  
R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342  
R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315  
R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151  
R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete c ds//5.1e-21:230:75//Hs.139648:AB014606  
R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mR NA, complete cds//1.5e-47:238:98//Hs.25664:AF089814  
R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202  
R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426  
R-HEMBA1002257  
R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTE IN IN YMA7-RP531A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91 //Hs.114673:W72675  
R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314  
R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595  
R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818  
R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679  
R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cd s//7.8e-130:642:96//Hs.6162:AB018314  
R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:HD4822  
R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094  
R-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCA P-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563  
R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435  
R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:HS8237  
R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-6 3:358:91//Hs.25527:AC005954  
R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]// 5.6e-87:429:96//Hs.13209:AI417849  
R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238:AA476267  
R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-2

## 【0902】

【表600】

2:181:80//Hs.74554:D38522	R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:A1220827
R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069	R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670
R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085	R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA
R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395	A, complete cds//1.2e-107:541:95//Hs.33787:AF037261
R-HEMBA1002475//ESTs. Weakly similar to F08G12.1 [C.elegans]//5.4	R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:1
e-95:488:95//Hs.108115:AA582193	03:71//Hs.95140:D80011
R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:2	R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820
81:80//Hs.43681:AL022394	R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-5
R-HEMBA1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:	0:308:88//Hs.154326:D42087
88//Hs.155464:AF088219	R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:A1188995	R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:A1254165
R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133	R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449	R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732
R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990	R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:A110892
R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like pro	R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
tein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972	R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//H
R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715	s.11214:AF019369
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cd	R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:A1000405
s//5.1e-106:564:93//Hs.129928:AB007923	R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cd
R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700	s//2.3e-30:162:99//Hs.5734:AB014579
R-HEMBA1002547//EST//8.7e-92:151:96//Hs.132145:A1041804	R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:A1281881	81//Hs.155464:AF088219
R-HEMBA1002555//EST//1.1e-77:461:91//Hs.38750:N30012	R-HEMBA1002997//ESTs//3.2e-18:102:100//Hs.146255:AA197064
R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:	R-HEMBA1002999//ESTs. Moderately similar to lamina associated poly
89//Hs.32567:AF073519	peptide 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:A1377682
R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:	R-HEMBA1003021//Homo sapiens PYRIN (NEFV) mRNA, complete cds//3.3
78//Hs.155464:AF088219	e-42:290:85//Hs.113283:AF018080
R-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, com	R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480
plete cds//1.4e-120:587:97//Hs.151411:AF075587	R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:A1038577
R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904	R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827
R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838	R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:A1240366
R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055	R-HEMBA1003041//ESTs. Highly similar to PUTATIVE SERINE/THREONIN
R-HEMBA1002621	E-PROTEIN KINASE C41C.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete c	s elegans]//5.6e-34:280:79//Hs.114905:AA088442
ds//2.2e-77:380:97//Hs.91338:AB018351	R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase be
R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881	ta-subunit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182
R-HEMBA1002629//EST//0.00014:50:100//Hs.119132:AA398715	R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627
R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041	R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.781
R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970	60:AF010238
R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-	R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903
4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//H	R-HEMBA1003077//ESTs. Weakly similar to KIAA0405 [H.sapiens]//1.1
s.108966:U48696	e-90:434:99//Hs.14146:W92235
R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete c	R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402
ds//1.1e-41:296:84//Hs.6232:AB018307	R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:A1075249
R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945	R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:
R-HEMBA1002678//EST. Moderately similar to !!!! ALU SUBFAMILY J WA	83//Hs.155464:AF088219
RNING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896	R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223
R-HEMBA1002679//EST//0.15:136:69//Hs.129570:AA895396	R-HEMBA1003096//ESTs. Weakly similar to Mouse 19.5 mRNA, complete
R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:24	cds [M.musculus]//4.2e-100:531:94//Hs.104800:AA709155
7:62//Hs.142023:M88282	R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624
R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477	R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:A1150058
R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete c	R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) m
ds//6.0e-46:302:86//Hs.15519:AB018315	RNA, complete cds//2.1e-13:109:88//Hs.118717:U86751
R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884	R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:A1370845
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cd	R-HEMBA1003136//ESTs. Weakly similar to MANNNOSE-1-PHOSPHATE GUANYL
s//3.8e-37:287:81//Hs.132942:AB014521	TRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:
R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168	A1088615
R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163	R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:
R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526	88//Hs.155464:AF088219
R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:A1375792	R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:
R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090	586:96//Hs.63931:AJ005670
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cd	R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933
s//4.0e-106:545:95//Hs.74750:AB011126	R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389
R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127	R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000
R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491	R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:
R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:3	328:57//Hs.83715:X69804
42:58//Hs.48824:D87717	R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cd
R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:4	s//1.3e-40:290:83//Hs.153026:AB014540
49:75//Hs.153563:AF011333	R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943
R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:A1279709	R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265
R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320	R-HEMBA1003220//ESTs. Weakly similar to MITOCHONDRIAL 40S RIBOSOMA
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, compl	L PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:
ete cds//1.4e-116:559:97//Hs.28307:AF071185	N32817
R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:28	R-HEMBA1003222//ESTs. Weakly similar to weak similarity to HSP90
1:62//Hs.79705:U53204	[C.elegans]//1.1e-42:310:85//Hs.23294:W27666
R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:A1092013	R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
R-HEMBA1002833//ESTs. Highly similar to ribosome-binding protein p	R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
34 [R.norvegicus]//4.3e-25:137:98//Hs.5337:AA243757	R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, c
R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514	omplete cds//7.4e-05:534:58//Hs.152663:AF068864
R-HEMBA1002863//EST//1.1e-67:359:94//Hs.124699:W27830	R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929

【0903】

【表601】

R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219	R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083
R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392	R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379
R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:A1084785	R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916
R-HEMBA1003281	R-HEMBA1003692//Human cytochrome P450-11B (h11B3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109	R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:A1279064
R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266	R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777
R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:A1148353	R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080
R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504	R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K <sup>+</sup> channel 1 (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872	R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847
R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869	R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839
R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119	R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
R-HEMBA1003328//H. sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173	R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:A1147040
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:54:76//Hs.117176:AF026029	R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357	R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:A1148540	R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651	R-HEMBA1003783//ESTs, Weakly similar to COH6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327
R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:A1139588	R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247	R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARRING ENTRY !!!! [H. sapiens]//1.8e-11:261:65//Hs.87578:A1125363	R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:A1357868
R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847	R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127	R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204	R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:A1264163
R-HEMBA1003408//ESTs//1.7e-24:188:85//Hs.70266:Z78309	R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-115:544:98//Hs.25812:AF058695
R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563	R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:A1225121
R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:A1421013	R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
R-HEMBA1003433//Homo sapiens fibrin (fibrin) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058695	R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080
R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:A1225121	R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516	R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080	R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688	R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760	R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058	R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN 1 [H. sapiens]//2.8e-93:495:93//Hs.91619:AA552351
R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817	R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673	R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN 1 [H. sapiens]//2.8e-93:495:93//Hs.91619:AA552351	R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:A1342058
R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734	R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H. sapiens]//4.0e-63:343:93//Hs.58598:AA625440
R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522	R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099
R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:A1342058	R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H. sapiens]//4.0e-63:343:93//Hs.58598:AA625440	R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099	R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:A1244212
R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892	R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087
R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065	R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:A1371042
R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:A1244212	R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:A1251374
R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087	R-HEMBA1003615
R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:A1371042	R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:M68167
R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:A1251374	R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
R-HEMBA1003615	R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888
R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:M68167	R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021
R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387	R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARRING ENTRY !!!! [H. sapiens]//9.3e-24:189:84//Hs.142208:AA209438
R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888	R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830
R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021	R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010
R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARRING ENTRY !!!! [H. sapiens]//9.3e-24:189:84//Hs.142208:AA209438	R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783
R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830	R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957
R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010	R-HEMBA1003662//Human TBX2 (TBX2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049
R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783	R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635
R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957	R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H. sapiens]//4.1e-87:434:97//Hs.9489:R84329
R-HEMBA1003662//Human TBX2 (TBX2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049	
R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635	
R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H. sapiens]//4.1e-87:434:97//Hs.9489:R84329	

【0904】

【表602】

R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754	R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frame s//2.9e-32:463:68//Hs.23094:M19503
R-HEMBA1004056//Homo sapiens PYRIN (MEFY) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080	R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
R-HEMBA1004074//EST//1.0:152:61//Hs.149093:A1243988	R-HEMBA1004461//EST//2.9e-102:503:98//Hs.16370:AA017033
R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652	R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172
R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251	R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:O50918	R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562	R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
R-HEMBA1004133	R-HEMBA1004507
R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736	R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271
R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320	R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947
R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219	R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972
R-HEMBA1004150//GRANULOCYTOGENESIS-INDUCING PROTEIN 1 (GIP1) mRNA, complete cds//0.99:357:59//Hs.79381:MB1637	R-HEMBA1004554
R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087	R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924
R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855	R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913
R-HEMBA1004199	R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243
R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701	R-HEMBA1004586//EST//2.6e-73:384:96//Hs.9582:R39769
R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.10092:AI189282	R-HEMBA1004596//ESTs//6.0e-22:190:82//Hs.42530:NA1661
R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518	R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767
R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748	R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970
R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617	R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:A1375915
R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-16:117:91//Hs.92033:AA255832	R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785
R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353	R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152
R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389	R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROT EIM R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393
R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:77//Hs.154103:AF061258	R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:A1278454
R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284	R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442
R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962	R-HEMBA1004669//EST//0.00039:116:74//Hs.138725:N76348
R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018	R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:A1057560
R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931	R-HEMBA1004672//EST//6.7e-76:315:97//Hs.20821:R19368
R-HEMBA1004275//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081	R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:A1093252
R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens: Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228	R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562
R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795	R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA598042
R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -p referring//1.7e-34:223:75//Hs.81884:U13061	R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:A1281881
R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-ori7 protein [C. elegans]//3.6e-93:496:94//Hs.14337:AA534961	R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219
R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426	R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:A1309235
R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679	R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequence//2.1e-44:467:73//Hs.91916:AF035317
R-HEMBA1004321//Zinc finger protein 44 (KIX 7)//2.6e-37:415:64//Hs.51199:X16281	R-HEMBA1004733//EST//0.99:84:65//Hs.161372:A1423151
R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904	R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275
R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714	R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828
R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561	R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651
R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:A1310231	R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:A1279428
R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336	R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081
R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240	R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498
R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667	R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679
R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353	R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:A1049504
R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494	R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380
R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869	R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POL YPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705
R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057	R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092
R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264	R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633
R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084	R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476
R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219	R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167
R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717	R-HEMBA1004795
R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933	R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732
R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein z-hx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:A1123518	R-HEMBA1004806
	R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:NA7676
	R-HEMBA1004816//EST//4.4e-18:246:72//Hs.150552:A1053784
	R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:W74002
	R-HEMBA1004847
	R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120
	R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267
	R-HEMBA1004864
	R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362
	R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409
	R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676
	R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:A1357470

【0905】

## 【表603】

R-HEMBA1004909//ESTs//7.3e-44:366.79//Hs.140329:AA714011  
R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-5  
0:313:89//Hs.40100:AB002390  
R-HEMBA1004923//ESTs//0.013:162.64//Hs.143655:AI128388  
R-HEMBA1004929//EST//2.3e-48:250.97//Hs.131589:AI025053  
R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-in-  
ducible), polypeptide 2//1.2e-70:547.80//Hs.1361:M55053  
R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-  
110:530:98//Hs.18029:AI422883  
R-HEMBA1004934//ESTs//1.3e-103:522.96//Hs.40415:AA037215  
R-HEMBA1004944//ESTs//6.0e-21:97.84//Hs.141973:N21434  
R-HEMBA1004954//ESTs//7.9e-112:596.93//Hs.6226:W61007  
R-HEMBA1004956//ESTs//3.1e-58:280.100//Hs.120750:AA741074  
R-HEMBA1004960//ESTs//6.9e-89:476.93//Hs.163738:AA601040  
R-HEMBA1004972//ESTs//3.0e-72:381.95//Hs.55014:AA934035  
R-HEMBA1004973//ESTs//2.7e-91:441.98//Hs.28144:AI292065  
R-HEMBA1004977//ESTs//2.0e-95:446.99//Hs.29690:AI168404  
R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F)  
mRNA, complete cds//0.43:187.67//Hs.129734:AJ001683  
R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-5  
3:305:91//Hs.146395:AB002329  
R-HEMBA1004983//ESTs//0.16:482.57//Hs.131929:AI021894  
R-HEMBA1004995  
R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapi-  
ens]//6.9e-51:482.78//Hs.141601:N63520  
R-HEMBA1005009//ESTs, Highly similar to ACTIN 1 [Naegleria fowler  
i]//3.8e-109:551.96//Hs.103180:AI365212  
R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cd  
s//2.0e-105:542.94//Hs.31921:AB014548  
R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTA  
SE HOMOLOG [Homo sapiens]//8.4e-95:491.94//Hs.16085:AI261382  
R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-6  
4:312:85//Hs.22271:D20607  
R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapi-  
ens]//2.6e-48:443.78//Hs.139019:N99348  
R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5  
A [Canis familiaris]//1.2e-87:542.87//Hs.16258:AI376436  
R-HEMBA1005050//ESTs//6.3e-46:311.86//Hs.159510:AA297145  
R-HEMBA1005062//ESTs//1.1e-14:216.68//Hs.129935:AA994451  
R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303.73//H  
s.79385:U90905  
R-HEMBA1005075//EST//0.65:214.62//Hs.133991:AI075789  
R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304.83//Hs.8  
5889:U17077  
R-HEMBA1005083//ESTs//2.8e-74:356.98//Hs.132272:AI393958  
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, com-  
plete cds//1.7e-111:545.96//Hs.11170:AF080561  
R-HEMBA1005113//ESTs//1.1e-101:512.95//Hs.7972:AI052739  
R-HEMBA1005123//Ley 1-L//3.6e-58:519.77//Hs.37062:AC005952  
R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:3  
09:85//Hs.19949:X98173  
R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcrip-  
t KIAA0488//4.7e-36:394.75//Hs.67619:AB007957  
R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//  
3.6e-32:362.77//Hs.132206:AF039694  
R-HEMBA1005159//EST//7.4e-47:252.94//Hs.134930:AI093397  
R-HEMBA1005185//ESTs//5.2e-48:305.89//Hs.14920:AA910914  
R-HEMBA1005201//ESTs//4.7e-58:293.97//Hs.23752:C05766  
R-HEMBA1005202//ESTs//1.0:169.59//Hs.153423:AI198239  
R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (12  
3F2) mRNA, complete cds//0.84:191.61//Hs.26931:AF061836  
R-HEMBA1005223//ESTs//0.75:90.70//Hs.127446:AA167284  
R-HEMBA1005232//EST//0.056:162.67//Hs.65649:F13687  
R-HEMBA1005241//ESTs//3.6e-113:564.96//Hs.12770:W84331  
R-HEMBA1005244//ESTs//6.4e-22:118.100//Hs.21396:AA114834  
R-HEMBA1005251//ESTs//8.5e-36:213.92//Hs.161554:AA393896  
R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cd  
s//6.1e-49:277.93//Hs.72660:AB011157  
R-HEMBA1005274//ESTs//3.7e-65:322.98//Hs.105166:AA668862  
R-HEMBA1005275//ESTs//2.1e-29:298.73//Hs.33393:R83391  
R-HEMBA1005293//ESTs//3.5e-93:448.98//Hs.12066:AI208611  
R-HEMBA1005296//ESTs//4.3e-33:168.100//Hs.13916:AI025750  
R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:  
82//Hs.155464:AF088219  
R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:  
83//Hs.32567:AF073519  
R-HEMBA1005314//ESTs//3.0e-103:491.98//Hs.41606:AI095046  
R-HEMBA1005315//EST//1.9e-29:370.72//Hs.161483:N59169  
R-HEMBA1005318//ESTs//3.9e-110:535.97//Hs.26771:AA126472  
R-HEMBA1005331//Interleukin adhesion molecule 2//7.6e-39:256.87/  
Hs.83733:X15606  
R-HEMBA1005353//ESTs//1.7e-81:406.96//Hs.155374:AI341467  
R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA  
A, complete cds//4.7e-46:294.81//Hs.129735:AF010144  
R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptid  
e//1.0:210.62//Hs.4:X03350  
R-HEMBA1005372//ESTs//6.2e-95:451.99//Hs.135219:AI091653  
R-HEMBA1005374//ESTs//1.5e-107:502.99//Hs.118208:AA947305  
R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311.80//  
Hs.54486:X54150  
R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cD  
NA yk30b3.5 [C.elegans]//4.0e-88:489.92//Hs.43864:AA131568  
R-HEMBA1005403//EST//0.0011:78.75//Hs.127061:AA863278  
R-HEMBA1005408//ESTs//3.2e-29:395.71//Hs.117532:AA676725  
R-HEMBA1005410//ESTs//1.5e-18:271.70//Hs.144604:AI052059  
R-HEMBA1005411//ESTs//1.1e-35:335.77//Hs.141181:R98757  
R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CD  
KN2C) mRNA, complete cds//1.8e-118:453.99//Hs.4854:AF041248  
R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:26  
4:61//Hs.136309:AB007960  
R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:3  
05:87//Hs.6445:L40391  
R-HEMBA1005447//ESTs//5.7e-83:529.86//Hs.114253:AA745961  
R-HEMBA1005468//ESTs//7.3e-23:249.73//Hs.61199:AA024494  
R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-4  
5:320:85//Hs.153014:AB002353  
R-HEMBA1005472//Human knpi repeat mRNA (cdna clone pcd-kpni-8), 3'  
end//8.4e-73:464.87//Hs.103948:K00627  
R-HEMBA1005475//ESTs//0.32:192.59//Hs.62694:AA100445  
R-HEMBA1005497  
R-HEMBA1005500//ESTs//2.2e-43:307.85//Hs.146811:AA410788  
R-HEMBA1005506//75 kda infertility-related sperm protein [human, t  
estis, mRNA Partial, 2427 nt]//0.11:295.60//Hs.62608:S58544  
R-HEMBA1005508//ESTs//2.8e-55:319.93//Hs.50150:N90870  
R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.e  
legans]//2.6e-82:387.99//Hs.67466:AI219740  
R-HEMBA1005517//ESTs//4.6e-77:469.90//Hs.126787:AA203322  
R-HEMBA1005518//ESTs//1.5e-108:561.94//Hs.123167:AA601045  
R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.  
5e-44:179.84//Hs.42674:U61981  
R-HEMBA1005526//ESTs//8.7e-46:308.86//Hs.146811:AA410788  
R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyc  
es cerevisiae]//8.6e-115:578.95//Hs.17035:AI080471  
R-HEMBA1005530//ESTs//1.5e-110:551.96//Hs.107294:W72350  
R-HEMBA1005548//ESTs//1.7e-100:510.96//Hs.9115:N90926  
R-HEMBA1005552//Interleukin 10//2.4e-38:306.80//Hs.2180:M57627  
R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.  
3e-77:439.91//Hs.22897:R43193  
R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARN1  
NG ENTRY !!!! [H.sapiens]//3.4e-31:182.76//Hs.133526:N21103  
R-HEMBA1005570//ESTs//3.3e-67:411.88//Hs.142245:AA489709  
R-HEMBA1005576//EST//0.91:52.73//Hs.149518:AI280497  
R-HEMBA1005577  
R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:  
561.64//Hs.57929:AB011538  
R-HEMBA1005582//ESTs//6.0e-73:371.97//Hs.103758:C06392  
R-HEMBA1005583//ESTs//8.3e-79:413.95//Hs.62348:AA419539  
R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403.83//Hs.75680:M1599  
0  
R-HEMBA1005593//ESTs//3.3e-30:139.80//Hs.142273:W37905  
R-HEMBA1005595//ESTs//1.1e-97:454.100//Hs.27497:AI274820  
R-HEMBA1005606//EST//1.0e-12:313.64//Hs.162402:AA573125  
R-HEMBA1005609//ESTs//0.49:278.58//Hs.76235:W56390  
R-HEMBA1005616//EST//1.3e-98:470.99//Hs.122230:AA781422  
R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.c  
erevisiae]//2.8e-95:539.92//Hs.19400:AA662845  
R-HEMBA1005627//Human mRNA for adipogenesis inhibitory factor//5.5  
e-38:317.78//Hs.1721:X58377  
R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-1  
1:279.65//Hs.15245:AF041081  
R-HEMBA1005632//EST//1.5e-10:181.70//Hs.120259:AA731522  
R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, com-  
plete cds//1.4e-25:234.80//Hs.10458:AF088219  
R-HEMBA1005666//ESTs//2.3e-103:534.95//Hs.14512:AA205973  
R-HEMBA1005670//ESTs//2.6e-39:166.81//Hs.139414:AI279477  
R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:32  
2:88//Hs.82193:M13450  
R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-  
43:343.81//Hs.154103:AF061258  
R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete

## 【0906】



【表604】

cds//0.0050:235:64//Hs.159437:U44060	A-BINDING PROTEIN NAB2 [S.cerevisiae]//1.6e-66:377:91//Hs.108674:W25021
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LER K-8 (Eplg8) mRNA, complete cds//1.7e-47:376:84//Hs.26988:U66406	R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:A1084735
R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055	R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:A1159943	R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:A1202037
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:AJ006470	R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:U33931
R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815	R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.m. usculus]//5.6e-76:417:94//Hs.111754:A1204587
R-HEMBA1005746//EST//0.098:125:68//Hs.136945:AA765672	R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219
R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:M47096	R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:U21936	R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204
R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974	R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROT E1N IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:A1417075
R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.10458:AF088219	R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:A1038601	R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960	R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:A1039201	R-HEMBA1006377//EST//0.0097:145:62//Hs.133027:A1049830
R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:A1080618	R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:AB011166
R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911	R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651
R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917	R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frame s//9.0e-87:582:84//Hs.23094:M19503
R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970	R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:A1218923
R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:A1022252	R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:HT2778
R-HEMBA1005894	R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878
R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:A1215686	R-HEMBA1006424//ESTs, Weakly similar to pot. ORF 11 [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004
R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:A1076363	R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964
R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632	R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:AB011098	R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033
R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867	R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784
R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:A1199418	R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895
R-HEMBA1005963	R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403
R-HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.26285:AF082516	R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441
R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199	R-HEMBA1006474
R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:A1080618	R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984
R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:A1379875	R-HEMBA1006486//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701
R-HEMBA1006005//EST//1.0:0:105:63//Hs.145273:A1249436	R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223
R-HEMBA1006031//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268	R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350
R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:M49951	R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720
R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508	R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387
R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490	R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:M33117
R-HEMBA1006067	R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505
R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:M25612	R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566
R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517	R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300
R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9558:AA506313	R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:A1057628
R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//Hs.73614:U83460	R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934
R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297	R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331
R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:A1279293	R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154
R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:A1198931	R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594
R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635	R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:A1283064
R-HEMBA1006138//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:AB007958	R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542	R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725
R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212	R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876
R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930	R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280
R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627	R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390
R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906	R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219
R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125	R-HEMBA1006612
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557	R-HEMBA1006617//ESTs//1.2e-25:225:80//Hs.138852:AA284247
R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//Hs.23617:AA928683	R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630
R-HEMBA1006252//Human mRNA for KIAA0880 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522	R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:AF083384	R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:A129988
R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881	
R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper inter active [M.musculus]//1.2e-97:529:93//Hs.10552:AA524401	
R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PRO TEASE [H.sapiens]//2.7e-88:484:92//Hs.104129:AA923278	
R-HEMBA1006278//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770	
R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RN	

【0907】

【表605】

9	R-HEMBA1006639//ESTs. Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185	R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777	R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987	R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M1599
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282	0	0
R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427	R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:AB018340	R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511	R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934	R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394
R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102	R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062	R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207
R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594	R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543	R-HEMBA1007286//EST//9.4e-43:344:81//Hs.162112:AA524804
R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842	R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:M52990	R-HEMBA1007301
R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435	R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917	R-HEMBA1007320//ESTs. Moderately similar to hypothetical protein 2 [H. sapiens]//5.5e-15:311:64//Hs.142764:AA205569
R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263	R-HEMBA1007322//Human kpni repeat mra (cdna clone pcn-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629	R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695	R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684	R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
R-HEMBA1006708//ESTs. Weakly similar to Miller-Dieker lissencephaly gene [H. sapiens]//1.1e-92:483:94//Hs.6525:AI205313	R-HEMBA1000005//ESTs. Weakly similar to putative p150 [H. sapiens]//3.3e-44:341:71//Hs.111730:AA604403	R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090
R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062	R-HEMBA1000018//H. sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969	R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418
R-HEMBA1006717	R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332	R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449
R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002	R-HEMBA1000036//ESTs. Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465	R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928
R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627	R-HEMBA1000044//EST//7.6e-70:367:95//Hs.140860:R42954	R-HEMBA1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702
R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099	R-HEMBA1000048//EST//1.5e-45:262:91//Hs.157627:AI357802	R-HEMBA1000050//EST//0.039:91:74//Hs.163189:AA236903
R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646	R-HEMBA1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107	R-HEMBA1000055//ESTs. Moderately similar to UBQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUBUNIT VI REQUIRING PROTEIN [H. sapiens]//1.1e-72:350:99//Hs.116490:AA659584
R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763	R-HEMBA1000059//ESTs//1.7e-10:200:70//Hs.163954:M57939	R-HEMBA1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997
R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881	R-HEMBA1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353	R-HEMBA1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562	R-HEMBA1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:AB014540	R-HEMBA1000103//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997
R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936	R-HEMBA1000113//EST//8.2e-94:437:100//Hs.136893:AA805239	R-HEMBA1000136//ESTs//0.043:262:59//Hs.61304:AA025692
R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:M52705	R-HEMBA1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521	R-HEMBA1000141//ESTs//5.0e-38:254:79//Hs.141658:M77915
R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978	R-HEMBA1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558	R-HEMBA1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333	R-HEMBA1000198//ESTs//1.0:123:62//Hs.116602:AA665965	R-HEMBA1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305	R-HEMBA1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353	R-HEMBA1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558
R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//7.6e-51:298:90//Hs.121493:D25272	R-HEMBA1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364	R-HEMBA1000198//ESTs//1.0:123:62//Hs.116602:AA665965
R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556	R-HEMBA1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019	R-HEMBA1000226//ESTs. Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C. elegans]//5.1e-73:449:89//Hs.15803:AA843214
R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087	R-HEMBA1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219	R-HEMBA1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106
R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665	R-HEMBA1000250//EST//8.8e-12:284:64//Hs.145960:AI276783	R-HEMBA1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219
R-HEMBA1006877//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:AB018315	R-HEMBA1000258//EST//4.5e-14:315:66//Hs.162551:AA584782	R-HEMBA1000250//EST//8.8e-12:284:64//Hs.145960:AI276783
R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453		
R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739		
R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117		
R-HEMBA1006926//ESTs. Weakly similar to ZK1053.6 [C. elegans]//2.9e-28:213:84//Hs.9096:AA029400		
R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308		
R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712		
R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:M52382		
R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:AJ010841		
R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321		
R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457		
R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827		
R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325		
R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679		
R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440		
R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:M70293		
R-HEMBA1007018//ESTs. Moderately similar to LIC-2 [R. norvegicus]//2.8e-112:558:96//Hs.107905:AI248363		
R-HEMBA1007045		
R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788		
R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839		
R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140		
R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272		
R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866		
R-HEMBA1007078//EST. Moderately similar to !!!! ALU SUBFAMILY SQ W ARNING ENTRY !!!! [H. sapiens]//7.2e-40:163:83//Hs.152369:AA504818		
R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087		
R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025		
R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597		
R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272		
R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438		
R-HEMBA1007147		
R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818		
R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674		
R-HEMBA1007174//Homo sapiens epsilon 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085		
R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954		

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【表606】

R-HEM8B1000264	4.0e-76:399:95//Hs.124106:AA948100
R-HEM8B1000266//ESTs. Weakly similar to similar to the beta transducin family [C. elegans]//2.7e-102:556:93//Hs.16079:AA083522	R-HEM8B1000652//ESTs//1.5e-14:271:64//Hs.163954:M57939
R-HEM8B1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385	R-HEM8B1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988
R-HEM8B1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:AB011129	R-HEM8B1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
R-HEM8B1000284//ESTs//4.8e-64:389:91//Hs.118043:M50458	R-HEM8B1000673//EST//0.58:46:82//Hs.142286:AA338293
R-HEM8B1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353	R-HEM8B1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
R-HEM8B1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601	R-nnnnnnnnnnnn//Homo sapiens neuroanl mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723
R-HEM8B1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034	R-HEM8B1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219
R-HEM8B1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219	R-HEM8B1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
R-HEM8B1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576	R-HEM8B1000709//ESTs. Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403
R-HEM8B1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480	R-HEM8B1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:35:0:59//Hs.10351:AB002306
R-HEM8B1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084	R-HEM8B1000726//EST//5.3e-49:303:88//Hs.149580:AI281881
R-HEM8B1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219	R-HEM8B1000738//Homo sapiens mRNA, clone:RE54-16//2.5e-49:302:89//Hs.121493:D25272
R-HEM8B1000339//EST//5.8e-41:336:79//Hs.151873:AA205736	R-HEM8B1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925
R-HEM8B1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651	R-HEM8B1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522
R-HEM8B1000343//EST//1.1e-77:396:95//Hs.162664:AA605020	R-HEM8B1000770//EST//1.0e-75:359:99//Hs.136564:AA642445
R-HEM8B1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008	R-HEM8B1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541
R-HEM8B1000369//ESTs//1.6e-21:234:73//Hs.111583:AA63590	R-HEM8B1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771
R-HEM8B1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.92381:AB007956	R-HEM8B1000790//PLATELET GLYCOPROTEIN V PRECURSOR//1.3e-37:193:75//Hs.73734:Z23091
R-HEM8B1000376//H. sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969	R-HEM8B1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
R-HEM8B1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840	R-HEM8B1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
R-HEM8B1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642	R-HEM8B1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219
R-HEM8B1000402//H. sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173	R-HEM8B1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447
R-HEM8B1000404//ESTs//0.088:298:59//Hs.61607:AA032026	R-HEM8B1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
R-HEM8B1000420//EST//2.2e-78:376:98//Hs.160787:AI336591	R-HEM8B1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219
R-HEM8B1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087	R-HEM8B1000827//EST//2.8e-40:295:84//Hs.149580:AI281881
R-HEM8B1000438//ESTs. Weakly similar to !!! ALU CLASS 8 WARNING ENTRY !!! [H.sapiens]//0.30:214:63//Hs.142209:AA873303	R-HEM8B1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
R-HEM8B1000441//Human c-myc mRNA//2.2e-46:280:90//Hs.75680:M15990	R-HEM8B1000835//ESTs//7.3e-21:124:82//Hs.102671:M52545
R-HEM8B1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221	R-HEM8B1000840//ATPase, Na+/K+ transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
R-HEM8B1000455//EST//4.8e-14:421:65//Hs.68832:AA088438	R-HEM8B1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137
R-HEM8B1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396	R-HEM8B1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
R-HEM8B1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390	R-HEM8B1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942
R-HEM8B1000487//EST//0.78:87:68//Hs.134601:AI081506	R-HEM8B1000876//EST//0.0022:211:63//Hs.125552:AA884141
R-HEM8B1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219	R-HEM8B1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
R-HEM8B1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080	R-HEM8B1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
R-HEM8B1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125	R-HEM8B1000888//EST//8.2e-07:196:64//Hs.118276:M15258
R-HEM8B1000510//EST//1.4e-45:139:97//Hs.152260:AA489703	R-HEM8B1000890//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.1e-46:327:83//Hs.51048:X68830
R-HEM8B1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087	R-HEM8B1000893//EST//4.7e-34:242:85//Hs.149580:AI281881
R-HEM8B1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080	R-HEM8B1000908//EST//0.95:27:100//Hs.142568:AA285066
R-HEM8B1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099	R-HEM8B1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
R-HEM8B1000550//EST//2.9e-11:113:79//Hs.161503:N68662	R-HEM8B1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325
R-HEM8B1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288	R-HEM8B1000915//ESTs//0.00018:188:61//Hs.144847:AI222742
R-HEM8B1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986	R-HEM8B1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874
R-HEM8B1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258	R-HEM8B1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784
R-HEM8B1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709	R-HEM8B1000947//ESTs. Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881
R-HEM8B1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618	R-HEM8B1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:M19503
R-HEM8B1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247	R-HEM8B1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354
R-HEM8B1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895	R-HEM8B1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007
R-HEM8B1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704	R-HEM8B1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
R-HEM8B1000592//ESTs//1.8e-97:455:99//Hs.94229:M65391	R-HEM8B1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
R-HEM8B1000598//Human antiserotransferrin factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199	R-HEM8B1000991//EST//0.99:58:72//Hs.100246:T23625
R-HEM8B1000632//ESTs//8.3e-47:277:92//Hs.6045:M67125	R-HEM8B1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258
R-HEM8B1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249	R-HEM8B1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
R-HEM8B1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152	R-HEM8B1001008//ESTs. Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:M58762
R-HEM8B1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531	R-HEM8B1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214
R-HEM8B1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522	R-HEM8B1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
R-HEM8B1000638//EST//2.2e-38:371:76//Hs.162236:AA551582	R-HEM8B1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080
R-HEM8B1000643//EST//0.0049:191:62//Hs.55445:M31963	R-HEM8B1001024//ESTs//8.5e-47:374:80//Hs.141602:M63562
R-HEM8B1000649//ESTs. Moderately similar to hTAF1168 [H.sapiens]//	R-HEM8B1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
	R-HEM8B1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
	R-HEM8B1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107

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R-HEM81001056//Homo sapiens mRNA for KIAA0518 protein, complete cds//1.1e-87:497:91//Hs.15832:AB014518	O.88:365:58//Hs.389:X76342
R-HEM81001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944	R-HEM81001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
R-HEM81001060//ESTs//1.9e-37:541:69//Hs.141534:N64785	R-HEM81001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
R-HEM81001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381	R-HEM81001429//ESTs//3.8e-59:543:76//Hs.158803:A1376846
R-HEM81001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803	R-HEM81001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
R-HEM81001096//Human HsLIM15 mRNA for HsLIM15, complete cds//1.2e-20:233:70//Hs.37181:D64108	R-HEM81001443//ESTs//4.8e-54:270:98//Hs.21898:A1088201
R-HEM81001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353	R-HEM81001449//ESTs//3.2e-43:170:84//Hs.150727:A1292236
R-HEM81001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080	R-HEM81001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
R-HEM81001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426	R-HEM81001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
R-HEM81001117//ESTs//1.1e-80:471:90//Hs.61935:T75092	R-HEM81001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881
R-HEM81001119//ESTs//4.0e-38:213:84//Hs.109140:A1289942	R-HEM81001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.2e-22:61//Hs.13275:A1341468
R-HEM81001126	R-HEM81001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481
R-HEM81001133//Human SS-A/Ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077	R-HEM81001500//EST//1.4e-13:310:67//Hs.162663:AA604515
R-HEM81001137//ESTs//4.6e-106:471:90//Hs.74924:A1332962	R-HEM81001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280
R-HEM81001142//EST//6.4e-48:315:85//Hs.149580:A1281881	R-HEM81001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
R-HEM81001151	R-HEM81001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159
R-HEM81001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197	R-HEM81001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459
R-HEM81001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878	R-HEM81001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353
R-HEM81001175//ESTs//3.5e-41:233:93//Hs.129218:AA991162	R-HEM81001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869
R-HEM81001177	R-HEM81001555//ESTs//2.6e-13:182:71//Hs.112671:A1377274
R-HEM81001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349	R-HEM81001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962
R-HEM81001199	R-HEM81001564//EST//1.3e-35:141:81//Hs.162197:AA535216
R-HEM81001208//ESTs//3.3e-43:216:99//Hs.121806:N71183	R-HEM81001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329
R-HEM81001209//ESTs//6.7e-80:409:96//Hs.141185:R99549	R-HEM81001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
R-HEM81001210//ESTs//2.2e-46:290:88//Hs.103329:D11573	R-HEM81001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
R-HEM81001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody 1A4))//3.1e-44:298:87//Hs.103458:X53795	R-HEM81001588//EST//8.3e-27:363:69//Hs.141603:N66015
R-HEM81001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817	R-HEM81001603//ESTs//1.2e-101:482:99//Hs.12403:A1090184
R-HEM81001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Callus gallus]//3.8e-80:400:96//Hs.71873:AA148213	R-HEM81001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
R-HEM81001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560	R-HEM81001619//EST//1.7e-38:476:70//Hs.139093:AA166888
R-HEM81001249//ESTs//3.8e-34:360:70//Hs.150727:A1292236	R-HEM81001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272
R-HEM81001253//EST//0.0011:84:77//Hs.124579:AA853987	R-HEM81001635//ESTs//9.5e-34:304:82//Hs.140444:A1002082
R-HEM81001254//ESTs//4.5e-95:444:99//Hs.161059:A1431268	R-HEM81001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
R-HEM81001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970	R-HEM81001641//EST//2.4e-06:67:86//Hs.162398:AA572813
R-HEM81001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087	R-HEM81001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438
R-HEM81001282//EST//2.9e-78:401:96//Hs.72871:AA169412	R-HEM81001665//ESTs//2.3e-44:372:79//Hs.132818:A1038577
R-HEM81001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021	R-HEM81001668//ESTs//0.73:212:62//Hs.8928:N32572
R-HEM81001289//ESTs//7.8e-45:440:75//Hs.44702:A1148840	R-HEM81001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439:AB014546
R-HEM81001294//ESTs//1.9e-100:476:99//Hs.109017:A1057112	R-HEM81001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534
R-HEM81001302	R-HEM81001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358
R-HEM81001304//ESTs//4.0e-92:431:99//Hs.113750:A1091154	R-HEM81001695//ESTs//3.7e-101:539:94//Hs.78289:R60867
R-HEM81001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627	R-HEM81001704//EST//0.96:248:57//Hs.163025:AA703038
R-HEM81001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627	R-HEM81001706//ESTs//1.3e-39:308:81//Hs.141318:N71080
R-HEM81001317//Human cytochrome P450-11B (h11B3) mRNA, complete cds//6.4e-45:357:81//Hs.110194:M29873	R-HEM81001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:AA205569
R-HEM81001326//ESTs//0.85:174:62//Hs.133487:A1393754	R-HEM81001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645
R-HEM81001331//ESTs, Weakly similar to OFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222	R-HEM81001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113
R-HEM81001335//EST//5.2e-80:381:99//Hs.116769:AA630365	R-HEM81001736//ESTs//0.0035:223:60//Hs.21354:AA203403
R-HEM81001337//ESTs//2.7e-84:404:99//Hs.148966:A1242639	R-HEM81001747//EST//9.9e-55:293:81//Hs.112866:AA620488
R-HEM81001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470	R-HEM81001749//ESTs//2.5e-13:95:91//Hs.139888:N25287
R-HEM81001346	R-HEM81001753//ESTs//2.6e-07:141:70//Hs.144604:A1052059
R-HEM81001348//ESTs//1.1e-43:295:85//Hs.163604:R94354	R-HEM81001756//EST//2.6e-06:165:64//Hs.121195:AA757211
R-HEM81001356//EST//6.0e-11:89:88//Hs.152366:AA486721	R-HEM81001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008:L00352
R-HEM81001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055	R-HEM81001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369
R-HEM81001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087	R-HEM81001785//ESTs//0.040:390:58//Hs.116651:AA993406
R-HEM81001377//ESTs//1.2e-19:165:82//Hs.146314:R99617	R-HEM81001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253
R-HEM81001389//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219	R-HEM81001802//Desmin//9.9e-95:497:93//Hs.119104:M63391
R-HEM81001380//ESTs//4.0e-08:216:63//Hs.143763:A1174205	R-HEM81001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247
R-HEM81001384//ESTs//6.6e-110:547:96//Hs.6671:A1341699	R-HEM81001816//Human Line-1 repeat mRNA with 2 open reading frame s//5.9e-13:143:76//Hs.23094:M19503
R-HEM81001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970	R-HEM81001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209
R-HEM81001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350	R-HEM81001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.67619:AB007957
R-HEM81001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//	R-HEM81001839

【0910】

【表608】

R-HEM881001850/EST//0.020:119:68//Hs.32767:H38125  
 R-HEM881001863/ESTs//4.5e-17:226:72//Hs.157253:A1357539  
 R-HEM881001867/ESTs//2.3e-16:254:68//Hs.123664:AA806106  
 R-HEM881001868/EST//9.8e-30:155:100//Hs.160572:AA888397  
 R-HEM881001869/ESTs//2.8e-42:376:78//Hs.141973:N21434  
 R-HEM881001872/EST//0.85:156:64//Hs.119501:AA487980  
 R-HEM881001874/EST//0.64:107:70//Hs.147482:A1215572  
 R-HEM881001875/EST//0.079:199:59//Hs.121810:AA775240  
 R-HEM881001880/Thromboxane A2 receptor//9.0e-47:237:88//Hs.89887:D38081  
 R-HEM881001899/ESTs//6.3e-68:323:100//Hs.121538:AA609310  
 R-HEM881001905/ESTs//4.4e-19:227:73//Hs.146173:AA906191  
 R-HEM881001906/ESTs//1.6e-90:463:95//Hs.28266:H46725  
 R-HEM881001908/Homo sapiens EV15 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915  
 R-HEM881001910/EST//6.0e-37:308:78//Hs.162197:AA535216  
 R-HEM881001911/Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750  
 R-HEM881001915/ESTs//3.1e-73:395:93//Hs.17054:A1139897  
 R-HEM881001921/Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390  
 R-HEM881001922/H.sapiens mRNA for novel member of serine-arginine domain protein, SRP129//7.4e-38:531:70//Hs.153086:Y11251  
 R-HEM881001925/Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325  
 R-HEM881001930/EST//1.9e-18:136:78//Hs.132635:A1032875  
 R-HEM881001944/EST//0.034:228:57//Hs.93664:N23366  
 R-HEM881001945/ESTs//1.8e-83:439:95//Hs.7341:N57875  
 R-HEM881001947/ESTs//5.6e-109:533:97//Hs.48855:AA134589  
 R-HEM881001950/ESTs//1.5e-107:583:93//Hs.8033:N94998  
 R-HEM881001952/ESTs//3.1e-40:283:85//Hs.146811:AA410788  
 R-HEM881001953/Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522  
 R-HEM881001957/EST//4.8e-50:382:81//Hs.149580:A1281881  
 R-HEM881001962/ESTs//1.5e-20:143:88//Hs.11924:W26972  
 R-HEM881001967/Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:AB011147  
 R-HEM881001973/ESTs//1.4e-48:303:88//Hs.132722:AA618531  
 R-HEM881001983/ESTs//2.6e-72:374:95//Hs.141022:H06475  
 R-HEM881001988/ESTs//2.0e-31:204:88//Hs.142531:N91572  
 R-HEM881001990/ESTs//9.4e-115:574:96//Hs.44426:AA173223  
 R-HEM881001996  
 R-HEM881001997/ESTs//7.6e-78:380:98//Hs.32682:H37798  
 R-HEM881002002/Human kni repeat mRNA (cdna clone pcd-kni-8), 3' end//3.0e-18:222:71//Hs.103948:K00627  
 R-HEM881002005/EST//2.2e-41:339:80//Hs.160833:A1345334  
 R-HEM881002009/EST//2.9e-44:245:94//Hs.28788:R66896  
 R-HEM881002015/EST//0.0027:198:63//Hs.160868:A1359052  
 R-HEM881002042/ESTs//1.1e-75:529:84//Hs.106919:AA523900  
 R-HEM881002043/ESTs//7.9e-40:292:83//Hs.70279:AA75426  
 R-HEM881002044/ESTs//2.1e-92:460:94//Hs.115897:AA156638  
 R-HEM881002045/Homo sapiens PYRIM (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080  
 R-HEM881002049/ESTs//3.8e-77:409:94//Hs.122624:R82638  
 R-HEM881002050/ESTs//8.7e-45:330:82//Hs.44702:A1148840  
 R-HEM881002068/ESTs//8.3e-70:333:99//Hs.134807:A1090671  
 R-HEM881002069/Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144  
 R-HEM881002092/ESTs//6.5e-46:331:83//Hs.22910:W18193  
 R-HEM881002094/EST//3.6e-45:280:88//Hs.149580:A1281881  
 R-HEM881002115  
 R-HEM881002139/ESTs//4.2e-45:318:85//Hs.107657:AA126814  
 R-HEM881002142/Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006  
 R-HEM881002152/EST//4.3e-39:250:89//Hs.156552:AA833553  
 R-HEM881002189/H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X59073  
 R-HEM881002190/ESTs//8.3e-05:122:70//Hs.41974:AF039185  
 R-HEM881002193/Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934  
 R-HEM881002217/EST//6.6e-50:303:89//Hs.149580:A1281881  
 R-HEM881002218/ESTs//2.3e-19:150:86//Hs.136031:W95841  
 R-HEM881002232/ESTs//8.9e-47:445:77//Hs.163971:N27584  
 R-HEM881002247/EST//6.6e-09:236:65//Hs.130578:A1004631  
 R-HEM881002249/ESTs//5.2e-16:325:64//Hs.156253:A1334807  
 R-HEM881002254/Human Line-1 repeat mRNA with 2 open reading frame s//3.8e-99:590:88//Hs.23094:M19503  
 R-HEM881002255/Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363  
 R-HEM881002266/ESTs//4.4e-98:472:98//Hs.65366:A1189112  
 R-HEM881002280/EST//2.9e-41:247:90//Hs.161917:AA483223  
 R-HEM881002300/ESTs//8.4e-19:229:75//Hs.138463:N72305  
 R-HEM881002306/Homo sapiens KIAA0432 mRNA, complete cds//0.0021:38:67//Hs.155174:AB007892  
 R-HEM881002327/EST//0.042:249:61//Hs.121097:AA714637  
 R-HEM881002329/ESTs//1.7e-94:453:99//Hs.7114:R24312  
 R-HEM881002340/ESTs//5.8e-15:163:77//Hs.26378:H10228  
 R-HEM881002342/Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841  
 R-HEM881002358/ESTs//2.0e-52:319:81//Hs.140255:AA708322  
 R-HEM881002359/ESTs//2.7e-106:517:97//Hs.13634:A1051613  
 R-HEM881002364/Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522  
 R-HEM881002371/Catalase//3.3e-22:235:77//Hs.76359:X04085  
 R-HEM881002381/Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467  
 R-HEM881002383/ESTs//3.5e-108:520:98//Hs.45140:D80055  
 R-HEM881002387  
 R-HEM881002415/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:168:77//Hs.133526:N21103  
 R-HEM881002425/Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280  
 R-HEM881002442/ESTs//2.7e-48:289:87//Hs.155243:N70293  
 R-HEM881002453/Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353  
 R-HEM881002457/Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087  
 R-HEM881002458/EST//1.8e-72:343:100//Hs.162006:AA508089  
 R-HEM881002477/ESTs//1.6e-38:215:93//Hs.18240:AA460083  
 R-HEM881002489/ESTs//1.2e-101:534:94//Hs.7981:H15176  
 R-HEM881002492/ESTs//5.0e-14:350:62//Hs.99205:AA204969  
 R-HEM881002495/ESTs//2.1e-19:147:86//Hs.163747:AA174017  
 R-HEM881002502/ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142  
 R-HEM881002509/ESTs//2.7e-97:459:99//Hs.127638:A1014615  
 R-HEM881002510/ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278  
 R-HEM881002520/EST//7.2e-40:198:84//Hs.140493:AA804538  
 R-HEM881002522/Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672  
 R-HEM881002531/EST//0.024:147:61//Hs.148305:AA909605  
 R-HEM881002534/EST//3.1e-22:168:84//Hs.146794:A1149478  
 R-HEM881002545/ESTs//9.2e-90:421:99//Hs.118317:A1033259  
 R-HEM881002550/ESTs, Weakly similar to similar to S. cerevisiae L AG1 [C.elegans]//5.1e-22:210:81//Hs.11896:T68813  
 R-HEM881002556//SLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344:82//Hs.51048:X68830  
 R-HEM881002579/ESTs//4.6e-47:326:85//Hs.155184:AA573189  
 R-HEM881002582/ESTs//0.00036:91:76//Hs.140039:AA047045  
 R-HEM881002590/ESTs//1.0e-37:210:84//Hs.36658:N91138  
 R-HEM881002596/Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087  
 R-HEM881002600/EST//2.5e-17:147:84//Hs.121918:AA777424  
 R-HEM881002601/ESTs//7.8e-68:358:95//Hs.101489:R66923  
 R-HEM881002603/EST//1.1e-47:281:90//Hs.149580:A1281881  
 R-HEM881002607/ESTs//5.4e-75:379:97//Hs.29438:H42896  
 R-HEM881002610/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265  
 R-HEM881002613/Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977  
 R-HEM881002614/ESTs//3.4e-81:383:99//Hs.13012:A1094150  
 R-HEM881002617/Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917  
 R-HEM881002623/ESTs//1.6e-45:288:87//Hs.138852:AA284247  
 R-HEM881002635/Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219  
 R-HEM881002664/EST//8.9e-49:315:87//Hs.149580:A1281881  
 R-HEM881002677/ESTs//0.65:159:62//Hs.163517:A1419775  
 R-HEM881002683/H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//6.6e-54:543:75//Hs.2638:Z28339  
 R-HEM881002684/ESTs//3.0e-18:148:87//Hs.158270:AA776646  
 R-HEM881002686/ESTs//6.1e-80:419:96//Hs.103002:W02753  
 R-HEM881002692/ESTs//3.3e-58:451:82//Hs.141254:A1334099  
 R-HEM881002697/ESTs//6.2e-86:423:98//Hs.129812:AA769487  
 R-HEM881002699/EST//5.6e-46:322:84//Hs.140231:A1054398  
 R-HEM881002702/ESTs//5.6e-36:412:72//Hs.154993:AA142842  
 R-HEM881002705/POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:W73547  
 R-HEM881002712/ESTs//9.0e-96:451:99//Hs.136806:AA805682  
 R-HEM881000009/ESTs//3.0e-78:392:96//Hs.166347:AA678701

【表609】

R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219	R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
R-MAMMA1000020//Zinc finger protein 2 (AI-5)//4.9e-49:384:80//Hs.155533:X60152	R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901	R-MAMMA1000386//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304	R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AI301060
R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA207165	R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973
R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350	R-MAMMA1000410//Archaea//1.8e-40:443:74//Hs.33642:X81198
R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531	R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958
R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065	R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099	R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171
R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241	R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARRING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713	R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352	R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390
R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARRING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172	R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452
R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577	R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
R-MAMMA1000133	R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171
R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017	R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179
R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970	R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881	R-MAMMA1000458
R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263	R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
R-MAMMA1000163//EST//2.8e-92:457:96//Hs.114413:AA884787	R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
R-MAMMA1000171//Homo sapiens mRNA for putative lipoid acid synthetase, partial//2.5e-39:173:83//Hs.53531:AJ224162	R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEIN [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069	R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886
R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611	R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054	R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219
R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881	R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [Mus musculus]//1.4e-41:272:90//Hs.68398:AA421103	R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390
R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425	R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946	R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.155119:AB018315	R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090	R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041	R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238	R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:73:77//Hs.6200:AB007872
R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814	R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548
R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977	R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219
R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369	R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694	R-MAMMA1000605//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267
R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956	R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN S1S1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105
R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066	R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180
R-MAMMA1000287	R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361
R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892	R-MAMMA1000623
R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:O26067	R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002
R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251	R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203
R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434	R-MAMMA1000664//Homo sapiens mRNA for putative lipoid acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162
R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491	R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881
R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998	R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TOMB 3' REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065
R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881	R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476
R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525	R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212
R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159	R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343
R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912	R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644
R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087	R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333
R-MAMMA1000361//EST//3.1e-17:188:68//Hs.164036:AA845659	R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569
	R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515
	R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329
	R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942
	R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267
	R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893
	R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN

【表610】

IN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:37 1:74//Hs.141429:AA631915	R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-5 0.298:91//Hs.40100:AB002390
R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1 e-58:253:98//Hs.31575:AF100141	R-MAMMA1001041//ESTs//3.6e-86:445:95//Hs.122625:R68650
R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridial steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632288	R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:A1281881
R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:A1224205	R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:A1015487
R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frame s//2.3e-90:568:86//Hs.23094:M19503	R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627	R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
R-MAMMA1000750//EST//5.0e-44:306:86//Hs.162404:AA573131	R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-3 8:544:68//Hs.153014:AB002353
R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256	R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:M38944
R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-4 6:465:76//Hs.153014:AB002353	R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frame s//1.7e-84:556:85//Hs.23094:M19503
R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204	R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439	R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150	R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing prot ein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF0355 87
R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163	R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, comp lete cds//4.2e-27:232:76//Hs.61840:U28686
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76/ Hs.73919:X81637	R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:A1421576
R-MAMMA1000831//ESTs//1.3e-104:510:97//Hs.17494:AA572675	R-MAMMA1001126//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:T9267
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:A1281881	R-MAMMA1001133//Homo sapiens tapasin (NCS-17) mRNA, complete cds// 1.8e-59:460:81//Hs.5247:AF029750
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902	R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358	R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097	R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.1357 2:AF068179
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955	R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251	R-MAMMA1001161//Homo sapiens tapasin (NCS-17) mRNA, complete cds// 1.1e-58:409:84//Hs.5247:AF029750
R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-4 7:281:91//Hs.40100:AB002390	R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-9 1:430:99//Hs.129982:A1420970
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212	R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:A1419311	R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922	R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:32 4:80//Hs.46918:AF052099	R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by t he epidermal growth factor receptor [M.musculus]//2.6e-80:358:96// Hs.163827:AA074202
R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399	R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:A1032875	R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79/ Hs.73919:X81637
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243	R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128	R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cd s//3.2e-40:542:68//Hs.154872:AB011166	R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107	R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:A1310215	R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-5 3:307:91//Hs.146395:AB002329	R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093	R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:A191307
R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634	R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989	R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
R-MAMMA1000921//Human S3K isoform of Type II phosphatidylinositol- 4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs. 108966:U48696	R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete c ds//2.0e-21:226:75//Hs.65238:AB014561
R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335	R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X 81001
R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:A1133727	R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONIN E-PROTEIN KINASE ENK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30 643
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281	R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cd s//4.4e-32:188:94//Hs.14409:AB011144
R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428	R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-in ducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053	R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178	R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete c ds//2.2e-27:348:70//Hs.15731:AB011135
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostat e: CD82 antigen (R2 leukocyte antigen, antigen detected by monoclo nal and antibody 1A4))//7.5e-49:340:85//Hs.103458:X53795	R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete c ds//2.0e-48:216:85//Hs.153468:AB011147	R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, co mplete cds//4.0e-43:300:85//Hs.46468:U45984
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:A1281881	R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRN A, complete cds//8.8e-12:188:70//Hs.55771:AF004709
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204	R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cd s//8.0e-39:338:79//Hs.93121:AB018304	R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:A1281881	R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285: 75//Hs.32567:AF073519
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263	R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:2 82:82//Hs.80738:X52075	R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-8 2:405:97//Hs.25863:AA630313	R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:3 09:86//Hs.153563:AF011333	R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814	R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:A1281881
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536	
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:AA7461	

【0913】

【表611】

R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831	R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659
R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275	R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-4
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957	6:325:87//Hs.44106:D86979
R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267	R-MAMMA1001818
R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168	R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881
R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618	R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:
R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:	75//Hs.32567:AF073519
328:67//Hs.155174:AB007892	R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140
R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:M57542	R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:3
R-MAMMA1001465	39:83//Hs.43681:AL022394
R-MAMMA1001476//Homo sapiens yeast sac permease-like molecule 3 (YSL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317	R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811
R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:3	R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:M47461
28:78//Hs.43681:AL022394	R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:
R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065	83//Hs.155464:AF088219
R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-1	R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840
5:220:69//Hs.74554:D38522	R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete c
R-MAMMA1001510	ds//7.8e-31:262:77//Hs.5737:AB007944
R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242	R-MAMMA1001868//Homo sapiens antigen NY-CO-16 mRNA, complete cds//
R-MAMMA1001547//H. sapiens mRNA for urea transporter//2.3e-45:282:8	9.2e-06:450:58//Hs.132206:AF039694
9//Hs.66710:X96969	R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1)
R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol	mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460
4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//H	R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethyla
s.108966:U48696	se)//1.2e-46:429:78//Hs.2379:U23942
R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140	R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W
R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo	ARRING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606
sapiens]//1.9e-111:549:96//Hs.21635:AI417305	R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788
R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441	R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostat
R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792	e; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclo
R-MAMMA1001604	nal and antibody 1A4))//6.7e-47:283:89//Hs.103458:X53795
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sap	R-MAMMA1001908//ESTs//0.043:134:65//Hs.145333:AI251374
iens]//1.9e-97:488:96//Hs.143263:AI057616	R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801
R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//	R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete c
Hs.121493:D25272	ds//1.4e-18:174:77//Hs.139648:AB014606
R-MAMMA1001621//Homo sapiens mRNA for KIAA0772 protein, complete c	R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790
ds//2.0e-49:472:76//Hs.15519:AB018315	R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sap
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]/	piens]//6.7e-24:331:71//Hs.140506:AA308018
/6.8e-15:168:73//Hs.115216:AA291074	R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734
R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:M36377	R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:M27084
R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606	R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:
R-MAMMA1001649	70//Hs.155464:AF088219
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA	R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054
A, complete cds//1.7e-54:272:81//Hs.129735:AF010144	R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MAR
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:	T-1) mRNA//3.7e-45:370:80//Hs.154069:U06452
89//Hs.155464:AF088219	R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248	R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412
R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation inhibitor	R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:
1//0.066:196:62//Hs.159161:X69550	76//Hs.32567:AF073519
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081	R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, com
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcrip	plete cds//1.9e-37:316:74//Hs.10458:AF088219
t KIAA0488//1.0e-17:246:73//Hs.67619:AB007957	R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-4	R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979
7:294:89//Hs.3094:D31884	R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTE
R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:M52088	IN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:
R-MAMMA1001715//ESTs//1.2e-73:399:93//Hs.124620:AI082338	78//Hs.138596:M38806
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596	R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gal	R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds
lus gallus]//3.7e-110:552:96//Hs.6923:AI161158	//1.7e-42:314:83//Hs.10887:AB013924
R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:M59651	R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-4
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666	6:308:87//Hs.40100:AB002390
R-MAMMA1001744	R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817	R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:HI1347
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:M25041	R-MAMMA1002118
R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413	R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:
R-MAMMA1001757//ESTs//1.0e-98:488:96//Hs.45184:C14904	D38081
R-MAMMA1001760//EST//8.7e-29:206:86//Hs.143310:AI142276	R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA
R-MAMMA1001764//EST//0.00012:434:58//Hs.120051:AA707847	A, complete cds//1.4e-58:396:78//Hs.129735:AF010144
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3	R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//
e-41:299:85//Hs.149323:AB002325	1.4e-37:422:75//Hs.128834:AF035835
R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825	R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276
R-MAMMA1001771//ESTs, Moderately similar to semaphorin B [M.muscul	R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:
us]//7.6e-43:257:91//Hs.7634:AA481246	371:69//Hs.97476:AB007886
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1)	R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548
mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460	R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frame
R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238	s//7.8e-39:506:69//Hs.23094:M19503
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644	R-MAMMA1002156//Homo sapiens mRNA for putative lipoid acid synthet
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744	ase, partial//2.9e-44:336:82//Hs.53531:AJ224162
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:M60313	R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040
R-MAMMA1001812//EST//2.4e-93:446:98//Hs.129034:AA776892	R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-3

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R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318.82//Hs.92381:AB007956  
 R-MAMMA1002209//ESTs//9.2e-34:111.88//Hs.141575:AA211734  
 R-MAMMA1002215//ESTs//3.6e-101:530.94//Hs.26780:N50038  
 R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283.88//Hs.153026:AB014540  
 R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330.77//Hs.108966:U48696  
 R-MAMMA1002236  
 R-MAMMA1002243  
 R-MAMMA1002250//Homo sapiens PYRIN (NEFV) mRNA, complete cds//1.2e-44:299.87//Hs.113283:AF018080  
 R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.6e-54:207.81//Hs.92381:AB007956  
 R-MAMMA1002268//ESTs//2.9e-94:439.100//Hs.68061:A1042283  
 R-MAMMA1002269//ESTs//7.4e-05:170.65//Hs.140466:AA766772  
 R-MAMMA1002282//ESTs//7.8e-09:69.78//Hs.159502:AA225141  
 R-MAMMA1002292//ESTs//5.6e-64:334.94//Hs.113606:A1138751  
 R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203.81//Hs.154257:A1275982  
 R-MAMMA1002294//EST//8.1e-43:326.82//Hs.149580:A1281881  
 R-MAMMA1002297//ESTs//6.5e-45:323.83//Hs.155475:AA761454  
 R-MAMMA1002298//ESTs//1.7e-68:355.96//Hs.52683:H87153  
 R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346.91//Hs.140385:AA773359  
 R-MAMMA1002308  
 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280.87//Hs.154069:U0452  
 R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503.81//Hs.23094:M19503  
 R-MAMMA1002312//EST//1.7e-31:144.80//Hs.135936:N36094  
 R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457.76//Hs.144563:AF057280  
 R-MAMMA1002319//ESTs//3.9e-38:297.76//Hs.140326:AA827183  
 R-MAMMA1002322//ESTs//1.1e-46:301.86//Hs.155498:W27084  
 R-MAMMA1002329//EST//2.6e-09:146.72//Hs.132366:A1026658  
 R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387.70//Hs.91916:AF035317  
 R-MAMMA1002333//EST//1.8e-09:139.74//Hs.137800:AA886897  
 R-MAMMA1002339//ESTs//4.2e-47:310.76//Hs.138865:W57618  
 R-MAMMA1002347//ESTs//1.5e-44:326.83//Hs.111723:H57439  
 R-MAMMA1002351//ESTs//3.0e-112:545.97//Hs.26209:A1143127  
 R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259.92//Hs.43628:Y15228  
 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360.77//Hs.40100:AB002390  
 R-MAMMA1002355//ESTs//1.4e-29:307.75//Hs.3769:A1085367  
 R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217.88//Hs.73919:X81637  
 R-MAMMA1002359//Homo sapiens PYRIN (NEFV) mRNA, complete cds//1.1e-70:483.84//Hs.113283:AF018080  
 R-MAMMA1002360//ESTs//3.5e-19:301.69//Hs.124701:AA701475  
 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244.81//Hs.129727:AF035587  
 R-MAMMA1002362//ESTs//2.3e-43:241.88//Hs.150727:A1292236  
 R-MAMMA1002380//ESTs//5.1e-36:322.79//Hs.136994:AA843542  
 R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298.84//Hs.155464:AF088219  
 R-MAMMA1002385//ESTs//0.57:203.63//Hs.146303:AA579061  
 R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305.83//Hs.86188:D87845  
 R-MAMMA1002411//ESTs//4.4e-68:385.92//Hs.53478:N92294  
 R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138.75//Hs.115325:D84488  
 R-MAMMA1002417//ESTs//1.6e-98:475.98//Hs.96345:N22588  
 R-MAMMA1002427//ESTs//3.1e-39:274.79//Hs.141130:H28477  
 R-MAMMA1002428//ESTs//8.4e-11:215.66//Hs.141022:H06475  
 R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-108:521.98//Hs.112152:AA87348  
 R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374.68//Hs.157142:U85996  
 R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323.81//Hs.89121:AB007954  
 R-MAMMA1002461//ESTs//4.7e-111:548.97//Hs.104281:AA147076  
 R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-HMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544.93//Hs.94570:A1192106  
 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263.79//Hs.38687:AA744496  
 R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159.79//Hs.133526:N21103  
 R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560.97//Hs.155223:AF055460  
 R-MAMMA1002494//ESTs//3.2e-47:303.88//Hs.155243:N70293  
 R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331.58//Hs.37035:U07664  
 R-MAMMA1002524//ESTs//0.0039:354.61//Hs.125797:AA806277  
 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529.95//Hs.18858:AF065214  
 R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317.88//Hs.153468:AB011147  
 R-MAMMA1002554//ESTs//2.3e-85:445.95//Hs.139140:AA218851  
 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280.65//Hs.12725:T65058  
 R-MAMMA1002566//ESTs//2.3e-88:421.99//Hs.17602:AA705681  
 R-MAMMA1002571//ESTs//5.1e-97:456.99//Hs.152834:AA595693  
 R-MAMMA1002573//ESTs//3.1e-38:258.87//Hs.163989:R74433  
 R-MAMMA1002585//ESTs//7.8e-96:533.91//Hs.26009:H49371  
 R-MAMMA1002590//ESTs//0.61:202.62//Hs.161190:A1419258  
 R-MAMMA1002597//Cytochrome P450, subfamily I1B (phenobarbital-inducible), polypeptide 6//2.9e-21:177.75//Hs.1360:W29874  
 R-MAMMA1002598//ESTs//3.4e-113:544.97//Hs.20263:AA573737  
 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225.80//Hs.51124:AF019369  
 R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424.75//Hs.1361:N55053  
 R-MAMMA1002617//ESTs//1.1e-38:229.92//Hs.96987:W27389  
 R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185.73//Hs.108287:L27670  
 R-MAMMA1002619//ESTs//1.7e-95:480.96//Hs.54873:AA526306  
 R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298.87//Hs.89887:D38081  
 R-MAMMA1002623//EST//4.3e-49:336.85//Hs.149580:A1281881  
 R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308.79//Hs.93332:AA811920  
 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283.86//Hs.115325:D84488  
 R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303.89//Hs.40100:AB002390  
 R-MAMMA1002637//ESTs//1.3e-55:391.85//Hs.95074:A1144421  
 R-MAMMA1002646//ESTs//7.4e-36:182.80//Hs.163937:N69915  
 R-MAMMA1002650//ESTs//1.6e-102:547.94//Hs.57841:W63776  
 R-MAMMA1002655  
 R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462.75//Hs.97476:AB007886  
 R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376.82//Hs.154326:D42087  
 R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans CDNA yk52e10.5 [C.elegans]//5.3e-108:544.96//Hs.16464:W19606  
 R-MAMMA1002673//EST//3.3e-35:169.79//Hs.140046:AA668213  
 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544.96//Hs.3363:D86987  
 R-MAMMA1002685//EST//1.9e-31:223.86//Hs.112540:AA601385  
 R-MAMMA1002698//ESTs//5.9e-43:292.85//Hs.144660:AA652675  
 R-MAMMA1002699//ESTs//3.2e-25:134.100//Hs.126049:F22510  
 R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70:353.96//Hs.138404:R70986  
 R-MAMMA1002708//ESTs//2.1e-76:413.94//Hs.57932:W59234  
 R-MAMMA1002711//ESTs//1.9e-44:236.96//Hs.138575:H67858  
 R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273.89//Hs.153563:AF011333  
 R-MAMMA1002727//ESTs//2.9e-84:395.100//Hs.162826:AA679571  
 R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266.88//Hs.155464:AF088219  
 R-MAMMA1002744//ESTs//4.2e-18:473.63//Hs.42826:AA846757  
 R-MAMMA1002746//ESTs//1.8e-100:473.99//Hs.117558:AA779907  
 R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330.80//Hs.154069:U0452  
 R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369.77//Hs.105292:AA504776  
 R-MAMMA1002758  
 R-MAMMA1002764//ESTs//4.2e-103:486.99//Hs.159909:A1393281  
 R-MAMMA1002765//ESTs//1.6e-37:338.76//Hs.37573:H59651  
 R-MAMMA1002769//ESTs//0.72:409.57//Hs.141376:A1301272  
 R-MAMMA1002780//ESTs//1.6e-52:292.92//Hs.135985:AA342750  
 R-MAMMA1002782//ESTs//1.0e-31:157.80//Hs.159510:AA297145  
 R-MAMMA1002796//ESTs//3.8e-49:284.92//Hs.156479:AA513812

【表613】

R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198	87:94//Hs.108112:AF070640
R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260	R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312
R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:A1248319	R-NT2RM4000027
R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:A1281881	R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663
R-MAMMA1002835	R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:A1186169
R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723	R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379
R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395	R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds
R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78150:AF010238	//4.0e-113:549:97//Hs.95665:AF070639
R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081	R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067	R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708
R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941	R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:A1052312
R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:A1243592	R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-99:536:92//Hs.127810:A1246301
R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194	R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397
R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:A1365871	R-NT2RM4000167//ESTs//1.0:214:61//Hs.119370:W52962
R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219	R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:A1382160
R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811	R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113
R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cD NA CEESB82F [C. elegans]//4.2e-92:438:99//Hs.155871:AA533783	R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723
R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915	R-NT2RM4000199//ESTs//0.020:95:65//Hs.146203:A1254528
R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087	R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876
R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179	R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219
R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002	R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:AB018255
R-MAMMA1002930//EST//4.4e-44:260:91//Hs.149580:A1281881	R-NT2RM4000215
R-MAMMA1002938	R-NT2RM4000229//ESTs//7.1e-92:457:97//Hs.162074:AA477760
R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frame s//1.1e-83:556:85//Hs.23094:W19503	R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602
R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243	R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031
R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353	R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974
R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081	R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:A1378742
R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630	R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128
R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835	R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673
R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279	R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219
R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (OFF40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019	R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637
R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179	R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-117:579:96//Hs.5216:AA534881
R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:A1127857	R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:A1224479
R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617	R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063
R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//Hs.92023:A1022248	R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542
R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189	R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140
R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268	R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:AA775879
R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315	R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAPI55-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977
R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358	R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285
R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321	R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C. elegans]//5.4e-75:470:90//Hs.69235:AA192359
R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160	R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173
R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940	R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:A1150687
R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:A1002941	R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865
R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862	R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:492:96//Hs.21090:AA418587
R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348	R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493:97//Hs.111279:W84558
R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:A1281881	R-NT2RM4000496
R-MAMMA1003056//EST//0.99:107:66//Hs.30348:A1038559	R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:A1358465
R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:AA878911	R-NT2RM4000514//ESTs//1.7e-112:552:96//Hs.6886:AA205496
R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X95969	R-NT2RM4000515//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014:AA074879
R-MAMMA1003089//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARMING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652	R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731
R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651	R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461
R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283	R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777
R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366	R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198
R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788	R-NT2RM4000585//EST//0.28:63:77//Hs.150024:A1291981
R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125	R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437
R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:A1149537	R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891
R-MAMMA1003146//Wingless-type LNTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861	R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589
R-MAMMA1003150	R-NT2RM4000611//ESTs//1.5e-89:431:97//Hs.26117:W16697
R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//Hs.6884:W30736	R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHET
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:5	

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ASE [Escherichia coli]//1.4e-102:519:96//Hs.14779:N64822	r protein Lnk [M.musculus]//4.0e-102:539:94//Hs.15744:A1055859
R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144	R-NT2RM4001412
R-NT2RM4000689//ESTs. Weakly similar to T01G9.4 [C.elegans]//2.9e-115:550:98//Hs.11820:AA205531	R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA75895
R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510	R-NT2RM4001437//EST//0.017:169:67//Hs.13207:FI0054
R-NT2RM4000700	R-NT2RM4001444//ESTs. Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812
R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128	R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277
R-NT2RM4000717//ESTs. Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.2e-103:519:95//Hs.6823:W18181	R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA69739
R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311	R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168:AB018303	R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121:AB014585
R-NT2RM4000741//ESTs//0.99:266:58//Hs.142718:AA034046	R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664
R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988	R-NT2RM4001522//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219
R-NT2RM4000764	R-NT2RM4001557//ESTs. Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165:83//Hs.29134:H43072
R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174	R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:AB007920	R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z98046
R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs.154069:U06452	R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009
R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:A1417008	R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946
R-NT2RM4000795//Human mRNA for KIAA0087 gene, complete cds//1.0:203:63//Hs.20991:D31891	R-NT2RM4001592
R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:A1003520	R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA. 3' end//2.5e-28:158:96//Hs.118249:M21868	R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:A1358871
R-NT2RM4000813	R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:AB018334
R-NT2RM4000820//ESTs. Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:A1219667	R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079
R-NT2RM4000833//ESTs. Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031	R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957
R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864	R-NT2RM4001650
R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:A1309597	R-NT2RM4001662
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:A1283343	R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:AB007938
R-NT2RM4000887	R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:A1367496
R-NT2RM4000895//ESTs. Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514	R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440
R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262	R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887	R-NT2RM4001715//ESTs//6.5e-104:487:99//Hs.153581:AA630465
R-NT2RM4000979//ESTs//1.6e-67:329:98//Hs.96927:AA349647	R-NT2RM4001731//ESTs. Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510:AA522887
R-NT2RM4000996//ESTs. Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:AA650126	R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs.120980:S83390
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:AB018272	R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:AB014539	R-NT2RM4001754//Human kpni repeat mRNA (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352	R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:A1290740
R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.32170:AB015132	R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300	R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956
R-NT2RM4001084//ESTs//3.4e-91:439:99//Hs.103177:W72798	R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:M22567
R-NT2RM4001092//ESTs//1.4e-86:517:89//Hs.132969:Z78324	R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:A1089920
R-NT2RM4001116//ESTs//5.2e-57:275:100//Hs.131115:A1016962	R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276	R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311	R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848	R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619
R-NT2RM4001160//EST//7.6e-25:308:68//Hs.147405:A1209085	R-NT2RM4001842//ESTs. Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.1e-10:274:62//Hs.161959:AA493652
R-NT2RM4001187//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174	R-NT2RM4001856//ESTs. Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292:86//Hs.14202:N46000
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942	R-NT2RM4001858//ESTs//6.2e-104:495:98//Hs.118686:AA682280
R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849	R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711
R-NT2RM4001203	R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252
R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307	R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149
R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410	R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178
R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677	R-NT2RM4001922//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438
R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184	R-NT2RM4001930//ESTs//4.1e-84:425:96//Hs.80042:N63143
R-NT2RM4001309	R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:A1205893
R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857	R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:AF098162
R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:A1128899	R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268
R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:A1042352	R-NT2RM4001965//ESTs. Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917
R-NT2RM4001340//ESTs. Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.18442:A1129307	R-NT2RM4001969//ESTs. Weakly similar to IP63 protein [R.norvegicus]//1.1e-21:121:98//Hs.8772:AA521097
R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339	
R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476	
R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA50211	
R-NT2RM4001382	
R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507	
R-NT2RM4001410//EST//0.13:50:82//Hs.157675:A1358790	
R-NT2RM4001411//ESTs. Weakly similar to lymphocyte specific adapt	

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R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265	R-NT2RM4002623//ESTs. Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//9.6e-28:194:87//Hs.59346:A112680
R-NT2RM4001984	2
R-NT2RM4001987	R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:M45096
R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:A1345528	R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081
R-NT2RM4002018	R-NT2RP2000008//Zinc finger protein 37a (KDX 21)//5.2e-25:366:67//Hs.54488:X69115
R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087	R-NT2RP2000007//ESTs//9.5e-74:377:96//Hs.96557:AA286713
R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435	R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290
R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226	R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749
R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887	R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798
R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179	R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:A1094910
R-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:AF071309	R-NT2RP2000067//ESTs. Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793:AA755879
R-NT2RM4002067//Human knpi repeat mra (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629	R-NT2RP2000070//ESTs. Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881
R-NT2RM4002073//ESTs. Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416	R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097
R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655	R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.54877:AF050078
R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:A1052528	R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.102576:A1010230
R-NT2RM4002109//ESTs//1.0e-95:69//Hs.25897:W65409	R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338
R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122507:Y13620	R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064
R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712	R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757
R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987	R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827
R-NT2RM4002146//ESTs//1.9e-93:439:99//Hs.119295:AA442090	R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535	R-NT2RP2000114//Homo sapiens mRNA for CM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356
R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258	R-NT2RP2000120//ESTs. Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//1.9e-19:153:86//Hs.5268:W22670
R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400	R-NT2RP2000126//ESTs//1.0e-55:293:95//Hs.14570:A1422099
R-NT2RM4002194//EST//0.22:68:72//Hs.149104:A1244343	R-NT2RP2000133//ESTs//0.24:354:59//Hs.157564:A1356513
R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678	R-NT2RP2000147//ESTs. Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-89:457:95//Hs.3832:A1208601
R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079	R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548
R-NT2RM4002226//ESTs. Highly similar to GTPASE ACTIVATING PROTEIN R0TUND [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984	R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820
R-NT2RM4002251//ESTs. Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190	R-NT2RP2000161//ESTs//1.6e-99:492:97//Hs.21738:A1188190
R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219	R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:A1143741
R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864	R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373
R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263	R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510
R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638	R-NT2RP2000205//ESTs. Moderately similar to !!! ALU SUBFAMILY J W ARNING ENTRY !!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897
R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461	R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382
R-NT2RM4002294	R-NT2RP2000232
R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164	R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:A1090683
R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498	R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379
R-NT2RM4002339//ESTs//5.0e-59:283:100//Hs.125048:AA682913	R-NT2RP2000248//ESTs. Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs.102057:AA649005
R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:W77198	R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:A1126840
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549	R-NT2RP2000258//EST//1.0e-67:68//Hs.61812:AA035649
R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594	R-NT2RP2000270//ESTs. Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-59:298:96//Hs.16085:A1261382
R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884	R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635
R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328	R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865
R-NT2RM4002409//ESTs. Weakly similar to coded for by C. elegans cDNA yk5210.5 [C.elegans]//1.3e-97:473:98//Hs.16464:W19606	R-NT2RP2000289
R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677	R-NT2RP2000297//ESTs. Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249
R-NT2RM4002446	R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712
R-NT2RM4002452//EST//1.0e-164:60//Hs.116619:AA668142	R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381
R-NT2RM4002457	R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSAs//2.9e-71:342:98//Hs.8768:AL022398
R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890	R-NT2RP2000329//ESTs. Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.8765:AF083255	R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:A1276062
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:AB014591	R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981
R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884	R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103
R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:A1088029	
R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA644464	
R-NT2RM4002527//ESTs. Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//Hs.31030:HS0467	
R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788	
R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:A1417057	
R-NT2RM4002537//ESTs//7.6e-41:272:87//Hs.7114:R24312	
R-NT2RM4002571//ESTs. Highly similar to POLYPEPTIDE N-ACETYLGLYCOSAMINYLTTRANSFERASE [Bos taurus]//2.3e-89:435:97//Hs.15830:AA165698	
R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569	

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R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010	R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775
R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:A1222324	R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265	R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205
R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:A1151425	R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]//2.3e-43:238:93//Hs.106632:N25679
R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAPI-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045	R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:A1341138
R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:A1352013	R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178
R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078	R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028
R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:A1290215	R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038
R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896	R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]//3.9e-74:411:93//Hs.47305:AA195153
R-NT2RP2000516//ESTs//9.9e-63:376:89//Hs.47546:AA181348	R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875
R-NT2RP2000523	R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97:469:97//Hs.20483:AA522505
R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144	R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030
R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446	R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514	R-NT2RP2001427//EST//1.7e-11:107:84//Hs.148584:A1201728
R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222	R-NT2RP2001436//ESTs, Weakly similar to F0208.3 [C.elegans]//2.9e-114:558:97//Hs.7627:A1341556
R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275	R-NT2RP2001440//EST//0.17:192:58//Hs.133442:A1061394
R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396	R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453
R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767	R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:A1076765
R-NT2RP2000678//ESTs//2.6e-53:271:96//Hs.23790:N99347	R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.181829:A1079539
R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:A1261368	R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:AF088219
R-NT2RP2000715//EST//1.2e-87:418:99//Hs.139425:AA429279	R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513
R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965	R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146
R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:N62642	R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545:95//Hs.4277:Y14494
R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419	R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240
R-NT2RP2000809	R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586
R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745	R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816
R-NT2RP2000814//ESTs//6.3e-87:433:97//Hs.145479:AA969404	R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387:96//Hs.67619:AB007957
R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918	R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:D14661
R-NT2RP2000819	R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:TS8884
R-NT2RP2000841//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR//4.6e-10:247:66//Hs.29352:M31165	R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:A1369995
R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:A1206552	R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:A1393767
R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345	R-NT2RP2001613
R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:AB018284	R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294
R-NT2RP2000892//ESTs//2.8e-50:258:96//Hs.119238:AA476267	R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090
R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266	R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:A1370845
R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:19:95//Hs.112318:AA186477	R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:A1201336
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:AB018298	R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:A1125323
R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021	R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579
R-NT2RP2000970//EST//8.7e-06:255:62//Hs.149202:A1246481	R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538
R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537	R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:A1147100
R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521	R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840
R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643	R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:AF091754
R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660	R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037
R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108	R-NT2RP2001861
R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665	R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:A1002941
R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068	R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088
R-NT2RP2001119	R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:AA113849
R-NT2RP2001127//Homo sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348	R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724
R-NT2RP2001137	R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423
R-NT2RP2001149//ESTs//5.1e-66:324:97//Hs.27475:AA704512	R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:A1097268
R-NT2RP2001168//ESTs//2.0e-98:539:97//Hs.77870:A1188145	R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087
R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:AB007949	R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:A1032180
R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287	R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594
R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510	R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588
R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:A1188402	R-NT2RP2001969
R-NT2RP2001222//EST//0.0074:154:63//Hs.128612:AA909358	R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745
R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//Hs.44014:AA632298	R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:89//Hs.18760:AA166678
R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996	R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:A1378233
R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353	R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332
R-NT2RP2001277//EST//2.0e-81:387:99//Hs.13751:AA908229	R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627
	R-NT2RP2002041
	R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938
	R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895
	R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068
	R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091
	R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265
	R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:17

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B:87//Hs.11039:AF052183	R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W
R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524	ARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein	R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031
//1.5e-60:376:89//Hs.155218:AJ007509	R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870
R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000	R-NT2RP2002880
R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134	R-NT2RP2002891
R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527	R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894
R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268	R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143
R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495	R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096
R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4	R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771
e-54:269:98//Hs.107201:W52859	R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:W57480
R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W	R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060
ARNING ENTRY !!!! [H.sapiens]//3.9e-15:245:71//Hs.87578:AI125363	R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213
R-NT2RP2002193//ESTs//3.5e-79:453:90//Hs.76578:AI290672	R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291
R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946	R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:7
R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499	8:74//Hs.146395:AB002329
R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341	R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.86337:AA149311
R-NT2RP2002252//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:AI188168	R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:AF005418	R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:HI2594
R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:54	R-NT2RP2003073//Human transporter protein (gl7) mRNA, complete cds
8:91//Hs.92137:W19720	//0.95:259:61//Hs.76460:U49082
R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//	R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:
4.8e-100:550:91//Hs.4029:Z78373	D38081
R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2	R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512
e-92:482:93//Hs.5570:AI377863	R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-4
R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2)	9:336:86//Hs.101996:AB002345
mRNA, partial cds//4.1e-103:527:94//Hs.24812:AF069532	R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355
R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015	R-NT2RP2003125
R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:95//Hs.31034:AB015594	R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986
R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372	R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506
R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:89//Hs.109051:AF038958	R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379
R-NT2RP2002394//ESTs//0.11:158:65//Hs.28792:AI343467	R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067
R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815	R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952
R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:80//Hs.15731:AB011135	R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156
R-NT2RP2002439//ESTs//3.2e-12:134:76//Hs.32246:AA464020	R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816
R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521	R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074
R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230	R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253
R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233	R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661
R-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605:92//Hs.125856:AB005289	R-NT2RP2003243//ESTs//3.6e-53:300:92//Hs.118793:AA192438
R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:W73180	R-NT2RP2003265//ESTs, Highly similar to protein NGDS [M.musculus]//
R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838	3.3e-110:557:96//Hs.24994:AA236937
R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:91//Hs.23255:AB018334	R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2
R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305	e-34:228:89//Hs.107201:W52859
R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA530990	R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cd
R-NT2RP2002546//Homo sapiens clone TUAB Cri-du-chat region mRNA//	s//1.4e-111:565:95//Hs.154919:AB014525
2.6e-109:570:93//Hs.49476:AF009314	R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427
R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325	R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106
R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564:97//Hs.94549:AA149547	R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-4
R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783	4:458:74//Hs.154326:O42087
R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:W40170	R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//
R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220	Hs.1087:L20321
R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615	R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874
R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881	R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126
R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944	R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948
R-NT2RP2002672	R-NT2RP2003339//ESTs//1.3e-85:441:96//Hs.24115:N32618
R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease 11B)//0.99:184:63//Hs.50727:U43572	R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825
R-NT2RP2002705//EST//2.8e-41:148:86//Hs.161917:AA483223	R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014
R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210	R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476
R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:W78626	R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502
R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300	R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52449
R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108	R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683
R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352	R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.13184
R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131	O:AI016073
R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:W62042	R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W
R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124	ARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N23360
R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:W03587	R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:34	105:529:96//Hs.8055:W60903
1:94//Hs.17481:AF070537	R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332
R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124	R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121

【表618】

B:566:94//Hs.78482:Y16270  
 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (s  
 ieian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.  
 1976:W12783  
 R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170  
 R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101  
 R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684  
 R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W  
 ARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439  
 R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696  
 R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719  
 R-NT2RP2003596//ESTs, Weakly similar to No definition line found  
 [C.elegans]//4.7e-101:495:98//Hs.34627:AA126463  
 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP)  
 mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067  
 R-NT2RP2003629//EST//0.032:440:59//Hs.135297:A1038981  
 R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTE  
 IN IN MURZ-RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.124  
 92:AA203188  
 R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951  
 R-NT2RP2003681//EST//5.9e-05:196:65//Hs.139064:AA135523  
 R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:2  
 02:62//Hs.65539:A1148540  
 R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific prote  
 in [R.norvegicus]//4.3e-99:492:96//Hs.93332:AA811920  
 R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246  
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cd  
 s//8.4e-47:265:93//Hs.78494:AB011097  
 R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401  
 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:A1365003  
 R-NT2RP2003727//Human 19.8 kDa protein mRNA, complete cds//0.84:22  
 1:60//Hs.2384:U18914  
 R-NT2RP2003737//ESTs, Highly similar to UBQUITIN-CONJUGATING ENZ  
 YME E2-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W7  
 4577  
 R-NT2RP2003751  
 R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808  
 R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709  
 R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606  
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complet  
 e cds//6.0e-106:531:96//Hs.90436:AF047437  
 R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:A1381811  
 R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836  
 R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955  
 R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077  
 R-NT2RP2003857//H.sapiens mRNA for C9a//2.8e-23:351:65//Hs.75196:X  
 69838  
 R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124  
 R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167  
 R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341  
 R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:A1094611  
 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, c  
 omplete cds//0.90:190:60//Hs.75875:U49278  
 R-NT2RP2003968//Homo sapiens HUBP mRNA for ubiquitin specific prot  
 ease, complete cds//7.6e-116:568:97//Hs.35086:AB014458  
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete c  
 ds//3.6e-109:540:97//Hs.7302:AB007916  
 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cd  
 s//2.5e-115:568:96//Hs.7316:AB018347  
 R-NT2RP2003984  
 R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087  
 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.s  
 apiens]//3.2e-110:519:99//Hs.36093:A1149968  
 R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:A1417478  
 R-NT2RP2004041  
 R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706  
 R-NT2RP2004066//ESTs//1.4e-110:559:96//Hs.71916:AA219699  
 R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204  
 R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461  
 R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036  
 R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:A1147500  
 R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:A1342241  
 R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIAR  
 Y [Anthocidaris crassispina]//1.0e-118:583:97//Hs.16520:A1224533  
 R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:A1348544  
 R-NT2RP2004172//ESTs//1.5e-109:565:95//Hs.159091:AA033974  
 R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589  
 R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167  
 R-NT2RP2004196  
 R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756  
 R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972  
 R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sap  
 iens]//5.2e-105:499:98//Hs.143460:AA483305  
 R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116  
 R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, compl  
 ete cds//3.4e-103:530:93//Hs.54900:AF039687  
 R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483  
 R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744  
 R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187  
 R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056  
 R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, comp  
 lete cds//4.7e-110:544:96//Hs.61152:AF000416  
 R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788  
 R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223  
 R-NT2RP2004347  
 R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:A1268173  
 R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:A1129310  
 R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:A1218624  
 R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N21892  
 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROT  
 EIN F09C8.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.4e-11:10  
 8:82//Hs.30490:AA146916  
 R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646  
 R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473  
 R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900  
 R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921  
 R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121  
 R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:A1168124  
 R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695  
 R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein  
 kinase-1 (PKD1) mRNA, complete cds//8.6e-34:143:98//Hs.154729:AF01  
 7995  
 R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:A1270700  
 R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320  
 R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:  
 D38081  
 R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:A1024347  
 R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470  
 R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:A1221661  
 R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126  
 R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666  
 R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862  
 R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNI  
 NG ENTRY !!!! [H.sapiens]//4.5e-07:149:76//Hs.12845:N28835  
 R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497  
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-1  
 18:587:96//Hs.5198:AJ006291  
 R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cd  
 s//5.9e-107:520:96//Hs.29956:AB007929  
 R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930  
 R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:N60858  
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cd  
 s//5.0e-120:600:96//Hs.154919:AB014525  
 R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:A1149793  
 R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433  
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete c  
 ds//1.3e-118:594:96//Hs.4236:AB007947  
 R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015  
 R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423  
 R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774  
 R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013  
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase  
 beta subunit (SCS) mRNA, partial cds//8.0e-116:564:96//Hs.40820:AF  
 058953  
 R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579  
 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds/  
 //8.7e-120:584:97//Hs.67052:AF054179  
 R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:A1219906  
 R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803  
 R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567  
 R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529  
 R-NT2RP2004959//ESTs//0.059:137:64//Hs.144109:A1345543  
 R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941  
 R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:A1275458  
 R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-5  
 1:506:75//Hs.154326:D42087  
 R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496  
 R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910  
 R-NT2RP2004985  
 R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:A1419902

【表619】

R-NT2RP2005000	//8.8e-108:560:94//Hs.159597:AJ012449
R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:AB014515	R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:AB007963
R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235	R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572
R-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141	R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567
R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161	R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169
R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507	R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240
R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887	R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733
R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220	R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060
R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757	R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788
R-NT2RP2005108	R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:AB014564	R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211
R-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.100555:X98743	R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740
R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383	R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173
R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180:AI341261	R-NT2RP2005651//ESTs. Highly similar to XF1N PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:AA868470
R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744	R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302
R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438	R-NT2RP2005669//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987
R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582	R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-IR) mRNA, complete cds//5.8e-91:434:98//Hs.25664:AF089814
R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648	R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229
R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein //2.4e-101:513:95//Hs.155218:AJ007509	R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236
R-NT2RP2005204//ESTs. Weakly similar to UBQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H. sapiens]//1.9e-115:577:96//Hs.7600:H98166	R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643
R-NT2RP2005227//Homo sapiens LIM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258	R-NT2RP2005701//ESTs. Highly similar to BUTYROPOLIN PRECURSOR [Bos taurus]//2.8e-68:376:93//Hs.9095:AA532630
R-NT2RP2005239//ESTs. Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587	R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:AB018342
R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503	R-NT2RP2005719//ESTs. Weakly similar to GPI-anchored protein p137 precursor [H. sapiens]//5.4e-105:500:98//Hs.14298:AI417523
R-NT2RP2005270//ESTs. Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596	R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982
R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272	R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455
R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001	R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219	R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258
R-NT2RP2005289//Homo sapiens mRNA for IPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590	R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:NT8064
R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261	R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//Hs.159651:AF068868
R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338	R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.26285:AF082516
R-NT2RP2005325//Human LIM-homeobox domain protein (LH-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701	R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163
R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699	R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463
R-NT2RP2005344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445	R-NT2RP2005773//ESTs. Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-112:559:96//Hs.14214:AI189379
R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:HI4544	R-NT2RP2005775//ESTs. Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.22151:AI214321
R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247	R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664
R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304	R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724
R-NT2RP2005407//ESTs. Weakly similar to OSHI PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697	R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398
R-NT2RP2005436//ESTs. Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN 80495.8 IN CHROMOSOME II [C. elegans]//8.1e-96:491:95//Hs.7194:AI185631	R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746
R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068	R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981
R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:HI4423	R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122
R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096	R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403
R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:NS1307	R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062
R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936	R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462
R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019	R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105
R-NT2RP2005476//ESTs//5.1e-40:205:98//Hs.101577:AI168526	R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133
R-NT2RP2005490//ESTs//1.3e-70:364:96//Hs.134382:AA083573	R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315
R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455	R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268
R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540	R-NT2RP2005908//ESTs. Weakly similar to weakly similar to gastrula zinc finger protein [C. elegans]//2.4e-73:397:94//Hs.16667:192427
R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426	R-NT2RP2005933//ESTs. Highly similar to nucleoporin p54 [R. norvegicus]//2.8e-114:560:97//Hs.9082:AA873170
R-NT2RP2005498//ESTs. Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:AI138993	R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419
R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755	R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988
R-NT2RP2005509//ESTs. Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071	R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080
R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:570:94//Hs.119023:AF092563	R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347
R-NT2RP2005525//ESTs. Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H. sapiens]//1.3e-84:433:95//Hs.36942:AA524535	R-NT2RP2006043//ESTs. Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN 80495.8 IN CHROMOSOME II [C. elegans]//1.2e-50:278:94//Hs.7194:AI185631
R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856	R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492
R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)	R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714
	R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093
	R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918
	R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//Hs.46440:U21943
	R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365
	R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522
	R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-

【0922】



【表620】

17:255:72//Hs.154103:AF061258	R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741
R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435	R-NT2RP3000361//ESTs. Weakly similar to PRE-MRNA SPLICING FACTOR RP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:AB014554	R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303
R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276	R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398	R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185
R-NT2RP2006219//H. sapiens mRNA for DGC6 protein//1.2e-94:532:90//Hs.153910:X86484	R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947
R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312	R-NT2RP3000433
R-NT2RP2006238//ESTs. Highly similar to rAB [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA04253	R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340
R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:M49928	R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254
R-NT2RP2006261//ESTs//3.4e-57:326:92//Hs.22523:W02999	R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262	R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492
R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015	R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.114963:L34408
R-NT2RP2006321//ESTs. Moderately similar to karyopherin beta 3 [H. sapiens]//1.9e-89:460:96//Hs.21889:W78664	R-NT2RP3000484//Heparin cofactor 1//0.98:166:62//Hs.1478:MS8600
R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771	R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141
R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412	R-NT2RP3000512//Homo box B3//2.0e-69:377:93//Hs.49931:X16667
R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321	R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151
R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411	R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161
R-NT2RP2006393//Cytochrome P450, subfamily 1 (aromatic compound-inducible), polypeptide 2//3.9e-48:403:77//Hs.1361:M55053	R-NT2RP3000531//ESTs. Weakly similar to TH1 protein [O.melanogaster]//0.95:85:71//Hs.5184:AA709151
R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.115325:D84488	R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180
R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092	R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI198036
R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146	R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:41:68//Hs.79077:D87071
R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595	R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447
R-NT2RP2006464//Homo sapiens mRNA for AMD-1 protein//2.1e-109:524:97//Hs.72160:AJ006266	R-NT2RP3000582//ESTs//2.1e-25:131:80//Hs.152465:AA563785
R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478	R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI241511
R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679	R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817
R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947	R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI190916
R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474	R-NT2RP3000596//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312
R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886	R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880
R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622	R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049
R-NT2RP2006573//ESTs//2.0e-112:533:98//Hs.18685:AI393829	R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394
R-NT2RP2006598//ESTs. Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112	R-NT2RP3000624//ESTs. Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545:98//Hs.4857:AI090739
R-NT2RP3000602//ESTs//1.3e-08:399:59//Hs.126044:AI301598	R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:AB018315
R-NT2RP3000631//Homo sapiens mRNA for histone deacetylase-like protein [JM21]//1.9e-116:560:97//Hs.6764:AJ011972	R-NT2RP3000632//ESTs. Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:99//Hs.152517:AA719022
R-NT2RP3000646//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219	R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084
R-NT2RP3000647//EST//0.91:130:66//Hs.140208:AA072213	R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185
R-NT2RP3000650//ESTs. Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202	R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185
R-NT2RP3000655//EST//2.4e-19:146:85//Hs.160497:AI255095	R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873
R-NT2RP3000672//ESTs//2.2e-82:424:96//Hs.21542:N49574	R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.146589:AI085578
R-NT2RP3000680//ESTs//2.1e-29:186:89//Hs.153372:AA424029	R-NT2RP3000736
R-NT2RP3000685//ESTs//4.5e-101:482:98//Hs.47649:AA838715	R-NT2RP3000742//ESTs. Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136065:W21960
R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241	R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:AI310447
R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000	R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243
R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:AB011164	R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI378583
R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418	R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810
R-NT2RP3000186	R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582
R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882	R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081
R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091	R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082
R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306	R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022
R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:M64817	R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154105:AI051657
R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819	R-NT2RP3000850
R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239	R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272
R-NT2RP3000251	R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895
R-NT2RP3000252//ESTs. Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177	R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741
R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073	R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:W70837
R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446	R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI014673
R-NT2RP3000299//ESTs. Weakly similar to enhancer of filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:AI191323	R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468
R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117	R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217
R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438	R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385
R-NT2RP3000324	R-NT2RP3000917//ESTs. Highly similar to mouse Dhml protein [M.musculus]//9.5e-113:566:96//Hs.5900:AA035728
R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267	R-NT2RP3000919
R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689	R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.5e-25:375:71//Hs.2953:X84407
R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225	R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178
R-NT2RP3000350//ESTs. Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177	R-NT2RP3000994//ESTs//3.5e-111:537:97//Hs.21146:AA683542
	R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405
	R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029
	R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044

【0923】

【表621】

R-NT2RP3001057//ESTs. Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//Hs.145956:AA007349	RC8 (TRC8) mRNA, complete cds//6.8e-112:549:97//Hs.28285:AF064801
R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD) //0.0012:447:58//Hs.2133:U18991	R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047
R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874	R-NT2RP3001529//Homo sapiens tapasin (NCS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750
R-NT2RP3001096//ESTs//1.1e-110:540:96//Hs.42824:AA873182	R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463
R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832	R-NT2RP3001554//ESTs. Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:AA524416
R-NT2RP3001109//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325	R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477
R-NT2RP3001111//ESTs. Weakly similar to Trf-proximal protein [D. melanogaster]//3.2e-104:543:95//Hs.93796:C06063	R-NT2RP3001587//Homo sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337
R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575	R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194
R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:164878	R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328
R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779	R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:A1279798
R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180	R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:A1193598
R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:A1190166	R-NT2RP3001629
R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188	R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149
R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761	R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989
R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305	R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
R-NT2RP3001147//ESTs. Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//9.6e-113:552:97//Hs.23900:U82984	R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717	R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:A1382189
R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266	R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:A1074460	R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:A1268225
R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139	R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:A122558
R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:A1254963	R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
R-NT2RP3001221//EST//0.010:106:66//Hs.147774:A1221196	R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:A1341312
R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399	R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
R-NT2RP3001235//ESTs. Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588	R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669
R-NT2RP3001239//ESTs. Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:AA524416	R-NT2RP3001716//ESTs. Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//4.1e-80:444:91//Hs.6823:W18181
R-NT2RP3001245//EST//0.53:237:62//Hs.161131:A1417631	R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:A1422099
R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:A1222997	R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135	R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
R-NT2RP3001268//Human Aac11 (aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857	R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440
R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:A1383965	R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.113184:N25651	R-NT2RP3001764//ESTs. Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:N92517
R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:A1247332	R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691	R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:AB007928
R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571	R-NT2RP3001792//ESTs. Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900
R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989	R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.12978:O75962
R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:U35234	R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:A1291292
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:AB007920	R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653	R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:W52900
R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798	R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:DB1792
R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090	R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
R-NT2RP3001383//ESTs//3.6e-101:118:78//Hs.111055:AA169778	R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
R-NT2RP3001384//ESTs. Weakly similar to A-kinase anchor protein 9 S. AKAP95 [R. norvegicus]//5.7e-92:522:90//Hs.96200:AA218942	R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375	R-NT2RP3001926//ESTs. Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:A123300
R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232	R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781
R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:A1276628	R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737
R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:A1041186	R-NT2RP3001938//ESTs. Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]//1.3e-95:483:96//Hs.5771:W74591
R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898	R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990
R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817	R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:A1291325
R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158	R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:A1025889
R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692	R-NT2RP3001989//ESTs. Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310:99//Hs.11449:A1201540
R-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397	R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088
R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:A1041374	R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779
R-NT2RP3001447//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//5.1e-101:482:98//Hs.124135:AA910560	R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729
R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:NA5994	R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:AF088219
R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219	R-NT2RP3002033
R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA644658	R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081
R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280	R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426
R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009	R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:A1365221
R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783	R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:D63486
R-NT2RP3001495//Human oxidoreductase (HCHMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395	R-NT2RP3002062
R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T	R-NT2RP3002063//ESTs//2.1e-113:552:97//Hs.9591:AA069657
	R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139
	R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148
	R-NT2RP3002102

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【表622】

R-NT2RP3002108	0143
R-NT2RP3002146//ESTs//5.5e-58:296.97//Hs.65328:AA625385	R-NT2RP3002972//ESTs//1.7e-97:502.96//Hs.7274:AA476850
R-NT2RP3002147//EST//2.5e-53:387.81//Hs.147928:A1249703	R-NT2RP3002978//ESTs//8.6e-104:498.98//Hs.118923:AA252116
R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//6.2e-107:534.96//Hs.59523:AA602837	R-NT2RP3002988//EST//1.2e-59:315.94//Hs.157743:A1360553
R-NT2RP3002163//ESTs//2.7e-106:520.97//Hs.21258:AA412293	R-NT2RP3003008//ESTs//1.4e-97:515.94//Hs.6544:AA524423
R-NT2RP3002165//ESTs//7.4e-93:479.95//Hs.27299:A1074024	R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POL YPROTEIN [Mus musculus]//3.0e-100:528.94//Hs.90353:N98551
R-NT2RP3002166//ESTs//1.0:261.59//Hs.132817:AA593713	R-NT2RP3003059//ESTs//1.7e-76:398.95//Hs.102971:W05355
R-NT2RP3002173//ESTs//2.7e-93:512.92//Hs.23648:H07120	R-NT2RP3003061//ESTs//4.9e-82:414.96//Hs.99603:A1141912
R-NT2RP3002181//ESTs//1.0e-84:435.96//Hs.47378:A1193598	R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans]//5.9e-83:392.99//Hs.101364:AA534439
R-NT2RP3002244//ESTs//2.7e-11:97.89//Hs.9412:W72446	R-NT2RP3003071//ESTs//6.3e-85:399.99//Hs.109755:AA180809
R-NT2RP3002248//ESTs//4.3e-90:459.95//Hs.9848:AA130588	R-NT2RP3003078//ESTs//1.0e-98:471.99//Hs.7995:A1359466
R-NT2RP3002255//ESTs//1.3e-45:289.88//Hs.9100:AA431672	R-NT2RP3003101//EST//0.032:235.60//Hs.147920:A1202441
R-NT2RP3002273//ESTs//2.3e-100:489.97//Hs.8258:AA744743	R-NT2RP3003121//ESTs//3.0e-47:238.97//Hs.43559:A1003520
R-NT2RP3002276//ESTs//1.2e-50:306.91//Hs.16160:AA778171	R-NT2RP3003133//EST//1.5e-77:395.96//Hs.142150:AA223982
R-NT2RP3002303//ESTs//1.1e-67:323.99//Hs.129761:AA836898	R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]//3.3e-107:535.96//Hs.27437:AA004208
R-NT2RP3002304//ESTs//2.8e-86:405.99//Hs.29643:AA418500	R-NT2RP3003139//ESTs//2.5e-106:504.98//Hs.106795:A1271632
R-NT2RP3002333//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]//1.8e-19:136.87//Hs.106928:A1041737	R-NT2RP3003150//ESTs//1.6e-99:539.91//Hs.46500:AA129774
R-NT2RP3002343//ESTs//1.0e-42:260.93//Hs.7797:W25667	R-NT2RP3003157//ESTs//1.5e-114:563.97//Hs.58608:AA081007
R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221.64//Hs.556:L41887	R-NT2RP3003185//ESTs//3.9e-93:443.98//Hs.9741:A1131226
R-NT2RP3002355//Homo sapiens mRNA for protein encoded by cxorf5 (7-17A) gene//5.8e-105:516.94//Hs.6483:Y16355	R-NT2RP3003193//ESTs//2.0e-37:428.71//Hs.33354:AA179944
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524.95//Hs.12707:AB014578	R-NT2RP3003197//ESTs//5.8e-56:312.94//Hs.7016:AA215796
R-NT2RP3002484//Human APRT gene for adenosine phosphoribosyltransferase//0.54:108.71//Hs.28914:Y00486	R-NT2RP3003203//EST//0.0073:212.63//Hs.161355:A1422634
R-NT2RP3002501//ESTs//2.7e-96:489.95//Hs.27335:W74185	R-NT2RP3003204//ESTs//7.4e-52:253.99//Hs.120146:AA708573
R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME 11 [C.elegans]//3.2e-90:526.90//Hs.8083:AA521436	R-NT2RP3003212//ESTs//1.8e-76:401.95//Hs.29067:W26107
R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN CG11.03C [Schizosaccharomyces pombe]//3.8e-101:497.96//Hs.6650:AA843246	R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:229.93//Hs.17377:A1078151
R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438.94//Hs.19542:AB018272	R-NT2RP3003242//ESTs//8.3e-97:458.99//Hs.23057:A1290343
R-NT2RP3002549//ESTs//3.8e-98:493.96//Hs.7358:AA191673	R-NT2RP3003251//ESTs//1.5e-60:320.95//Hs.36495:AA151628
R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNM3) mRNA, complete cds//0.14:184.63//Hs.89230:AF031815	R-NT2RP3003264//ESTs//2.1e-103:521.95//Hs.4094:AA173960
R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138.78//Hs.129883:AB007880	R-NT2RP3003278//ESTs//8.2e-109:536.96//Hs.23788:AA524061
R-NT2RP3002590//ESTs//2.9e-51:290.93//Hs.162942:A1243850	R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550.93//Hs.11702:L36983
R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673	R-NT2RP3003290//EST//4.3e-27:372.70//Hs.159131:A1384035
R-NT2RP3002603	R-NT2RP3003301//ESTs//4.4e-56:285.97//Hs.95370:AA601055
R-NT2RP3002631//ESTs//4.8e-54:367.85//Hs.13109:AA192514	R-NT2RP3003302//EST//7.2e-10:395.63//Hs.162554:AA584818
R-NT2RP3002659//ESTs//5.3e-30:229.85//Hs.152114:AA401365	R-NT2RP3003311//ESTs//4.2e-110:538.97//Hs.62180:A1341261
R-NT2RP3002660//ESTs//1.9e-88:452.95//Hs.120146:AA708573	R-NT2RP3003313//ESTs//2.1e-106:531.96//Hs.22630:C05931
R-NT2RP3002663//EST//3.2e-89:469.95//Hs.105767:AA525172	R-NT2RP3003327//ESTs//4.3e-102:518.95//Hs.120355:AA625445
R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109:537.97//Hs.19348:AA151678	R-NT2RP3003330//ESTs//8.6e-104:497.97//Hs.72071:A125289
R-NT2RP3002682//ESTs//2.3e-98:541.91//Hs.75844:AA115502	R-NT2RP3003344//ESTs//2.5e-105:494.99//Hs.112188:AA872993
R-NT2RP3002687//ESTs//5.5e-103:498.97//Hs.72782:AA910871	R-NT2RP3003346//ESTs//1.0:123.69//Hs.116029:AA813102
R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARMING ENTRY !!!! [H.sapiens]//5.0e-101:524.95//Hs.32580:A1123601	R-NT2RP3003353//EST//0.0014:162.68//Hs.149191:A1246155
R-NT2RP3002701//EST//0.87:131.63//Hs.161916:AA483169	R-NT2RP3003377//EST//4.5e-15:119.85//Hs.148129:AA885567
R-NT2RP3002713//ESTs//4.7e-106:542.95//Hs.14479:AA160945	R-NT2RP3003384//EST//0.0057:86.74//Hs.127735:AA962272
R-NT2RP3002763//ESTs//1.3e-54:290.94//Hs.142031:AA809159	R-NT2RP3003385//ESTs//0.64:347.59//Hs.5646:W72721
R-NT2RP3002770//ESTs//0.047:275.61//Hs.122984:AA526973	R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418.67//Hs.139488:A1124095
R-NT2RP3002785//ESTs//2.4e-52:255.99//Hs.132959:A1376958	R-NT2RP3003409//ESTs//5.3e-98:479.97//Hs.155198:AA767372
R-NT2RP3002799//EST//8.2e-61:321.94//Hs.140992:R71377	R-NT2RP3003411//ESTs//4.8e-86:416.97//Hs.129059:AA126041
R-NT2RP3002810//EST//0.19:116.68//Hs.121810:AA775240	R-NT2RP3003427//ESTs//7.4e-103:510.96//Hs.25303:AA641023
R-NT2RP3002818//ESTs//1.3e-109:531.98//Hs.58924:A1348080	R-NT2RP3003433//ESTs//3.5e-85:405.99//Hs.63131:AA664156
R-NT2RP3002861//ESTs//2.5e-84:429.95//Hs.23920:AA909678	R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479.96//Hs.14934:AF004828
R-NT2RP3002869//EST//0.00011:116.71//Hs.161606:AA019641	R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527.93//Hs.26450:AB018268
R-NT2RP3002876//ESTs//0.0024:182.63//Hs.117306:AA687262	R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549.94//Hs.7886:A1057529
R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146.72//Hs.129727:AF035587	R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401.60//Hs.75307:U02556
R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570.95//Hs.6162:AB018314	R-NT2RP3003543//Human clone A9A2BR87 (CAC)n/(GTC)n repeat-containing mRNA//4.1e-33:217.88//Hs.8068:U00952
R-NT2RP3002911//ESTs//3.6e-92:436.99//Hs.143917:A1206286	R-NT2RP3003552//ESTs//3.1e-106:546.94//Hs.101754:A1123430
R-NT2RP3002948//EST//1.0:102.65//Hs.144730:A1191975	R-NT2RP3003555//ESTs//3.4e-106:537.95//Hs.85550:AA187681
R-NT2RP3002953//ESTs//1.8e-107:513.98//Hs.119693:A1201698	R-NT2RP3003564
R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563.56//Hs.127338:AB007961	R-NT2RP3003572//ESTs//1.2e-20:122.88//Hs.8253:N48721
R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID-COA LIGASE 1 [Saccharomyces cerevisiae]//2.0e-56:387.86//Hs.144597:W2	R-NT2RP3003576//ESTs//2.7e-71:394.94//Hs.151136:R99944
	R-NT2RP3003589//EST//0.58:242.59//Hs.130804:AA894759
	R-NT2RP3003625//ESTs//7.6e-41:349.80//Hs.140608:N53448
	R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222.60//Hs.17217:U49957
	R-NT2RP3003659//ESTs//2.0e-113:547.97//Hs.23389:AA769310
	R-NT2RP3003665//ESTs//1.6e-80:415.95//Hs.141084:H11714
	R-NT2RP3003672
	R-NT2RP3003686//ESTs//6.8e-114:552.97//Hs.43299:W23036
	R-NT2RP3003701//ESTs//2.1e-16:282.66//Hs.115512:A1208768
	R-NT2RP3003716//ESTs//2.1e-45:195.91//Hs.41296:W71923
	R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete c

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【表623】

ds//5.6e-103:492:97//Hs.48513:AB018300  
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863  
 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747  
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:HI8913  
 R-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754  
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446  
 R-NT2RP3003809//ESTs. Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:AI285198  
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:W57627  
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761  
 R-NT2RP3003828//ESTs. Weakly similar to unknown [H.sapiens]//9.6e-98:511:95//Hs.26955:AI333224  
 R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743  
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611  
 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888  
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962  
 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298  
 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:W40170  
 R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726  
 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933  
 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:HS0221  
 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409  
 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19583  
 R-NT2RP3004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142  
 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714  
 R-NT2RP3004041  
 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820  
 R-NT2RP3004070//EST//5.5e-108:552:95//Hs.23392:AI310139  
 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W45387  
 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104  
 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045  
 R-NT2RP3004110//ESTs. Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402:95//Hs.55847:W31092  
 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:CD1696  
 R-NT2RP3004145//EST//2.6e-96:451:99//Hs.59584:AA587334  
 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425  
 R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093  
 R-NT2RP3004206//ESTs. Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200:100//Hs.26089:AA195126  
 R-NT2RP3004207//ESTs. Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:89//Hs.6314:AA522619  
 R-NT2RP3004209//ESTs. Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:AI346680  
 R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:W64794  
 R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:W46252  
 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827  
 R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628  
 R-NT2RP3004258//ESTs. Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:468:95//Hs.5117:AA831530  
 R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:W78723  
 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630  
 R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264  
 R-NT2RP3004348//Homo sapiens LIM protein mRNA. complete cds//5.9e-61:299:85//Hs.154103:AF061258  
 R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223  
 R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044  
 R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224  
 R-NT2RP3004424//EST. Highly similar to F21G4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934  
 R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985  
 R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621  
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein. complete cds//9.3e-108:526:98//Hs.27349:AB007917  
 R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616  
 R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332  
 R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406  
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein. partial cds//5.0e-107:521:97//Hs.5003:AB007925  
 R-NT2RP3004480  
 R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:W42504  
 R-NT2RP3004498//ESTs. Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.47393:AA218858  
 R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735  
 R-NT2RP3004504//ESTs. Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//1.8e-83:465:92//Hs.137064:AA318257

R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971  
 R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865  
 R-NT2RP3004534  
 R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232  
 R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461  
 R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674  
 R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493  
 R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456  
 R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213  
 R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157  
 R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723  
 R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST). complete cds//7.2e-57:291:95//Hs.8786:AB014680  
 R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335  
 R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560  
 R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219  
 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA. complete cds//6.7e-60:289:82//Hs.51233:AF016266  
 R-NT2RP4000051//ESTs. Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:AI345945  
 R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030  
 R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287  
 R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538  
 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein. partial cds//3.5e-112:554:97//Hs.64691:AB007952  
 R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014  
 R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294  
 R-NT2RP4000151//ESTs. Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436  
 R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295  
 R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:W66569  
 R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257  
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein. partial cds//1.5e-100:505:96//Hs.13999:AB014600  
 R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788  
 R-NT2RP4000214//Human mRNA for KIAA0392 gene. partial cds//6.2e-43:272:90//Hs.40100:AB002390  
 R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185  
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354:96//Hs.155481:AJ006470  
 R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757  
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA. complete sequence//9.3e-79:379:99//Hs.43728:AF091092  
 R-NT2RP4000263  
 R-NT2RP4000290//ESTs. Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//4.7e-104:525:96//Hs.152069:AA548972  
 R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631  
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524  
 R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760  
 R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390  
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein. complete cds//7.6e-111:520:99//Hs.107479:AB018281  
 R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA. complete cds//2.8e-110:527:98//Hs.31323:AF044195  
 R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130  
 R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498  
 R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376  
 R-NT2RP4000415//ESTs. Weakly similar to coded for by C. elegans CDNA yk30b.5 [C.elegans]//3.9e-87:499:91//Hs.26156:AA630975  
 R-NT2RP4000417//ESTs. Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPSTA-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-95:468:96//Hs.93871:AI191318  
 R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011  
 R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955  
 R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953  
 R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA. complete cds//0.35:153:63//Hs.113286:U77783  
 R-NT2RP4000457//ESTs//4.5e-89:455:96//Hs.62638:AA127740  
 R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167  
 R-NT2RP4000481  
 R-NT2RP4000500//ESTs. Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R0503.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:AI424792

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【表624】

R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713	R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514
R-NT2RP4000517//Aldehyde dehydrogenase 7//T.5e-28:183:76//Hs.8315	R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495
5:U10868	R-NT2RP4001213//ESTs. Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//4.4e-123:624:95//Hs.22744:AI379892
R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874	R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750
R-NT2RP4000519	R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103
R-NT2RP4000524//ESTs. Highly similar to rsec8 [R.norvegicus]//3.4e-93:496:93//Hs.107394:M07126	R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120
R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213	R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255
R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328	R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430
R-NT2RP4000556//ESTs. Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//8.2e-92:448:98//Hs.25597:H93026	R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933
R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840	R-NT2RP4001276//ESTs//2.9e-34:213:91//Hs.43100:AA186588
R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263	R-NT2RP4001313
R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531	R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892
R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393	R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612
R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704	R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732
R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651	R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837
R-NT2RP4000724//ESTs//1.5e-83:442:94//Hs.142114:AA205615	R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616
R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399	R-NT2RP4001372
R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211	R-NT2RP4001373//ESTs. Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]//1.7e-108:546:96//Hs.32271:AA203680
R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312	R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299
R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:94//Hs.25132:AB007939	R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501
R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA288834	R-NT2RP4001389//ESTs. Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAPI-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.8e-79:438:93//Hs.21938:W81045
R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028	R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132
R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104	R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649
R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356	R-NT2RP4001433//ESTs. Moderately similar to PROHIBITIN [H.sapiens]//1.6e-102:498:97//Hs.62386:AA512948
R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185	R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339433
R-NT2RP4000879//ESTs//1.8e-42:211:95//Hs.89991:AI374617	R-NT2RP4001447
R-nnnnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594	R-NT2RP4001474
R-nnnnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI277106	R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655
R-NT2RP4000925//ESTs. Weakly similar to KIAA0405 [H.sapiens]//5.9e-17:134:85//Hs.14146:W92235	R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846
R-NT2RP4000927//ESTs//4.3e-14:84:100//Hs.155360:AA984683	R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511
R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95//Hs.24812:AF069532	R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385
R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905	R-NT2RP4001524//ESTs. Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:AI377863
R-NT2RP4000955//ESTs//3.5e-10:119:78//Hs.42946:N21111	R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292
R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986	R-NT2RP4001547//ESTs. Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928
R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179	R-NT2RP4001551//ESTs. Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:88//Hs.136189:AA133224
R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017	R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552
R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98//Hs.12457:AF052123	R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285
R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018	R-NT2RP4001568//ESTs//8.4e-55:300:94//Hs.57442:N63437
R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620	R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251
R-NT2RP4000997//Homo sapiens neuronal thread protein ADTC-NTP mRNA, complete cds//1.1e-28:439:68//Hs.129735:AF010144	R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906
R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769	R-NT2RP4001575
R-NT2RP4001006//ESTs. Moderately similar to ORF2: function unknown [H.sapiens]//6.6e-124:574:99//Hs.47393:AA218858	R-NT2RP4001592//ESTs. Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//8.7e-112:557:97//Hs.7558:AA526812
R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI418635	R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776
R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI336292	R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657
R-NT2RP4001041//ESTs. Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//3.6e-114:569:96//Hs.6762:AA088424	R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737
R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94//Hs.100955:AB007859	R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:AF007151
R-NT2RP4001064//ESTs. Weakly similar to protein B [H.sapiens]//2.1e-103:485:99//Hs.10114:AI345945	R-NT2RP4001644//ESTs. Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361
R-NT2RP4001078	R-NT2RP4001656//ESTs. Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734
R-NT2RP4001079//Homo sapiens mRNA for putative Ca2+-transporting ATPase, partial//1.7e-119:569:98//Hs.106778:AJ010953	R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805
R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668	R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.15562:U96629
R-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164	R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:W25941
R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:AI344055	R-NT2RP4001730//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:AI141922
R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617	R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692
R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:723737	R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:W78926
R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357	R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315
R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476	R-NT2RP4001790//ESTs. Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:W28098
R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890	R-NT2RP4001803
R-NT2RP4001143//ESTs. Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAPI55-WMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//5.4e-113:573:96//Hs.5249:U55977	R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133
R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453	R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434
R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:HI6171	R-NT2RP4001828//EST//3.3e-101:536:92//Hs.18851:AA857826
R-NT2RP4001150//ESTs//1.9e-90:422:100//Hs.125490:AI138884	
R-NT2RP4001159	
R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278	
R-NT2RP4001206//ESTs//1.1e-25:140:97//Hs.83756:AI002822	

【表625】

R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663  
 R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210  
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-3  
 4:212:88//Hs.154326:D42087  
 R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602  
 R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:A1345528  
 R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:A1018606  
 R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:A1417099  
 R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848  
 R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436  
 R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:A1341793  
 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//  
 Hs.73919:X81637  
 R-NT2RP4001966//ESTs. Weakly similar to tenascin-like protein [D.m  
 elanogaster]//8.3e-87:457:94//Hs.41793:AA775879  
 R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252  
 R-NT2RP4002018  
 R-NT2RP4002047//ESTs. Highly similar to GTP-BINDING PROTEIN LEPA  
 [Pseudomonas fluorescens]//4.7e-09:90:86//Hs.41127:AA555184  
 R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738  
 R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106  
 R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679  
 R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:A1284198  
 R-NT2RP4002078//ESTs. Highly similar to ZINC FINGER PROTEIN 35 [H  
 omo sapiens]//1.6e-61:464:82//Hs.144228:N99507  
 R-NT2RP4002081//ESTs. Weakly similar to HYPOTHETICAL 139.1 KD PROT  
 EIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.618  
 5:AA428565  
 R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407  
 R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592  
 R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555  
 R-NT2RP4002888//ESTs. Highly similar to ENV POLYPROTEIN [Avian sp  
 leen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272  
 R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090  
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cd  
 s//2.8e-115:605:94//Hs.108258:AB007934  
 R-OVARC1000004  
 R-OVARC1000006//ESTs//1.5e-119:139:89//Hs.143034:A1126929  
 R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635  
 R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273  
 R-OVARC1000017  
 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:A1078286  
 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//  
 3.8e-46:331:83//Hs.96247:X95073  
 R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041  
 R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367  
 R-OVARC1000071//ESTs//2.5e-60:321:96//Hs.25010:R67871  
 R-OVARC1000085//Proteasome component CS//8.6e-67:366:92//Hs.75748:  
 AL031259  
 R-OVARC1000087//ESTs//1.0e-111:526:98//Hs.129020:A1380703  
 R-OVARC1000091//ESTs. Weakly similar to HOST CELL FACTOR C1 [H.sap  
 iens]//3.9e-112:596:94//Hs.20597:W58370  
 R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:A1289942  
 R-OVARC1000106  
 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein  
 (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250  
 R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7  
 e-45:489:74//Hs.101238:Y11312  
 R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482  
 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:A133214  
 R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090  
 R-OVARC1000151  
 R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023  
 R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629  
 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-  
 44:339:81//Hs.154103:AF061258  
 R-OVARC1000209//ESTs. Moderately similar to ZINC FINGER PROTEIN 93  
 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864  
 R-OVARC1000212//EST//0.20:178:61//Hs.133031:A1049874  
 R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958  
 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:A123130  
 R-OVARC1000288//ESTs. Highly similar to HYPOTHETICAL 54.2 KD PROT  
 EIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.  
 3e-74:403:93//Hs.108117:A1097079  
 R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476  
 R-OVARC1000304//ESTs. Highly similar to PUTATIVE GTP-BINDING PROT  
 EIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:A1027777  
 R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449  
 R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743  
 R-OVARC1000326//ESTs. Moderately similar to lamina associated poly

peptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:A1377682  
 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:A1050863  
 R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672  
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423  
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928  
 R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219  
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-  
 27:211:79//Hs.108287:L27670  
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237  
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034  
 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:A1123426  
 R-OVARC1000437  
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:A1018671  
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1)  
 mRNA, complete cds//4.3e-45:320:84//Hs.73614:U83460  
 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete c  
 ds//3.6e-79:418:94//Hs.12334:AB014583  
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582  
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA475756  
 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:A1421211  
 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926  
 R-OVARC1000479//ESTs. Highly similar to TIP120 [R.norvegicus]//1.1  
 e-102:514:96//Hs.11833:A1299947  
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983  
 R-OVARC1000496  
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484  
 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:  
 87//Hs.155464:AF088219  
 R-OVARC1000533//ESTs. Moderately similar to integrase [H.sapiens]/  
 /8.5e-48:264:92//Hs.49860:AA702248  
 R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021  
 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:20  
 2:85//Hs.90859:X85106  
 R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:A1244285  
 R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:A1141587  
 R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627  
 R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:  
 84//Hs.155464:AF088219  
 R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053  
 R-OVARC1000605  
 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcrip  
 t KIAA0501//6.4e-47:417:77//Hs.159897:AB007970  
 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//  
 1.9e-28:366:72//Hs.96247:X95073  
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete c  
 ds//5.1e-31:162:100//Hs.111862:AB011162  
 R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480  
 R-OVARC1000679//ESTs//0.94:416:59//Hs.130754:AA279522  
 R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:A1032875  
 R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//  
 0.053:160:64//Hs.108447:AJ000517  
 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:  
 141:73//Hs.32511:AB007901  
 R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461  
 R-OVARC1000730//ESTs. Weakly similar to C27F2.7 gene product [C.el  
 egans]//1.7e-17:137:86//Hs.7049:A1141736  
 R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918  
 R-OVARC1000769//ESTs. Weakly similar to eukaryotic initiation fact  
 or eIF-2 alpha kinase [D.melanogaster]//4.6e-28:430:69//Hs.42457:A  
 A523306  
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016  
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793  
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659  
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-1  
 9:119:95//Hs.3069:L11066  
 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:A1419764  
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CA  
 LC//1.2e-106:536:95//Hs.61628:Y17711  
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87/  
 Hs.73919:X81637  
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:57  
 9:96//Hs.18910:AF045584  
 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096  
 R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:A1150674  
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:A1336292  
 R-OVARC1000885//ESTs. Highly similar to HYPOTHETICAL OXIDOREDUCTA  
 SE IN ROCC-PTA INTERGENIC REGION [Bacillus subtilis]//7.9e-98:525:  
 93//Hs.10366:W21953  
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777  
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401

【表626】

R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350	R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.1186
R-OVARC1000912	90:X67247
R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814	R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216
R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127	R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.33
R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696	37:M90657
R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215	R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844
R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794	R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777
R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971	R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415
R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219	R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete c
R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:3	ds//1.1e-53:344:72//Hs.153468:AB011147
48:80//Hs.43681:AL022394	R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958
R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909	R-OVARC1001391
R-OVARC1000984//ESTs. Weakly similar to No definition line found	R-OVARC1001399//ESTs//0.0039:48:95//Hs.117964:W20913
[C.elegans]//3.5e-68:346:96//Hs.25544:AA532784	R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:56
R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811	1:95//Hs.21586:AB006651
R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:5	R-OVARC1001419
13:73//Hs.127649:AB007874	R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136
R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:M53448	R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427
R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3'	R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345
end//1.7e-28:181:77//Hs.139107:X00629	R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592
R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270	R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700
R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117	R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694
R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630	R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089
R-OVARC1001034//Homo sapiens apoptotic protease activating factor	R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, co
1 (Apat-1) mRNA, complete cds//2.1e-09:137:74//Hs.77579:AF013263	mplete cds//3.0e-117:585:96//Hs.6534:AF016507
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1	R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:
e-101:501:96//Hs.9899:AF099149	90//Hs.155464:AF088219
R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046	R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539
R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:W94384	R-OVARC1001542//Homo sapiens NJTB mRNA, complete cds//1.6e-111:56
R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.1081	6:95//Hs.6396:AB016492
24:Z12962	R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388
R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231	R-OVARC1001577//Homo sapiens SRP46 splicing factor retropseudogene
R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:W98652	mRNA//4.4e-20:150:89//Hs.155160:AF031166
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, p	R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//6.8e-2
artial cds//7.3e-97:463:98//Hs.3426:AF082657	1:282:72//Hs.154326:D42087
R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844	R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:W32019
R-OVARC1001074	R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965
R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:9	R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:1
4:69//Hs.103126:U57029	14:78//Hs.5158:AB007869
R-OVARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (c	R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659
lone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q	R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854
7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897	R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080
R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete c	R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784
ds//3.3e-75:386:95//Hs.26584:AF051782	R-OVARC1001726//ESTs. Highly similar to APICAL PROTEIN [Xenopus l
R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, co	aevis]//1.2e-27:236:81//Hs.15485:AA046954
mplete cds//3.9e-37:283:84//Hs.46468:U45984	R-OVARC1001731//Tropomyosin 4 (fibroblast)//7.9e-74:422:90//Hs.102
R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548	824:X05276
R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312	R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.
R-OVARC1001161//ESTs. Moderately similar to !!!! ALU SUBFAMILY SX	4)//1.7e-62:300:83//Hs.144563:AF057280
WARNING ENTRY !!!! [H.sapiens]//2.2e-66:346:95//Hs.53263:AA173226	R-OVARC1001762//ESTs. Weakly similar to N-TERMINAL ACETYLTRANSFERA
R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223	SE 1 [S.cerevisiae]//6.8e-100:540:92//Hs.117741:AA903456
R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727	R-OVARC1001766//Homo sapiens eukaryotic translation initiation fac
R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200	tor eIF3, p35 subunit mRNA, complete cds//1.1e-109:567:94//Hs.1553
R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:	77:U97670
84//Hs.155464:AF088219	R-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete c
R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223	ds//2.0e-109:529:97//Hs.15869:AB014575
R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC)	R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127
mRNA, complete cds//6.6e-64:247:80//Hs.97203:U83171	R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604
R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343	R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978
R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826	R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:2
R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025	76:81//Hs.153563:AF011333
R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668	R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688
R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361	R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831
R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166	R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cd
R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929	s//2.1e-15:519:63//Hs.25639:AB011110
R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708	R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705
R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532	R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621
R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113	R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160
R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885	R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809
R-OVARC1001306//Homo sapiens mRNA for KIAA0518 protein, partial cd	R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence/
s//3.8e-70:334:100//Hs.23763:AB011090	/1.9e-105:571:91//Hs.25300:AF070611
R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83/	R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476
/Hs.73919:X81637	R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete c
R-OVARC1001330//Proline arginine-rich end leucine-rich repeat prot	ds//2.2e-49:302:90//Hs.153468:AB011147
ein//1.0:147:63//Hs.76494:U41344	R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310
R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:	R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56
76//Hs.155464:AF088219	homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF0617
R-OVARC1001341//ESTs. Moderately similar to !!!! ALU SUBFAMILY SQ	49
WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356	R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435
	R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855

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R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842	R-PLACE1000562//ESTs. Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN INXRI-TFAI INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-26:220:81//Hs.163791:W25348
R-OVARC1001928	R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:A1380485
R-OVARC1001942//ESTs. Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S. cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456	R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353
R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637	R-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:W55542
R-OVARC1001949//ESTs. Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:A1379892	R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030
R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:A1032875	R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087
R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:A1183729	R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301
R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887	R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308
R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531	R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265
R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934	R-PLACE1000656//Homo sapiens mRNA for JMA protein, complete CDS (clone IMAGE 546750 and LLNLcl10F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896
R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315	R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353
R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860	R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485
R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:A1347130	R-PLACE1000716
R-OVARC1002138//ESTs. Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN IN C07A9.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691	R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701
R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825	R-PLACE1000749//EST//0.019:186:61//Hs.135443:A1077396
R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923	R-PLACE1000755//ESTs. Weakly similar to HYPOTHETICAL HELICASE K12H.48 IN CHROMOSOME III [C. elegans]//3.9e-40:224:94//Hs.87889:AA262008
R-OVARC1002158//ESTs//7.7e-81:412:96//Hs.12211:AA908631	R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536
R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160	R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548
R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478	R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482
R-PLACE1000004//ESTs. Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337	R-PLACE1000793//H. sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219
R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920	R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189
R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557	R-PLACE1000841//ESTs. Highly similar to guanine nucleotide regulatory protein [H. sapiens]//7.7e-31:220:86//Hs.117576:R33135
R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223	R-PLACE1000849//ESTs//1.8e-87:459:94//Hs.43100:AA186588
R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870	R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:A1275039
R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:A1310440	R-PLACE1000863//ESTs. Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118:A1141558
R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503	R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:A1392846
R-PLACE1000050//ESTs//9.7e-90:453:96//Hs.27410:N25612	R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:A1097091
R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499	R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697
R-PLACE1000066//ESTs. Weakly similar to coded for by C. elegans C01NA yk10c10.3 [C. elegans]//1.4e-61:331:94//Hs.30026:A1356771	R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:A1002941
R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659	R-PLACE1000977//EST//0.085:153:65//Hs.131646:A1025689
R-PLACE1000081	R-PLACE1000979
R-PLACE1000094	R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725
R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505	R-PLACE1001007//ESTs. Moderately similar to MNK1 [H. sapiens]//5.2e-63:343:93//Hs.5662:AA868361
R-PLACE1000142//ESTs. Weakly similar to enoyl-CoA hydratase [H. sapiens]//5.5e-103:538:94//Hs.9870:AA632135	R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146
R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.151017:AF058291	R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878
R-PLACE1000185//ESTs. Weakly similar to No definition line found [C. elegans]//2.0e-19:114:95//Hs.7036:W22072	R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736
R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:A1262946	R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:A1025762
R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916	R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120
R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U17077	R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124
R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545	R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580
R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912	R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141
R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940	R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268
R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424	R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610
R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:A1423126	R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594
R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:A1334994	R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834
R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708	R-PLACE1001171//ESTs. Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H. sapiens]//0.91:77:71//Hs.115211:AA287527
R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959	R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297
R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089	R-PLACE1001238//ESTs. Moderately similar to RNA polymerase I associated factor [M. musculus]//1.9e-99:512:94//Hs.24884:AA176812
R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799	R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:A1073464
R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125	R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131
R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131	R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371
R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF023456	R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780
R-PLACE1000444//ESTs. Moderately similar to platelet glycoprotein IIb precursor [H. sapiens]//2.0e-58:410:81//Hs.97579:AA398118	R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:A1334460
R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793	R-PLACE1001294//ESTs. Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M. musculus]//2.7e-22:181:84//Hs.48320:AA149548
R-PLACE1000481//ESTs. Weakly similar to Ndr protein kinase [H. sapiens]//3.2e-109:549:95//Hs.19074:U69566	R-PLACE1001304//ESTs. Weakly similar to ZINC FINGER PROTEIN 135 [H. sapiens]//4.2e-34:195:92//Hs.86276:W27601
R-PLACE1000492//ESTs. Highly similar to vacuolar protein sorting homolog r-vps33b [R. norvegicus]//3.5e-83:435:94//Hs.26510:AA700425	R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:A1339056
R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729	R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA
R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88//Hs.153026:AB014540	

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【表628】

NA, complete cds//5.5e-44:215:86//Hs.50984:UD1160  
R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:A1097077  
R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219  
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615  
R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030  
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419  
R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:A1298280  
R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555  
R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348  
R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:AF091087  
R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800  
R-PLACE1001440  
R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115  
R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:A1017547  
R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:A1248625  
R-PLACE1001502//ESTs//8.1e-31:161:98//Hs.126264:AA455617  
R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361  
R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969  
R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:A1042153  
R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265  
R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431  
R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249  
R-PLACE1001602//EST//0.33:297:57//Hs.149839:A1287601  
R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904  
R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608583  
R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174  
R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.114547:AA167095  
R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:A1168526  
R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640  
R-PLACE1001672//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804  
R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250  
R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124  
R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:A1374903  
R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667  
R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993  
R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171  
R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113  
R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266  
R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479  
R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:A1423937  
R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243  
R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662  
R-PLACE1001761  
R-PLACE1001771//ESTs//0.92:165:62//Hs.47387:N51980  
R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236  
R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352  
R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//1.3e-93:463:95//Hs.40820:AF058953  
R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219  
R-PLACE1001845  
R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868  
R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009  
R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098  
R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936  
R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:AB014523  
R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313  
R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941  
R-PLACE1002046  
R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595  
R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094  
R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619  
R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:A1028552  
R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632  
R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311  
R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293  
R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937  
R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:A1167614  
R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189  
R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:A1185965  
R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745  
R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793  
R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788  
R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892  
R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:A1004257  
R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frame s//5.8e-67:501:81//Hs.23094:W19503  
R-PLACE1002319//ESTs//1.4e-28:178:92//Hs.7353:AA209308  
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271  
R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291  
R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381  
R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959  
R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110  
R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804  
R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333  
R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320  
R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263  
R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132  
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2 A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273  
R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429  
R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869  
R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:A1140609  
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256  
R-PLACE1002532//Homo sapiens BAC clone RC300E22 from Tq21-q31.1//2.7e-19:116:93//Hs.99348:AC004774  
R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491  
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437  
R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131  
R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:A1339738  
R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778  
R-PLACE1002598//ESTs, Highly similar to PROTEIN H11715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208  
R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147  
R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749  
R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130  
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180  
R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830  
R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586  
R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865  
R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:A1334099  
R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:A1149014  
R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593  
R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA465955  
R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:A1304392  
R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916  
R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094  
R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142  
R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:A1096756  
R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539  
R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:A1066762  
R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:A1249332  
R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995  
R-PLACE1002962  
R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202  
R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941  
R-PLACE1002993//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268  
R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:A1144268  
R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:A1151499  
R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:15

【表629】

6:60//Hs.82042:D87075	R-PLACE1003768//Human PO42 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965
R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840	R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798
R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777	R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757
R-PLACE1003100//ESTs, Highly similar to MODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:367//Hs.6318:AI131178	R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909
R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359	R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:AB011147
R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920	R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092
R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757	R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059
R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467	R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058
R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924	R-PLACE1003864
R-PLACE1003176	R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871
R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453	R-PLACE1003885
R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017	R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595
R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802	R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915
R-PLACE1003238//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123	R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259
R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460	R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:AA100804
R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131	R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760
R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326	R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236
R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986	R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110
R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993	R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567
R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:97//Hs.155050:AA908765	R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330
R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438	R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231
R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701	R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715	R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770
R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636	R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244
R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234	R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:HI1714
R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591	R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080
R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941	R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601
R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909	R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11 (COX11) mRNA, complete cds//4.7e-78:434:91//Hs.153504:AF044321
R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755	R-PLACE1004197
R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020	R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.5e-105:501:98//Hs.24640:AF069493
R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840	R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952
R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697	R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630
R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671	R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209
R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270	R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.11729:J00124
R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952	R-PLACE1004270//ESTs//0.011:264:59//Hs.110044:AA181800
R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505	R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:121:66//Hs.1938:S82362
R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980	R-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//1.4e-107:581:91//Hs.127007:AF084830
R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461	R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114
R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.110439:N93209	R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:279:77//Hs.38687:AA744496
R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321	R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.71435:AI253099
R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591	R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588
R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956	R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:77//Hs.1361:MS5053
R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:R86178	R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:379:93//Hs.16232:AF100153
R-PLACE1003584	R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309
R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542	R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556
R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AI377106	R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-98:572:90//Hs.14202:N46000
R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875	R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467
R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:O83200	R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:NS3665
R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299	R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101
R-PLACE1003611//ESTs//1.0:78:71//Hs.101248:T26446	R-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283
R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943	R-PLACE1004451
R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285	R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980
R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247	R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721
R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607	R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578
R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521	R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194
R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866	R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:278:61//Hs.89663:U13286
R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639	R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117
R-PLACE1003723//ESTs//1.7e-89:448:96//Hs.157222:AA766987	
R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087	
R-PLACE1003760//Human globin gene//1.9e-98:538:91//Hs.100090:M69023	
R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512	

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R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:A1420493	R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:A1201336
R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164	R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:U91985
R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553	R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225
R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.115325:DB4488	R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423
R-PLACE1004550	R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349
R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742	R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:A1089013
R-PLACE1004629//ESTs. Weakly similar to OS-9 precursor [H. sapiens]//8.1e-40:272:87//Hs.7100:W07181	R-PLACE1005176//ESTs//5.4e-75:366:97//Hs.48119:AA454227
R-PLACE1004645//ESTs//8.3e-14:83:100//Hs.17270:AA701903	R-PLACE1005181//EST//0.012:172:66//Hs.147107:A1190589
R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734	R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:A1022830
R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113	R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:HA5211
R-PLACE1004664//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.132129:AB018257	R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532
R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:A1144254	R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767
R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.8e-90:510:91//Hs.80019:AF035606	R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524
R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482	R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633
R-PLACE1004686	R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516
R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552	R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:A1251374	R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:A1197937
R-PLACE1004716//ESTs. Weakly similar to No definition line found [C. elegans]//3.4e-80:413:94//Hs.23528:A1279571	R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997	R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614
R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N63911	R-PLACE1005327//Chromosome I specific transcript KIAA0491//1.7e-10:4:537:94//Hs.136309:AB007960
R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619	R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:A1189343
R-PLACE1004743//EST//0.45:94:69//Hs.147174:A1192195	R-PLACE1005335//ESTs. Weakly similar to F23B2.4 [C. elegans]//3.8e-90:442:97//Hs.70202:AA732975
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:A1223374	R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901
R-PLACE1004773//Homo sapiens invertin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367	R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:3:44:80//Hs.43681:AL022394
R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548	R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619	R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304
R-PLACE1004804//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178	R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856	R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frame s//2.3e-88:561:86//Hs.23094:M19503
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250	R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607
R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356	R-PLACE1005480//EST//0.99:39:82//Hs.157275:A1364046
R-PLACE1004824//Protein kinase, interferon-inducible double strand ed RNA dependent//4.8e-46:450:76//Hs.73821:M35663	R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:A1032875
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185	R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220
R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299	R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:AF071185
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901	R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325
R-PLACE1004840//ESTs. Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]//6.5e-71:381:93//Hs.8383:AA013272	R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:AJ006470
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308	R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:A1291325
R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456	R-PLACE1005550//ESTs. Highly similar to HYPOTHETICAL 40.2 KD PROT EIM K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:45:8:98//Hs.38114:N62927
R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:A1281881	R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555
R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597	R-PLACE1005557//ESTs. Highly similar to MITOCHONDRIAL GDS RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261
R-PLACE1004913//ESTs//4.5e-75:375:96//Hs.91115:A1221563	R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835
R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:A124948	R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612
R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//5.6e-102:532:93//Hs.17839:AF099936	R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:A1276023
R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980	R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:A1026927
R-PLACE1004937//ESTs. Weakly similar to F55B12.3 [C. elegans]//6.4e-80:409:95//Hs.31945:AA702166	R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857
R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013	R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA089964
R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106	R-PLACE1005630
R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789	R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452
R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:A1291776	R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:AF083255
R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:A1420335	R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169
R-PLACE1005026	R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587
R-PLACE1005027//ESTs. Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R. norvegicus]//0.72:145:66//Hs.11215:N56719	R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355
R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:AB011147	R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332
R-PLACE1005052//ESTs. Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C. elegans]//1.2e-106:543:95//Hs.18625:A1074605	R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259
R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103	R-PLACE1005739//ESTs. Moderately similar to unknown intracellular protein [M. musculus]//1.3e-42:236:94//Hs.23889:A1341137
R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985	R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070
R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080	R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087
R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364	R-PLACE1005799//ESTs. Highly similar to HYPOTHETICAL 68.7 KD PROT EIM ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:8:98//Hs.109857:AA088385
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99:531:92//Hs.75437:L40401	R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941
	R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327
	R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:A1287693

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【表631】

R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058	R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053
R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58//Hs.75770:L41870	R-PLACE1006382
R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:A1050965	R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748
R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:A1203471	R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:A1281881
R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305	R-PLACE1006414//Homo sapiens LIM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258
R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:A1041842	R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:A1278629
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558	R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:A1339981	R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501	R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:A1341793	R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418
R-PLACE1005925//Human Line-1 repeat mRNA with 2' open reading frame s//2.8e-27:382:70//Hs.23094:M19503	R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722
R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361	R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:A1251374
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142	R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913	R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:A1183729	R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368
R-PLACE1005953	R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532
R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROT E1N IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.108117:A1097079	R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214
R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:A1016239	R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:A1128443
R-PLACE1005968//EST//0.26:103:66//Hs.161300:A1420897	R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//9.3e-118:590:95//Hs.155377:U97670
R-PLACE1005990	R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322
R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353	R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615
R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROT E1N IN APE1/LAP4-CWPI INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449:A1192946	R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384
R-PLACE1006011//ESTs, Moderately similar to MAD(+) ADP-RIBOSYLTRANSFERASE [D. melanogaster]//5.7e-100:596:88//Hs.24284:AA595596	R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522
R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:A1056276	R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627
R-PLACE1006037//ESTs, Weakly similar to T2308.3 [C. elegans]//4.1e-102:491:98//Hs.61164:A1096332	R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736
R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765	R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214
R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007:H74314	R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98//Hs.12472:AF038172
R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904	R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861
R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002	R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622
R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROT E1N IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249:U55977	R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658
R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.038:463:58//Hs.904:U84010	R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234
R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:A1357886	R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515
R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925	R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335
R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128	R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989
R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894:AC005239	R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847
R-PLACE1006170//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121:A1125280	R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433	R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPT ASE HOMOLOG [Homo sapiens]//1.0e-87:481:92//Hs.141263:H64113
R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:532:91//Hs.105216:A1361807	R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933
R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507	R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA828359
R-PLACE1006205//EST//1.7e-89:448:96//Hs.116665:AA669114	R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008
R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664	R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536
R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:A1079555	R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131
R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:A1341472	R-PLACE1006901//ESTs//3.0e-95:496:94//Hs.47546:AA181348
R-PLACE1006239//Homo sapiens BAC clone RG18D07 from Tg31//3.2e-99:497:95//Hs.3781:AC004142	R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089
R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M. musculus]//1.3e-104:532:95//Hs.41151:A1301961	R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548	R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:A1379514
R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321:62//Hs.53057:W67839	R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078
R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132	R-PLACE1006958//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956
R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265	R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520
R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:A1246503	R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:A1275982
R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900	R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:A1017636
R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168	R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257
R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044	R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366
R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:A1079284	R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971

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R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450  
 R-PLACE1007243//ESTs. Weakly similar to transporter protein [H.sapiens]//3.7e-73:357:98//Hs.18272:N78499  
 R-PLACE1007251//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909  
 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:A1275071  
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419  
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812  
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087  
 R-PLACE1007301  
 R-PLACE1007317  
 R-PLACE1007342  
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870  
 R-PLACE1007367//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488:96//Hs.24359:AA699594  
 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614  
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:A1129945  
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877  
 R-PLACE1007409//Homo sapiens mitoxanthrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771  
 R-PLACE1007416//ESTs. Weakly similar to OIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.72165:A1243857  
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171  
 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514  
 R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:A1028230  
 R-PLACE1007478  
 R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975  
 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533  
 R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072  
 R-PLACE1007511//ESTs. Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657  
 R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377  
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087  
 R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612  
 R-PLACE1007547//EST//0.00010:107:71//Hs.146867:A1161404  
 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:A1148840  
 R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257  
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:54:93//Hs.21838:AF038179  
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923  
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176  
 R-PLACE1007632  
 R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:A1344106  
 R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:A1262946  
 R-PLACE1007677//ESTs. Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//9.0e-37:190:97//Hs.23437:AA707331  
 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:A1376944  
 R-PLACE1007690//ESTs. Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]//3.4e-61:384:89//Hs.92918:AA133274  
 R-PLACE1007697//ESTs. Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs.91251:U66685  
 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407  
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812:AF061243  
 R-PLACE1007725//ESTs. Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797:AA476815  
 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619  
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121:AB014585  
 R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:M39322  
 R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778  
 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903  
 R-PLACE1007791//ESTs. Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//8.6e-27:143:98//Hs.144194:AA706337  
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M19503  
 R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:A1279044  
 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050  
 R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:A1308839  
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503

R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:MS2017  
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:AB018309  
 R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:HO1178  
 R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:A1207832  
 R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:A1189060  
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.92381:AB007956  
 R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510  
 R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:A1217966  
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.5671:AF084530  
 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:465:93//Hs.78106:AF079529  
 R-PLACE1007969//ESTs. Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900  
 R-PLACE1007990//ESTs. Highly similar to DOSAGE COMPENSATION REGULATORY [Drosophila melanogaster]//3.8e-97:493:95//Hs.6141:U69564  
 R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:A1206835  
 R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:A1263612  
 R-PLACE1008044//ESTs. Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]//2.0e-115:575:95//Hs.92395:AA779854  
 R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:MS1935  
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:A1054269  
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469  
 R-PLACE1008111//ESTs. Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:A1309334  
 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:A1028617  
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511  
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381  
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:A1028266  
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267  
 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107  
 R-PLACE1008201//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102  
 R-PLACE1008209//ESTs//1.2e-72:366:96//Hs.92308:A1052701  
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871  
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990  
 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808  
 R-PLACE1008275  
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:A1338705  
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852  
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog g/0.53:206:62//Hs.79070:K02276  
 R-PLACE1008330//ESTs. Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//Hs.146477:A1128445  
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656  
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579  
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:A1359052  
 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009  
 R-PLACE1008392//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-41:448:72//Hs.139007:H74314  
 R-PLACE1008398//ESTs. Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242  
 R-PLACE1008401//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:536:87//Hs.7570:W31010  
 R-PLACE1008402//Homo sapiens mRNA for p15, complete cds//5.1e-103:521:95//Hs.7763:D86326  
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440  
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:A1379778  
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757  
 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562  
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928  
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761  
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:A1289387  
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:A1299636  
 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180  
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:M62816  
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560  
 R-PLACE1008532  
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850  
 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:A1423223  
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:M50064  
 R-PLACE1008621//ESTs. Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:AA778649  
 R-PLACE1008625  
 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454  
 R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:A1004972  
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512

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R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612	R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872
R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353	R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.147967:AF044333	R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67 AI//1.3e-42:266:89//Hs.155049:AC004531
R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:U68830	R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925
R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:76//Hs.1361:M55053	R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596
R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600	R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698
R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303	R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131
R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408	R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:289:63//Hs.77579:AF013263
R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313	R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326
R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930	R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.sapiens]//0.0012:56:91//Hs.12151:AA001818
R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217	R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:AB014535
R-PLACE1008808//Homo sapiens putative checkpoint control protein H RAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905	R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735
R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA c10e3 [C.elegans]//4.2e-92:490:93//Hs.110454:HI1810	R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482
R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428	R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680
R-PLACE1008854	R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243338
R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502	R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858
R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:U64878	R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701
R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893	R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308	R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:AB011159
R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018	R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483:79//Hs.140416:AA778649
R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653	R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534
R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680	R-PLACE1009708//ESTs//3.0e-94:471:96//Hs.40091:M48582
R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573	R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529:92//Hs.3945:AA004210
R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419	R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489:89//Hs.26194:AA033989
R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112	R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024
R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520	R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:M20989
R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195	R-PLACE1009798//Human DNA sequence from clone 1189824 on chromosome Xq25-26.3. Contains MADH-Ubiquitin Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-113:549:97//Hs.16411:AL030996
R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008	R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056888
R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142	R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748
R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:M53448	R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328
R-PLACE1009094//Human splicing factor Srp30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546	R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031
R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136	R-PLACE1009908//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:AI219740
R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549	R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563
R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983	R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276
R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:AA703945	R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI304317
R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747	R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543
R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.93332:AA811920	R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074
R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005	R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:AI160540
R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322	R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698
R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948	R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347
R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707	R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219
R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717	R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:AI141736
R-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:Z78396	R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204
R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701	R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//7.6e-104:546:94//Hs.8215:AA521150
R-PLACE1009200//Hs.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248	R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905
R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680	R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.11183:AF065482
R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018	R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375
R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423	R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424
R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.108654:N91279	R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615
R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503	R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:U69567
R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397	R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015
R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782	R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103
R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760	R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270
R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AI61260	R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130
R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883	R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:
R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186	
R-PLACE1009404//ESTs//3.6e-94:452:98//Hs.103177:W72798	
R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255	
R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632	
R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269	

【0936】

【表634】

M90359	cds//8.9e-82:441:93//Hs.66392:AF064244
R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:AI139897	R-PLACE1010944
R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313	R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519
R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:TS8466	R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219
R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037	R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.0e-103:565:92//Hs.23259:AA532437
R-PLACE1010231	R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580
R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478	R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846
R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545	R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867
R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535	R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249
R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788	R-PLACE1011046//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153
R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081	R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135
R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568	R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219
R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219	R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ W ARNING ENTRY !!!! [H.sapiens]//9.9e-32:190:77//Hs.152369:AA504818	R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.6e-54:398:84//Hs.108740:W20094
R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327	R-PLACE1011099//EST//1.3e-40:321:85//Hs.146794:AI149478
R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594	R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA095587
R-PLACE1010383//Homo sapiens mRNA for putative lipoid acid synthetase, partial//4.9e-35:166:86//Hs.53531:AJ224162	R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//3.0e-105:552:93//Hs.31257:AA875998
R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152	R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795
R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816	R-PLACE1011160//Homo sapiens mRNA for HRHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:AF039081	R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673
R-PLACE1010492	R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B W ARNING ENTRY !!!! [H.sapiens]//3.4e-85:442:95//Hs.136910:AA810782
R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031	R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438
R-PLACE1010547//ESTs//3.4e-36:228:89//Hs.128724:AA215455	R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671
R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306	R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299
R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033	R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693
R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116	R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602
R-PLACE1010599	R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772
R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418	R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913
R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:M57895	R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849
R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475	R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807
R-PLACE1010628//ESTs, Weakly similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//6.4e-74:391:95//Hs.163495:W57637	R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291
R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805	R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578
R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719	R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102	R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:HI1376
R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN P BS13 [Mus musculus]//4.8e-83:467:91//Hs.22383:R51067	R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194
R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN C LUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794:AA701659	R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337
R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973	R-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102
R-PLACE1010714//Human organic anion transporting polypeptide (OAT P) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943	R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607
R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:95//Hs.50758:AF092564	R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887
R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189	R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255
R-PLACE1010743	R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278
R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250	R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294
R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024	R-PLACE1011520//ESTs//5.8e-99:477:97//Hs.85077:AA968576
R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN 1B [Acanthamoeba castellanii]//7.6e-111:575:94//Hs.10260:AI126627	R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421
R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558	R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985
R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:AI091203	R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672
R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896	R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548
R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472	R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067
R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048	R-PLACE1011641//ESTs//2.5e-71:338:100//Hs.153085:AA993965
R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917	R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900
R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090	R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182	R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036
R-PLACE1010891	R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838
R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983	R-PLACE1011675
R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023	R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025
R-PLACE1010916//Plasminogen activator inhibitor, type II (arginin e-serpin)//0.25:190:61//Hs.75716:Y00630	R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frame s//8.5e-57:410:83//Hs.23094:W19503
R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093	R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392
R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479	R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126	R-PLACE1011749//Myelin oligodendrocyte glycoprotein (alternative p roducts)//7.3e-40:361:77//Hs.53217:Z48051
R-PLACE1010942//Homo sapiens intersectin short form mRNA, complete	R-PLACE1011762//Human kni repeat mRNA (cdna clone pcd-kni-8), 3'

【表635】

end//3.0e-60:319:76//Hs.103948:K00627  
 R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080  
 R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179  
 R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563  
 R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067  
 R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648  
 R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913  
 R-PLACE1011895//ESTs//2.8e-23:176:84//Hs.121540:A1275497  
 R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268  
 R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617  
 R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:A1031969  
 R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H. sapiens]//2.6e-06:284:63//Hs.124102:AA701285  
 R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890  
 R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247  
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:AB018256  
 R-PLACE20000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069  
 R-PLACE20000007//ESTs//2.4e-110:564:95//Hs.65135:W89120  
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:AF091080  
 R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211  
 R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:A1049504  
 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:A1302868  
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.154069:U06452  
 R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013  
 R-PLACE2000039//H. sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073  
 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622  
 R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652  
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:AB011147  
 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390  
 R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:AF027219  
 R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179  
 R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:A1292236  
 R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941  
 R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds//0.00043:127:71//Hs.42400:AF022789  
 R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662  
 R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988  
 R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558  
 R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:AB011134  
 R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:A1052357  
 R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219  
 R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:A1379778  
 R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:A1360292  
 R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067  
 R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:A1382378  
 R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191  
 R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717  
 R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600  
 R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363  
 R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H. sapiens]//1.9e-87:422:98//Hs.9740:A1004779  
 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664  
 R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:A1344055  
 R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380  
 R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058  
 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789  
 R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:A1347618  
 R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848  
 R-PLACE2000366//Thromboxane A2 receptor//7.5e-53:392:82//Hs.89887:

D38081

R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731  
 R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277  
 R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781  
 R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814  
 R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189  
 R-PLACE2000399  
 R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA088424  
 R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:M25941  
 R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739  
 R-PLACE2000425//Homo sapiens DEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333  
 R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans CDNA CEES142F [C.elegans]//3.0e-113:543:97//Hs.16933:AA976002  
 R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523  
 R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986  
 R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:A1279887  
 R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390  
 R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714  
 R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638  
 R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228  
 R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642  
 R-PLACE2000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838  
 R-PLACE20000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:AB011147  
 R-PLACE2000059//EST//0.028:175:61//Hs.159873:R92763  
 R-PLACE2000070//ESTs//3.8e-16:200:74//Hs.138771:N70979  
 R-PLACE2000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830  
 R-PLACE2000119//ESTs//1.2e-45:330:83//Hs.35254:A1133727  
 R-PLACE2000124//EST//3.1e-75:391:96//Hs.161515:N71739  
 R-PLACE2000136//ESTs//8.3e-18:152:84//Hs.10043:D81792  
 R-PLACE2000142//ESTs//0.047:183:62//Hs.43102:AA131369  
 R-PLACE2000147//ESTs//6.6e-53:310:90//Hs.8230:W07142  
 R-PLACE2000148//EST//1.9e-16:184:76//Hs.146570:A1139815  
 R-PLACE2000155//ESTs//1.2e-19:192:79//Hs.131350:AA052233  
 R-PLACE2000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//Hs.31532:H18272  
 R-PLACE2000157  
 R-PLACE2000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219  
 R-PLACE2000160  
 R-PLACE2000169//ESTs//1.5e-64:329:97//Hs.129864:R20798  
 R-PLACE2000194  
 R-PLACE2000197//ESTs//1.4e-38:197:98//Hs.146341:A1269930  
 R-PLACE2000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.131370:AA927516  
 R-PLACE2000207//EST//1.3e-15:154:78//Hs.136617:AA630476  
 R-PLACE2000208//ESTs//1.6e-18:151:82//Hs.155498:W27084  
 R-PLACE2000218//ESTs//1.8e-85:463:93//Hs.7849:A129964  
 R-PLACE2000220//ESTs//6.4e-44:308:84//Hs.136839:H93717  
 R-PLACE2000226//ESTs//1.3e-49:269:95//Hs.9059:A1359014  
 R-PLACE2000230//EST//2.3e-34:258:83//Hs.4382:T02878  
 R-PLACE2000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811  
 R-PLACE2000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emmericella nidulans]//7.5e-110:549:95//Hs.13692:AA632002  
 R-PLACE2000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307  
 R-PLACE2000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:82//Hs.97203:U83171  
 R-PLACE2000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782  
 R-PLACE2000304//Human S3K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//4.0e-59:456:80//Hs.108966:U48696  
 R-PLACE2000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830  
 R-PLACE2000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627  
 R-PLACE2000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.114531:N74103  
 R-PLACE2000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:AB018315  
 R-PLACE2000339//ESTs//1.3e-109:548:96//Hs.7871:A1041837  
 R-PLACE2000341//EST//1.1e-11:231:68//Hs.131328:AA922688  
 R-PLACE2000350//Human mRNA for adipogenesis inhibitory factor//8.0



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e-40:291:76//Hs.1721:X58377	R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380	R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683	R-THYR01000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888	R-THYR01000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524
R-PLACE3000363	R-THYR01000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881	R-THYR01000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430	R-THYR01000070//ESTs//6.7e-43:283:86//Hs.37573:HS9651
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W	R-THYR01000072//ESTs//1.3e-57:313:96//Hs.127827:HI3438
ARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534	R-THYR01000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435
R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570	R-THYR01000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-4
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528	1:344:79//Hs.153014:AB002353
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230	R-THYR01000107//Interleukin 10//2.8e-43:292:84//Hs.2180:W57627
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:6	R-THYR01000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPT
2//Hs.142570:AF052160	ASE HOMOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359
R-PLACE3000405//Human HsLIM15, complete cds//5.3	R-THYR01000121//EST//0.24:78:74//Hs.156632:AI345108
e-43:315:82//Hs.37181:D64108	R-THYR01000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764
R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1)	R-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds//
mRNA, complete cds//4.4e-47:302:87//Hs.73614:U83460	6.8e-90:449:96//Hs.87619:AF087142
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077	R-THYR01000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:	ARNING ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217
85//Hs.155464:AF088219	R-THYR01000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426
R-PLACE3000425//Homo sapiens cF55 mRNA, complete cds//1.6e-46:307:	R-THYR01000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-
85//Hs.32567:AF073519	38:278:84//Hs.154103:AF061258
R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461	R-THYR01000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PR
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA,	OTEIN AP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946
A, complete cds//6.1e-84:440:92//Hs.153487:U43899	R-THYR01000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980	R-THYR01000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227	81//Hs.155464:AF088219
R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cd	R-THYR01000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:
s//8.8e-85:433:95//Hs.105399:AB018352	85//Hs.155464:AF088219
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240	R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031	a//3.6e-110:535:97//Hs.43445:AJ005698
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292	R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete c
R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444	ds//4.3e-115:559:97//Hs.79672:AB014552
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547	R-THYR01000206//ESTs//3.1e-90:507:90//Hs.32456:W29063
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739	R-THYR01000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J W
R-PLACE4000100	ARNING ENTRY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cd	R-THYR01000241//Homo sapiens mRNA for KIAA0688 protein, complete c
s//2.7e-98:419:91//Hs.129937:AB007931	ds//7.8e-69:524:82//Hs.141874:AB014588
R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W	R-THYR01000242//ESTs//4.2e-27:222:85//Hs.77554:W87927
ARNING ENTRY !!!! [H.sapiens]//3.8e-111:184:71//Hs.154278:N45985	R-THYR01000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:3
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript	18:80//Hs.80738:X52075
t KIAA0500//5.2e-21:118:100//Hs.118164:AB007969	R-THYR01000270//ESTs//1.9e-99:531:94//Hs.17767:N62925
R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582	R-THYR01000279//EST//2.7e-54:266:99//Hs.149527:AI280674
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete c	R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5
ds//3.0e-47:306:88//Hs.153468:AB011147	e-100:566:91//Hs.25846:AB016068
R-PLACE4000192//ESTs, Weakly similar to Human zinc finger protein (ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186	R-THYR01000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:W7
R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734	3547
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949	R-THYR01000327//Autocrine motility factor receptor//9.2e-54:289:93
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5	//Hs.80731:M63175
e-72:307:85//Hs.113283:AF018080	R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cd
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:	s//3.4e-113:559:96//Hs.12002:AB018333
83//Hs.155464:AF088219	R-THYR01000358//Human selenium-binding protein (hSBP) mRNA, comple
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216	te cds//1.5e-48:317:87//Hs.7833:U29091
R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442	R-THYR01000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586	R-THYR01000381//ESTs//1.0:253:57//Hs.128783:AA436250
R-PLACE4000270//Homo sapiens apoptotic protease activating factor	R-THYR01000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2
1 (Apat-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263	G2) mRNA, complete cds//4.6e-69:294:84//Hs.151614:AF032456
R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782	R-THYR01000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:
R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131	D38081
R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454	R-THYR01000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429
R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460	R-THYR01000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601
R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414	R-THYR01000438//ESTs//2.1e-48:360:83//Hs.141203:HS2638
R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478	R-THYR01000452//ESTs, Weakly similar to No definition line found
R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656	[C.elegans]//8.5e-40:239:90//Hs.84009:AI309761
R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425	R-THYR01000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426
R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ W	R-THYR01000484//Homo sapiens mRNA for KIAA0737 protein, complete c
ARNING ENTRY !!!! [H.sapiens]//1.1e-44:379:78//Hs.152369:AA504818	ds//2.2e-49:479:75//Hs.17630:AB018280
R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sap	R-THYR01000488//Homo sapiens mRNA for HRIHFB2038, partial cds//4.1
iens]//2.3e-70:482:83//Hs.140416:AA778649	e-89:471:94//Hs.28719:AB015333
R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502	R-THYR01000501//ESTs//1.5e-46:287:89//Hs.125300:R62360
R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780	R-THYR01000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005
R-PLACE4000445//ESTs, Weakly similar to CDS9.6 gene product [C.el	R-THYR01000505//ESTs, Weakly similar to KIAA0281 [H.sapiens]//3.9
egans]//2.6e-111:530:98//Hs.12003:AA643063	e-57:286:96//Hs.105861:AI206965
R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-in	R-THYR01000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511
ducible), polypeptide 2//8.5e-58:409:72//Hs.1361:M55053	R-THYR01000569//ESTs//3.2e-89:463:94//Hs.20555:W22193
R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932	R-THYR01000570//ESTs//2.8e-97:471:97//Hs.8245:AA15485
R-PLACE4000494//ESTs//1.4e-109:525:98//Hs.22539:AI334210	R-THYR01000585//Homo sapiens protein associated with Myc mRNA, com
R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290	plete cds//2.6e-108:533:97//Hs.15141:AF075587

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【表637】

R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247  
 R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223  
 R-THYRO1000605//ESTs. Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//Hs.21907:N24415  
 R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742  
 R-THYRO1000637  
 R-THYRO1000641//ESTs. Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.sapiens]//4.9e-46:245:95//Hs.97398:AA398634  
 R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840  
 R-THYRO1000662//ESTs//1.5e-82:389:99//Hs.155573:AA487384  
 R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866  
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:A1061063  
 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109  
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713  
 R-THYRO1000712  
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287  
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713  
 R-THYRO1000756//ESTs. Weakly similar to CMP-N-ACETYLNEURAMINATE-6-ETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624  
 R-THYRO1000777  
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932  
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897  
 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144  
 R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381  
 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594  
 R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067  
 R-THYRO1000829  
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:W57627  
 R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:A1281881  
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011  
 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663  
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871  
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234  
 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529  
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182  
 R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859  
 R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761  
 R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440  
 R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:A1281881  
 R-THYRO1000983//ESTs. Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:A1027524  
 R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:A1020777  
 R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131  
 R-THYRO1001003//ESTs. Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489  
 R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717  
 R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070  
 R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223  
 R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497  
 R-THYRO1001100  
 R-THYRO1001120//ESTs. Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:A1138834  
 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417  
 R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399  
 R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922  
 R-THYRO1001142//ESTs//0.2e-84:69//Hs.153434:A1287853  
 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075  
 R-THYRO1001177  
 R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744  
 R-THYRO1001204//ESTs. Weakly similar to THI protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151  
 R-THYRO1001213//EST//1.3e-75:409:92//Hs.140213:AA828932  
 R-THYRO1001262//Human kpn1 repeat mRNA (cdna clone pcd-kpn1-4), 3' end//1.3e-48:349:83//Hs.139107:K00629  
 R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640  
 R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561  
 R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269  
 R-THYRO1001320//EST//1.4e-61:403:79//Hs.139555:AA8230  
 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Ny

han syndrome)//8.5e-05:326:60//Hs.82314:M31642  
 R-THYRO1001322//ESTs//0.16:422:59//Hs.23876:AA082935  
 R-THYRO1001347//ESTs. Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250  
 R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033  
 R-THYRO1001365  
 R-THYRO1001374  
 R-THYRO1001401//Human HsLIM15 mRNA for HsLIM15, complete cds//2.5e-48:467:75//Hs.37181:D64108  
 R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627  
 R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733  
 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197  
 R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979  
 R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977  
 R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172  
 R-THYRO1001458//ESTs. Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082  
 R-THYRO1001480//Small inducible cytokine A5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219  
 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135  
 R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:A1093110  
 R-THYRO1001537//ESTs. Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094  
 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936  
 R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594  
 R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413  
 R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958  
 R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741  
 R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:RS4247  
 R-THYRO1001602//Insulin-like growth factor 1 (somatomedin C)//7.4e-12:288:67//Hs.85112:IX7025  
 R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886  
 R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:diacylglycerol phosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:43:493//Hs.12482:AJ002190  
 R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874  
 R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:A1080282  
 R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446  
 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562:95//Hs.118633:AJ225089  
 R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957  
 R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:A1341726  
 R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:A1147691  
 R-THYRO1001721  
 R-THYRO1001738//ESTs. Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184  
 R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172  
 R-THYRO1001746//EST//0.0073:226:61//Hs.146544:A1125323  
 R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474  
 R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224  
 R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788  
 R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956  
 R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:A1352123  
 R-THYRO1001907//ESTs. Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//3.7e-41:362:79//Hs.139007:HT4314  
 R-VESEN1000122  
 R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289  
 R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:A1359321  
 R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178  
 R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs.153026:AB014540  
 R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629  
 R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792  
 R-Y79AA1000181//ESTs. Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159:AA113849  
 R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991  
 R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103  
 R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:A1421812  
 R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:A1246624  
 R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:A1092936  
 R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-4

【0940】

【表638】

4:320:84//Hs.84123:AB002363	R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084
R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826	R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143
R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635	R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819
R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210	R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859
R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808	R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891
R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//4.4e-66:339:97//Hs.8215:AA521150	R-Y79AA1001493//ESTs, Highly similar to UBQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//4.4e-109:553:95//Hs.106616:A1027524
R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-44:279:88//Hs.139007:H74314	R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704
R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018	R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46:260:94//Hs.24884:AA176812
R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613	R-Y79AA1001541//EST//0.62:126:67//Hs.137020:AA868563
R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758	R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AFD12872
R-Y79AA1000420//EST//0.17:99:69//Hs.160859:A1352292	R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177
R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-60:362:80//Hs.6381:A1185509	R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508
R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320	R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:A1126237
R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:A1281881	R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:A1336204
R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.41723:U37426	R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81:400:97//Hs.13323:AA897542
R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848	R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486
R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:A1125280	R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19:112:97//Hs.26252:AA643235
R-Y79AA1000574//ESTs, Weakly similar to MD4B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:A1147455	R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99:553:92//Hs.108896:R54040
R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:AF060503	R-Y79AA1001692
R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELI CASE IN ATSI-TPD3 INTERGENIC REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818	R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6605:AA211783
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586:95//Hs.83023:AF093670	R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA418490
R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN P2585.5 IN CHROMOSOME III [C.elegans]//9.8e-111:563:95//Hs.19845:A1005330	R-Y79AA1001711//Human DNA sequence from clone 111809 on chromosome 20p12. Contains part of a gene for a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phospholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and CDSs//0.0085:251:63//Hs.21864:AL031652
R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405	R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87:427:97//Hs.18645:A1023798
R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463	R-Y79AA1001805//ESTs//1.1e-112:558:97//Hs.109755:AA180809
R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433	R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//0.8e-95:530:91//Hs.72444:W23217
R-Y79AA1000784//EST//0.80:87:67//Hs.158558:A1368359	R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582
R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512	R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.99931:L34355
R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642	R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:A1278630
R-Y79AA1000802//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405	R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094
R-Y79AA1000805	R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:A1333652
R-Y79AA1000824//ESTs//0.9e-276:61//Hs.153992:AA280227	R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404
R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:A1334650	R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275
R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.55836:U85647	R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB011135
R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079	R-Y79AA1002089//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080
R-Y79AA1000968	R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//Hs.78185:L38933
R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181	R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:A1417785
R-Y79AA1000976//ESTs//1.7e-86:299:95//Hs.120125:M86049	R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275
R-Y79AA1000985	R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399
R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851	R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858
R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067	R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725
R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407	R-Y79AA1002208//ESTs//1.7e-55:478:76//Hs.154554:AA552715
R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:A1271325	R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.50441:AA747428
R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:AB011135	R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349
R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047	R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//6.5e-86:518:90//Hs.25682:AA857843
R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA61260	R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:A1016274
R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155	R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:A1039977
R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015	R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:AB014592
R-Y79AA1001167	R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOMYME [D.melanogaster]//9.0e-102:507:96//Hs.25895:A1341537
R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884	R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555
R-Y79AA1001185	R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288
R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051	R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:AB014534
R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933	R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:A1187985
R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:A1025750	R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371
R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674	R-Y79AA1002361
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//1.1e-110:549:95//Hs.23170:AJ005892	R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908
R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271	R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:A1042000
R-Y79AA1001299//Human Inil mRNA, complete cds//9.6e-25:133:100//Hs.155626:U04847	
R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:A1191149	

## 【表639】

R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753  
R-Y79AA1002431//EST//6.6e-23:128:98//Hs.128417:AA975026  
R-Y79AA1002433//ESTs, Highly similar to CELL DIVISION CONTROL PRO  
TEIN 68 [Saccharomyces cerevisiae]//4.4e-62:390:88//Hs.143930:AI20  
7821  
R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870  
R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788  
R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

## 【0942】

全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データ。ただし、タンパク質コード領域の推定が困難であったものや、推定アミノ酸配列が100アミノ酸残基未満であったものについてはアミノ酸配列を示していない。以下に示す検索結果には、比較配列の長さの単位にaaとbpが混在している。

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

## 【0943】

【表640】

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%/Q61712  
 C-HEMBA1000030  
 C-HEMBA1000046  
 C-HEMBA1000050  
 C-HEMBA1000076  
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%/P08553  
 C-HEMBA1000158//HEPATOCTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5E-16//166aa//36%/P35584  
 C-HEMBA1000168//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%/P35662  
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%/P48555  
 C-HEMBA1000193  
 C-HEMBA1000227  
 C-HEMBA1000288  
 C-HEMBA1000302  
 C-HEMBA1000304  
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91%/Q35594  
 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%/AL049654  
 C-HEMBA1000387  
 C-HEMBA1000392  
 C-HEMBA1000460  
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%/Q04652  
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%/P22279  
 C-HEMBA1000501  
 C-HEMBA1000508  
 C-HEMBA1000520  
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%/P02826  
 C-HEMBA1000534  
 C-HEMBA1000555  
 C-HEMBA1000568  
 C-HEMBA1000588  
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%/Q43295  
 C-HEMBA1000636  
 C-HEMBA1000682  
 C-HEMBA1000686  
 C-HEMBA1000719  
 C-HEMBA1000727  
 C-HEMBA1000752  
 C-HEMBA1000817  
 C-HEMBA1000851  
 C-HEMBA1000867  
 C-HEMBA1000869  
 C-HEMBA1000872  
 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN).//1.6E-30//127aa//40%/P43366  
 C-HEMBA1000918  
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%/Q19124  
 C-HEMBA1000946  
 C-HEMBA1000968  
 C-HEMBA1000971  
 C-HEMBA1000975  
 C-HEMBA1001009  
 C-HEMBA1001022  
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//1.4E-12//131aa//38%/Q01485  
 C-HEMBA1001052  
 C-HEMBA1001080  
 C-HEMBA1001085  
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%/P48059  
 C-HEMBA1001109  
 C-HEMBA1001122  
 C-HEMBA1001133  
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN K0X3 I) (K1A0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%/Q06730  
 C-HEMBA1001140  
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%/P51646  
 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%/AB020678  
 C-HEMBA1001235  
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%/AJ130733  
 C-HEMBA1001281  
 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.0000002//198aa//29%/Q60401  
 C-HEMBA1001303  
 C-HEMBA1001310  
 C-HEMBA1001326  
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds.//1.4E-133//614bp//99%/AF057358  
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%/P17081  
 C-HEMBA1001388  
 C-HEMBA1001398  
 C-HEMBA1001405  
 C-HEMBA1001407  
 C-HEMBA1001413  
 C-HEMBA1001415  
 C-HEMBA1001446  
 C-HEMBA1001450  
 C-HEMBA1001455  
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%/P18850  
 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%/P29166  
 C-HEMBA1001533  
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%/AB020657  
 C-HEMBA1001581  
 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%/Q14141  
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSG A).//1.6E-10//155aa//28%/Q63679  
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROEIN).//4.6E-36//365aa//33%/P33450  
 C-HEMBA1001702  
 C-HEMBA1001714//Homo sapiens mRNA: cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%/AL050386  
 C-HEMBA1001731  
 C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%/P53009  
 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%/P11675  
 C-HEMBA1001815  
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%/Q99676  
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%/Q07230  
 C-HEMBA1001864  
 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%/P20659  
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.9.2) (ME2GLYDH).//9.3E-36//395aa//26%/Q63342  
 C-HEMBA1001987  
 C-HEMBA1002018  
 C-HEMBA1002049  
 C-HEMBA1002084  
 C-HEMBA1002125  
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%/P79293  
 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%/P43694  
 C-HEMBA1002191  
 C-HEMBA1002199  
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%/P18161  
 C-HEMBA1002237  
 C-HEMBA1002265  
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%/AF125537  
 C-HEMBA1002349  
 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCA P-E) mRNA, complete cds.//0//1847bp//99%/AF092563  
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%/P22793  
 C-HEMBA1002430  
 C-HEMBA1002439  
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%/Q00994  
 C-HEMBA1002460  
 C-HEMBA1002462  
 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%/P98175

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C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%/P17437	C-HEMBA1003395
C-HEMBA1002477	C-HEMBA1003402
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%/P48732	C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%/AB020712
C-HEMBA1002515	C-HEMBA1003417//Homo sapiens mRNA: cDNA DKFZp586C021 (from clone D KFP586C021).//1.6E-312//1414bp//99%/AL050287
C-HEMBA1002542	C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%/P37709
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%/AF075587	C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%/AB013139
C-HEMBA1002583	C-HEMBA1003447
C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%/AB011169	C-HEMBA1003461
C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%/AB018351	C-HEMBA1003463
C-HEMBA1002688	C-HEMBA1003528
C-HEMBA1002696	C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%/P50480
C-HEMBA1002750	C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%/P53384
C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%/AJ000414	C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-1).//1.2E-31//71aa//100%/P16874
C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%/AB020636	C-HEMBA1003568//52 KD RO PROTEIN (SJOJEN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-49//279aa//32%/P19474
C-HEMBA1002777	C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%/Q13330
C-HEMBA1002794	C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%/P26039
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2E-314//1437bp//99%/AF071185	C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28R NP).//4.4E-10//118aa//35%/P19682
C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2E-304//1383bp//99%/AJ132819	C-HEMBA1003615
C-HEMBA1002850	C-HEMBA1003617//Homo sapiens HRHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%/AB015344
C-HEMBA1002863	C-HEMBA1003621
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME 11.//1.5E-44//188aa//52%/Q09297	C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%/Q13207
C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%/AB011148	C-HEMBA1003690//HISTONE DEACETYLASE HDAC1.//2.1E-59//249aa//47%/P53973
C-HEMBA1002937	C-HEMBA1003711
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%/P16157	C-HEMBA1003807
C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%/AB020710	C-HEMBA1003864
C-HEMBA1002954	C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//89aa//46%/P16372
C-HEMBA1002971	C-HEMBA1003959
C-HEMBA1002973//CAMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (OPDE4).//1.2E-27//63aa//100%/P14646	C-HEMBA1003989
C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa//24%/Q02224	C-HEMBA1004074
C-HEMBA1003033	C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.5E-221//1188bp//78%/AF091234
C-HEMBA1003035	C-HEMBA1004146
C-HEMBA1003041	C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1893bp//98%/AB023145
C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%/Q75439	C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%/U50748
C-HEMBA1003067	C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.7E-217//1217bp//88%/AF095927
C-HEMBA1003096	C-HEMBA1004246
C-HEMBA1003117	C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.8E-257//738bp//99%/AF092094
C-HEMBA1003129	C-HEMBA1004289
C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%/P41940	C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%/AF132955
C-HEMBA1003148//Homo sapiens mRNA full length insert cDNA clone EU ROIMAGE 381801.//0//1583bp//99%/AL079278	C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2E-316//1445bp//99%/AF089841
C-HEMBA1003175	C-HEMBA1004596
C-HEMBA1003179//PROBABLE tRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%/P44551	C-HEMBA1004693
C-HEMBA1003199	C-HEMBA1004736
C-HEMBA1003222	C-HEMBA1004753
C-HEMBA1003235//TROPOMYOSIN.//0.000023//109aa//33%/Q02088	C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%/U49082
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%/Q06548	C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%/L39060
C-HEMBA1003257	C-HEMBA1004763
C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%/P32506	C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%/P08547
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229//1043bp//99%/AB024436	C-HEMBA1004771
C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%/AB011109	C-HEMBA1004776
C-HEMBA1003322	C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%/P50851
C-HEMBA1003327	C-HEMBA1004806
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0000002//248aa//23%/Q02224	C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%/Q00004
C-HEMBA1003370	C-HEMBA1004850
C-HEMBA1003380	C-HEMBA1004863//Homo sapiens mRNA: cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//100%/AL080114

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C-HEMBA1004923  
 C-HEMBA1004929  
 C-HEMBA1004930//26S PROTEASOME SUBUNIT 55B (K1A0072) (HA1357).//3.3E-27//65aa//100%/Q16401  
 C-HEMBA1004933  
 C-HEMBA1004954  
 C-HEMBA1004972//NEUROFILAMENT TRIPLET M PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%/P12036  
 C-HEMBA1005475  
 C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%/AF133270  
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%/P16372  
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1 (PACS-1) mRNA, complete cds.//3.7E-22//1189bp//88%/AF076183  
 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%/P26043  
 C-HEMBA1006377  
 C-HEMBA1006467  
 C-HEMBA1006530  
 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//0.00000043//111aa//40%/Q01485  
 C-HEMBA1006795  
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%/P16258  
 C-HEMBA1006936  
 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-26//1215bp//99%/AF078849  
 C-HEMBA1007342  
 C-HEMBA1000008  
 C-HEMBA1000018  
 C-HEMBA1000024  
 C-HEMBA1000025  
 C-HEMBA1000036  
 C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-18//1582bp//80%/AF084928  
 C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%/P17799  
 C-HEMBA1000103  
 C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%/Y15521  
 C-HEMBA1000136  
 C-HEMBA1000215  
 C-HEMBA1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEDD8.5.//2.7E-12//112aa//47%/Q09530  
 C-HEMBA1000244  
 C-HEMBA1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%/Q23256  
 C-HEMBA1000338  
 C-HEMBA1000339  
 C-HEMBA1000391  
 C-HEMBA1000438  
 C-HEMBA1000449  
 C-HEMBA1000589  
 C-HEMBA1000591  
 C-HEMBA1000623  
 C-HEMBA1000630  
 C-HEMBA1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//232aa//28%/P78970  
 C-HEMBA1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%/P27671  
 C-HEMBA1000671  
 C-HEMBA1000673  
 C-HEMBA1000705  
 C-HEMBA1000706  
 C-HEMBA1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%/U53475  
 C-HEMBA1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%/AF151847  
 C-HEMBA1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.2E-126//613bp//97%/AF111110  
 C-HEMBA1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-54//232aa//43%/P39956  
 C-HEMBA1000807  
 C-HEMBA1000810  
 C-HEMBA1000848  
 C-HEMBA1000852  
 C-HEMBA1000870  
 C-HEMBA1000887  
 C-HEMBA1000908  
 C-HEMBA1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%/AF120102  
 C-HEMBA1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%/AF116910  
 C-HEMBA1000973//Mus musculus schlafen3 (Sifn3) mRNA, complete cds.//3.4E-120//580bp//67%/AF099974  
 C-HEMBA1000975  
 C-HEMBA1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-18//178aa//30%/P28575  
 C-HEMBA1000991  
 C-HEMBA1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%/P51523  
 C-HEMBA1001014  
 C-HEMBA1001024  
 C-HEMBA1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%/P46087  
 C-HEMBA1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//80%/AF010144  
 C-HEMBA1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%/AF034803  
 C-HEMBA1001096  
 C-HEMBA1001105  
 C-HEMBA1001117  
 C-HEMBA1001126  
 C-HEMBA1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%/AB018435  
 C-HEMBA1001151//Rattus norvegicus golgi stacking protein homolog G RASPS5 mRNA, complete cds.//4.2E-210//1835bp//76%/AF110267  
 C-HEMBA1001153  
 C-HEMBA1001169  
 C-HEMBA1001175//ANKYRIN.//6.9E-11//169aa//31%/Q02357  
 C-HEMBA1001182  
 C-HEMBA1001199  
 C-HEMBA1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%/AB023187  
 C-HEMBA1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%/AF089897  
 C-HEMBA1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%/AF132966  
 C-HEMBA1001289  
 C-HEMBA1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%/P17081  
 C-HEMBA1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%/U92703  
 C-HEMBA1001331  
 C-HEMBA1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%/P98175  
 C-HEMBA1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%/AF097441  
 C-HEMBA1001369  
 C-HEMBA1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%/AF100757  
 C-HEMBA1001387  
 C-MAHMA1002317  
 C-MAHMA1002319  
 C-MAHMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%/Q02926  
 C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%/Q21190  
 C-NT2RM1000242  
 C-NT2RM1000257//MAGO WASHI PROTEIN.//7.9E-69//143aa//91%/P49028  
 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%/P39942  
 C-NT2RM1000669  
 C-NT2RM1000781  
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%/AF092138  
 C-NT2RM1001008  
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.00000002//980bp//95%/AF085360  
 C-NT2RM1001074  
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%/P39942  
 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to NM52. ESTs and GSS s. complete sequence.//0//1740bp//99%/AL031291  
 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE

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(EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%/P25167	7E-53//266aa//43%/P41877
C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.0000043//136aa//31%/P54703	C-NT2RM2000795
C-NT2RM2000032	C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.5E-279//545aa//98%/P23514
C-NT2RM2000042	C-NT2RM2000837
C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%/P50102	C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%/AB015046
C-NT2RM2000093	C-NT2RM2000952
C-NT2RM2000101	C-NT2RM2000984
C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%/AF067223	C-NT2RM2001004
C-NT2RM2000192	C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%/Q60809
C-NT2RM2000239	C-NT2RM2001065
C-NT2RM2000250//Homo sapiens mRNA: cDNA DKFp564L232 (from clone D KFp564L232).//4.2E-314//1416bp//100%/AL080069	C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOM E III.//2.4E-15//266aa//26%/P46577
C-NT2RM2000259	C-NT2RM2001131
C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181aa//34%/P14918	C-NT2RM2001141
C-NT2RM2000287	C-NT2RM2001152
C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%/AB020666	C-NT2RM2001177//Homo sapiens mRNA: cDNA DKFp586G1822 (from clone DKFp586G1822).//2.1E-293//1335bp//99%/AL080109
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%/AB011132	C-NT2RM2001194
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%/P11274	C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%/P05143
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK 7 mRNA, partial cds.//0//1506bp//99%/U48251	C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//0.0000015//95aa//35%/P48724
C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE).//1.7E-68//419aa//36%/P50849	C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.6E-10//177aa//32%/P97924
C-NT2RM2000374	C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//1.3E-180//328aa//99%/P13264
C-NT2RM2000395	C-NT2RM2001243
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LAT ENDOCYTIC INTERMEDIATE COMPONENT).//1.6E-54//344aa//33%/P32802	C-NT2RM2001247
C-NT2RM2000407	C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%/P53995
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NNT73.//1E-222//237aa//89%/Q08469	C-NT2RM2001291
C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//157aa//28%/P36113	C-NT2RM2001306//Homo sapiens mRNA: cDNA DKFp564I052 (from clone D KFp564I052).//0//1694bp//99%/AL080063
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.0000089//377aa//24%/P22211	C-NT2RM2001312
C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.8E-13//166aa//34%/P41823	C-NT2RM2001319
C-NT2RM2000502	C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%/Q04584
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%/AF061243	C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN MET-E-1.//0.0000029//334aa//22%/Q00808
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//32%/P17437	C-NT2RM2001370
C-NT2RM2000540	C-NT2RM2001393
C-NT2RM2000567	C-NT2RM2001420
C-NT2RM2000569	C-NT2RM2001424//Homo sapiens mRNA: cDNA DKFp586D0920 (from clone DKFp586D0920).//0//1621bp//100%/AL050146
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//1.7E-187//741aa//46%/P73505	C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//437aa//57%/P52569
C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%/D86987	C-NT2RM2001504
C-NT2RM2000588//HISTONE DEACETYLASE HDAC1.//2.8E-60//384aa//40%/P53973	C-NT2RM2001524
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%/AF156487	C-NT2RM2001544
C-NT2RM2000599//Homo sapiens F-box protein Liliina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%/AF179221	C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//90aa//42%/P38660
C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.4E-32//319aa//35%/Q08170	C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.3E-61//312aa//44%/P19474
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%/AB018272	C-NT2RM2001582
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%/AB014558	C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%/AB014610
C-NT2RM2000639	C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%/P28692
C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%/AB014576	C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%/AB007931
C-NT2RM2000669	C-NT2RM2001930
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%/P32391	C-NT2RM2001935
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.8E-23//184aa//36%/Q15404	C-NT2RM2001936//32.3 KD PROTEIN IN CWPI-MBRI INTERGENIC REGION.//2.7E-27//216aa//34%/P28320
C-NT2RM2000718//Homo sapiens HRIHF82436 mRNA, partial cds.//4.4E-231//1065bp//99%/AB015342	C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%/P38250
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%/P41877	C-NT2RM2001982
	C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%/P37838
	C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PD1) (EC 5.3.4.1).//1.3E-10//232aa//28%/Q12730
	C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOM E I.//3.1E-12//206aa//30%/Q09782
	C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.00000029//83aa//44%/P40796
	C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FE0A INTERGENIC REGION.//1.1E-89//425aa//41%/P46837
	C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phospha

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te amidotransferase, complete cds. //0//1959bp//99%/AB016789	C-NT2RP1000191
C-NT2RM2002049	C-NT2RP1000202//ANKYRIN. //1E-25//302aa//34%/Q02357
C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13. //0.00000099//338aa//24%/Q07878	C-NT2RP1000243
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP). //5E-62//104aa//57%/Q61990	C-NT2RP1000259
C-NT2RM2002091	C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds. //5.8E-114//616bp//93%/AF067730
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial. //0//1807bp//99%/AJ010840	C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds. //1.3E-275//1249bp//99%/AF053551
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds. //0//1858bp//99%/AF030435	C-NT2RP1000333//ANTI-SILENCING PROTEIN 1. //8.7E-47//155aa//58%/P32447
C-NT2RM2002126//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKNA (EC 2.7.1.-). //4.9E-13//487aa//26%/P49695	C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161. //1.7E-15//162aa//30%/P25343
C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12. //8E-31//105aa//47%/P47805	C-NT2RP1000357
C-NT2RM2002178//Homo sapiens mRNA: cDNA DKFpZp434E0335 (from clone DKFpZp434E0335). //0//1683bp//99%/AL117402	C-NT2RP1000376//Homo sapiens mRNA: cDNA DKFpZp434A102 (from clone D KFpZp434A102). //0//2265bp//95%/AL080187
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2). //7.1E-155//381aa//72%/P25167	C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds. //0//1056bp//99%/AB011159
C-NT2RM4000061	C-NT2RP1000416
C-NT2RM4000104//ZINC FINGER PROTEIN 135. //1.5E-81//251aa//53%/P52742	C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCA P-C mRNA, complete cds. //1.8E-94//1019bp//63%/AF111423
C-NT2RM4000139//R. norvegicus trg mRNA. //2.3E-114//1161bp//72%/X68101	C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN). //2.4E-10//227aa//25%/Q08257
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1. //4.8E-13//686aa//23%/P25386	C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III. //2.6E-94//254aa//47%/P34580
C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10. //9.2E-75//439aa//41%/P16381	C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V). //4.5E-240//445aa//97%/P09653
C-NT2RM4000197	C-NT2RP1000481
C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds. //0//1926bp//100%/AB018255	C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds. //0//2728bp//99%/D87686
C-NT2RM4000229//Gallus gallus actin filament-associated protein (A FAP-110) mRNA, complete cds. //1.1E-27//633bp//64%/L20303	C-NT2RP1000541//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT). //1.1E-27//193aa//35%/P49020
C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds. //2.2E-276//1124bp//97%/M99438	C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1). //3.5E-75//151aa//94%/P97367
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L. //0//2030bp//99%/AJ132637	C-NT2RP1000581
C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds. //0//1827bp//99%/AF083246	C-NT2RP1000630//NECDIN. //2.4E-44//227aa//41%/P25233
C-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL83 PROTEIN). //1.5E-21//208aa//35%/Q24371	C-NT2RP1000688
C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds. //0//2156bp//86%/AB025412	C-NT2RP1000695
C-NT2RM4000395	C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds. //0//2057bp//99%/E14379
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor. //0//1730bp//99%/AJ133769	C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds. //0//2186bp//99%/AF101434
C-NT2RM4000451//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1. //8E-20//393aa//24%/Q10297	C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN). //1.2E-30//232aa//30%/Q35566
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds. //0//2092bp//99%/AF097025	C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P5-RHOGAP). //8.2E-83//334aa//50%/Q07960
C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 1B-6; PEPTIDE P-H]. //4.8E-11//242aa//31%/P04280	C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds. //0//1494bp//99%/AF067223
C-NT2RM4000496//SAP1 PROTEIN. //8.3E-53//434aa//29%/P39955	C-NT2RP1000846
C-NT2RM4000511	C-NT2RP1000851
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT). //1.1E-11//394aa//24%/P16884	C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN). //1.2E-30//232aa//30%/Q35566
C-NT2RM4000520	C-NT2RP1000915//AUTOANTIGEN NGP-1. //1.7E-19//343aa//25%/Q13823
C-NT2RM4000585	C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds. //4.6E-105//504bp//99%/U39317
C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds. //1.1E-285//1293bp//99%/AF186273	C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN). //1.4E-23//370aa//28%/Q04652
C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds. //0//1940bp//95%/AB014587	C-NT2RP1000958//AUTOANTIGEN NGP-1. //1.4E-19//343aa//25%/Q13823
C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds. //0//1652bp//99%/AB020657	C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds. //2.5E-236//966bp//99%/M17885
C-NT2RP1000040	C-NT2RP1000966//NUCLEOLIN (PROTEIN C23). //8.9E-299//554aa//99%/P19338
C-NT2RP1000063	C-NT2RP1000980
C-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12. //0//1162bp//99%/X98834	C-NT2RP1000988
C-NT2RP1000101	C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (T H1) mRNA, complete cds. //2.2E-78//1529bp//61%/L01790
C-NT2RP1000111//COP1 REGULATORY PROTEIN. //4E-116//296aa//51%/P93471	C-NT2RP1001014
C-NT2RP1000112	C-NT2RP1001395
C-NT2RP1000124	C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3. //8.9E-141//396aa//67%/P91917
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HGF). //4.5E-50//181aa//60%/P51859	C-NT2RP1001424
C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds. //0//1889bp//98%/AB023165	C-NT2RP1001449
C-NT2RP1000170	C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative). //1.2E-137//629bp//100%/AJ005257
	C-NT2RP1001466
	C-NT2RP1001475
	C-NT2RP1001482

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【表645】

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%/Q08891	mRNA, complete cds.//0//1757bp//99%/AF102265
C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IP S).//1.6E-166//506aa//60%/P42803	C-NT2RP2000438
C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%/Q35566	C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%/P35844
C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//271aa//89%/P47758	C-NT2RP2000503
C-NT2RP1001616	C-NT2RP2000510
C-NT2RP1001665//CALMODULIN.//0.0000051//83aa//30%/P02594	C-NT2RP2000516
C-NT2RP2000008//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%/Q01730	C-NT2RP2000603
C-NT2RP2000007	C-NT2RP2000617
C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%/P51523	C-NT2RP2000634//Homo sapiens mRNA for KIAA0514 protein, partial cd s.//0//2482bp//99%/AB014514
C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//1.8E-22//184aa//34%/Q01730	C-NT2RP2000656
C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%/AF061749	C-NT2RP2000658
C-NT2RP2000054	C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%/Q01577
C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//9.4E-16//45aa//100%/P49446	C-NT2RP2000704
C-NT2RP2000067	C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE).//2.7E-100//488aa//44%/Q32038
C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROTEIN).//3.4E-51//383aa//32%/P33450	C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%/P12623
C-NT2RP2000079	C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cd s.//0//3347bp//99%/AB020680
C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cd s.//0//2286bp//100%/AB018338	C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.00000056//179aa//29%/Q99104
C-NT2RP2000091	C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN I20) (ABP-1 20).//0.0000011//96aa//29%/P13466
C-NT2RP2000097	C-NT2RP2000816//MAGNESIUM-CHLATASE 30 KD SUBUNIT.//0.00000079//172aa//28%/P26174
C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%/AB018356	C-NT2RP2000819
C-NT2RP2000120	C-NT2RP2000841
C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SMF2L.//2.5E-117//541aa//42%/P41877	C-NT2RP2000845
C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cd s.//0//2286bp//99%/AB023206	C-NT2RP2000863
C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (COLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIAN CHAIN).//4.4E-226//423aa//99%/P35585	C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/Q60841
C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%/P41891	C-NT2RP2000892
C-NT2RP2000157//ML02 PROTEIN.//2.6E-11//62aa//40%/Q09329	C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244
C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete c ds.//3.4E-315//1430bp//99%/AB023225	C-NT2RP2000932//Homo sapiens mRNA: cDNA DKFZp5640043 (from clone D KFZp5640043).//0//2487bp//99%/AL050390
C-NT2RP2000173	C-NT2RP2000938
C-NT2RP2000175	C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete c ds.//0//3458bp//99%/AB018298
C-NT2RP2000195	C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704
C-NT2RP2000205	C-NT2RP2000985
C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cd s.//0//2898bp//99%/AB020699	C-NT2RP2001036
C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%/P35568	C-NT2RP2001044
C-NT2RP2000232	C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0488.//0//2749bp//99%/AB007957
C-NT2RP2000233	C-NT2RP2001065
C-NT2RP2000239	C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.8E-46//222aa//45%/Q20939
C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMI NYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P 110 SUBUNIT).//3.4E-21//210aa//33%/P56558	C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%/P50232
C-NT2RP2000270	C-NT2RP2001094
C-NT2RP2000274	C-NT2RP2001119
C-NT2RP2000283	C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440
C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMO SOME 1.//1.6E-27//576aa//25%/Q10297	C-NT2RP2001218
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%/Q99676	C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEA VY CHAIN) (NMHC).//2.2E-10//366aa//28%/P14105
C-NT2RP2000298	C-NT2RP2001381
C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//1193bp//99%/U82381	C-NT2RP2001397//Homo sapiens mRNA: cDNA DKFZp434B174 (from clone D KFZp434B174).//0//1495bp//100%/AL080146
C-NT2RP2000328	C-NT2RP2001427
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//7E-111//226aa//92%/P08760	C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cd s.//0//1748bp//99%/AB018340
C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN M YD116.//6.3E-115//674aa//46%/P17564	C-NT2RP2001675
C-NT2RP2000369	C-NT2RP2001721
C-NT2RP2000412	C-NT2RP2001907
C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//100%/P52597	C-NT2RP2001969
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase	C-NT2RP2001976//Mus musculus calmodulin-binding protein SHAI (Sha 1) mRNA, complete cds.//4.7E-177//1538bp//74%/AF062378
	C-NT2RP2002046
	C-NT2RP2002154
	C-NT2RP2002208
	C-NT2RP2002270//AF-9 PROTEIN.//0.0000012//74aa//36%/P42568
	C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%/V16521
	C-NT2RP2002325//Homo sapiens mRNA for Pax1lp, complete cds.//8.4E-254//1158bp//99%/AB015594
	C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced var iant mRNA, complete cds.//4.3E-240//1105bp//99%/AF038958
	C-NT2RP2002426

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C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%/AB005289	C-NT2RP2004802
C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%/Q11073	C-NT2RP2004841
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815	C-NT2RP2004936
C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345	C-NT2RP2004959//PS4 PROTEIN PRECURSOR.//0.0000095//297aa//20%/P13692
C-NT2RP2002621	C-NT2RP2004999
C-NT2RP2002672	C-NT2RP2005000
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME 11.//1.9E-14//210aa//30%/O14345	C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%/AB014515
C-NT2RP2002769	C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%/AJ011779
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764	C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%/P32447
C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%/AF038392	C-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%/X98743
C-NT2RP2002954	C-NT2RP2005140
C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%/P51669	C-NT2RP2005147
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.0000001//98aa//35%/P10129	C-NT2RP2005159
C-NT2RP2002985//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%/AB026190	C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%/AF097025
C-NT2RP2003108	C-NT2RP2005270
C-NT2RP2003117	C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%/D89053
C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.3E-82//642bp//68%/AF079765	C-NT2RP2005293
C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%/Q04652	C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%/AB014576
C-NT2RP2003177	C-NT2RP2005358//Homo sapiens methyl-CoG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%/AF072247
C-NT2RP2003194	C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%/Q13823
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%/AF151811	C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%/Q08170
C-NT2RP2003295//Homo sapiens RNP mRNA for RPB5 mediating protein, complete cds.//0//1526bp//99%/AB006572	C-NT2RP2005441
C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%/P26337	C-NT2RP2005453
C-NT2RP2003367	C-NT2RP2005464
C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%/P38378	C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN R1M2.//3E-44//252aa//41%/P38127
C-NT2RP2003446	C-NT2RP2005472
C-NT2RP2003533	C-NT2RP2005495
C-NT2RP2003543//HYPOTHETICAL TRNA/RNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%/P74261	C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%/P36876
C-NT2RP2003596	C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%/AF151803
C-NT2RP2003629	C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%/AF092563
C-NT2RP2003687	C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%/AF035526
C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%/Q05481	C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%/AB007963
C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%/P51669	C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%/Q39366
C-NT2RP2003793	C-NT2RP2005555
C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%/O09175	C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%/AF062529
C-NT2RP2003986	C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9E-313//1455bp//98%/AF062085
C-NT2RP2004042	C-NT2RP2005622
C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%/AL096820	C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%/P47623
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%/P38120	C-NT2RP2005637
C-NT2RP2004392//RNA4 PROTEIN.//1.4E-11//143aa//27%/P36044	C-NT2RP2005640
C-NT2RP2004463	C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%/P56101
C-NT2RP2004602	C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%/AJ010973
C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%/AB023139	C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%/AF089814
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%/AJ006291	C-NT2RP2005683
C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1.//5.6E-64//616aa//33%/Q92355	C-NT2RP2005690
C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%/Q10490	C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%/AB018342
C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%/P53588	C-NT2RP2005723//HORN ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODI PROTEIN).//0.00000003//169aa//28%/P38074
	C-NT2RP2005748
	C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%/AF068868
	C-NT2RP2005753//Homo sapiens l-1 receptor candidate protein mRNA.

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complete cds. //0//1966bp//99%/AF082516  
 C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A). //1.7E-61  
 //374aa//38%/P47943  
 C-NT2RP2005767//G. gallus PB1 gene. //5E-163//1158bp//81%/X90849  
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase iso  
 form (P5CR2) mRNA, complete cds. //2.7E-180//656bp//99%/AF151351  
 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN E  
 NDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEP  
 TIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP). //2.1E-  
 213//249aa//85%/Q02038  
 C-NT2RP2005781  
 C-NT2RP2005804  
 C-NT2RP2005835//SHP1 PROTEIN. //1.8E-28//208aa//32%/P34223  
 C-NT2RP2005853  
 C-NT2RP2005868  
 C-NT2RP2005886  
 C-NT2RP2005890  
 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete c  
 ds. //0//1977bp//99%/AB023188  
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57). //5  
 E-11//155aa//34%/P48837  
 C-NT2RP2006038  
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA  
 SPLICING FACTOR SRP75). //1.5E-13//185aa//38%/Q08170  
 C-NT2RP2006052  
 C-NT2RP2006069  
 C-NT2RP2006071  
 C-NT2RP2006100//Homo sapiens mRNA: cDNA DKFp564B102 (from clone D  
 KFp564B102). //0//1759bp//99%/AL049970  
 C-NT2RP2006106  
 C-NT2RP2006141  
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cd  
 s. //3.3E-189//899bp//97%/AB014554  
 C-NT2RP2006196  
 C-NT2RP2006200  
 C-NT2RP2006219//H. sapiens mRNA for DGCR6 protein. //1.1E-214//1026b  
 p//97%/X96484  
 C-NT2RP2006237  
 C-NT2RP2006238  
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT  
 CHAIN LC1]. //2E-59//388aa//32%/P46821  
 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds. //2.  
 8E-274//1236bp//99%/AF035262  
 C-NT2RP2006333  
 C-NT2RP2006365  
 C-NT2RP2006393  
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATNKE POUCH  
 HOMEO BOX). //0.0000034//50aa//50%/Q61658  
 C-NT2RP2006456  
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein. //0//2181bp//9  
 9%/AJ006266  
 C-NT2RP2006467  
 C-NT2RP2006472  
 C-NT2RP2006565//Sus scrofa mRNA for SCAMP1 protein. //0//1276bp//84  
 %//Y15710  
 C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P45  
 0-KMB) (OLFACTIVE). //4.2E-134//486aa//50%/P24461  
 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC  
 3.1.4.37) (CNP). //0.000055//169aa//25%/P09543  
 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete c  
 ds. //0//2547bp//99%/AB020708  
 C-NT2RP3000072  
 C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cd  
 s. //0//1404bp//97%/AB011164  
 C-NT2RP3000220  
 C-NT2RP3000251  
 C-NT2RP3000252//Homo sapiens GTP-binding protein NCB mRNA, complet  
 e cds. //0//2388bp//99%/AF120334  
 C-NT2RP3000312  
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protei  
 n which interacts with transcription factor Spl. //0//1544bp//100%  
 /AJ242978  
 C-NT2RP3000333  
 C-NT2RP3000348  
 C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303. //0.00000028/  
 //185aa//31%/Q25074  
 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.  
 4.10) (AK3). //2E-111//226aa//92%/P08760  
 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast  
 pre-mRNA splicing factors, Prp1/Zer1 and Prp6. //0//2072bp//98%/AB  
 019219  
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18. //2.1E-107//206aa//99%  
 /P35293  
 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DE  
 AH BOX PROTEIN 13). //1.7E-139//679aa//41%/Q43143  
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, compl  
 ete cds. //0//2354bp//99%/AF071185  
 C-NT2RP3000484  
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6). //4.8E-  
 28//536aa//27%/P28160  
 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN). //1.  
 9E-12//192aa//30%/P15151  
 C-NT2RP3000596//TRICHOHYALIN. //2.5E-17//304aa//28%/Q07283  
 C-NT2RP3000599  
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).  
 //3E-140//499aa//46%/P51523  
 C-NT2RP3000644  
 C-NT2RP3000661  
 C-NT2RP3000665  
 C-NT2RP3000690  
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR. //7E-28//176aa//34%/Q9465  
 0  
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN. //2.5E-36//417aa/  
 //31%/Q61982  
 C-NT2RP3000836  
 C-NT2RP3000841  
 C-NT2RP3000850  
 C-NT2RP3000852  
 C-NT2RP3000859  
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy ch  
 ain homolog (Doc1) mRNA, complete cds. //6.9E-69//1611bp//61%/U5134  
 45  
 C-NT2RP3000869  
 C-NT2RP3000901  
 C-NT2RP3000917//Homo sapiens Dhel-like protein mRNA, complete cds.  
 //0//3199bp//99%/AF064257  
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protei  
 n p65 (GRASP65) mRNA, complete cds. //2.7E-185//585bp//88%/AF01526  
 4  
 C-NT2RP3000980  
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN. //0.0000006//78aa  
 //48%/P25159  
 C-NT2RP3001004  
 C-NT2RP3001081  
 C-NT2RP3001084  
 C-NT2RP3001096//Rattus norvegicus leprecan (leprel) mRNA, complete  
 cds. //1.7E-94//787bp//66%/AF087433  
 C-NT2RP3001107//PEREGRIN (BRI40 PROTEIN). //3E-44//260aa//40%/P552  
 01  
 C-NT2RP3001109  
 C-NT2RP3001116  
 C-NT2RP3001119  
 C-NT2RP3001133  
 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cd  
 s. //0//2802bp//99%/AB018305  
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein. //0//2732bp//9  
 9%/AJ006266  
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MADI-SCY1 INTERGEN  
 IC REGION. //1.7E-10//196aa//27%/P53154  
 C-NT2RP3001214  
 C-NT2RP3001216//CYLICIN 1 (MULTIPLE-BAND POLYPEPTIDE 1) (FRAGMENT  
 ). //0.000023//137aa//33%/P35663  
 C-NT2RP3001221//GAMMA-BUTYROBETAIN, 2-OXOGLUTARATE DIOXYGENASE (EC  
 1.14.11.1) (GAMMA-BUTYROBETAIN HYDROXYLASE). //1.9E-31//353aa//30  
 %//P80193  
 C-NT2RP3001236  
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1  
 X) [CONTAINS: LIGHT CHAIN LC1]. //1.2E-166//395aa//51%/P14873  
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete c  
 ds. //0//2497bp//99%/AB020718  
 C-NT2RP3001307  
 C-NT2RP3001325  
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase  
 anchoring protein 95, complete cds. //0//1213bp//99%/AB025905  
 C-NT2RP3001392  
 C-NT2RP3001396  
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF. //1.3E-61//374aa//3  
 6%/P49711  
 C-NT2RP3001407//SCY1 PROTEIN. //0.0000033//143aa//25%/P53009  
 C-NT2RP3001420

【0951】

【表648】

C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%/033529  
 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//  
 /33%/009053  
 C-NT2RP3001457  
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//  
 /43%/P11632  
 C-NT2RP3001495//Human oxidoreductase (HMCMA56) mRNA, complete cds.  
 //0//1475bp//99%/U13395  
 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T  
 RC8 (TRC8) mRNA, complete cds.//0//2295bp//99%/AF064801  
 C-NT2RP3001529//SPODB-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345a  
 a//42%/P20964  
 C-NT2RP3001621  
 C-NT2RP3001629  
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIA0210.//6.8E-18//91aa//38%  
 //Q92609  
 C-NT2RP3001646//WD-40 REPEAT PROTEIN MS12.//8.8E-09//132aa//31%/Q  
 22468  
 C-NT2RP3001676  
 C-NT2RP3001679  
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348  
 aa//27%/P24733  
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249a  
 a//30%/Q04652  
 C-NT2RP3001896  
 C-NT2RP3001915  
 C-NT2RP3001929  
 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%/PS2  
 742  
 C-NT2RP3004466  
 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.  
 //3.3E-113//466aa//42%/P34110  
 C-NT2RP3004539//Homo sapiens mRNA for KIA0532 protein, partial cd  
 s.//0//1520bp//99%/AB014532  
 C-NT2RP3004544//Homo sapiens mRNA for KIA0554 protein, partial cd  
 s.//0//974bp//95%/AB011126  
 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NON  
 ERYTHROID).//0.00000038//150aa//28%/Q01484  
 C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15  
 0) mRNA, complete cds.//0//1770bp//99%/AF026445  
 C-NT2RP3004578//Homo sapiens mRNA for KIA0477 protein, complete c  
 ds.//0//1639bp//99%/AB007946  
 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//9  
 9%/AJ006266  
 C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%/Q0  
 2084  
 C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA  
 A, complete cds.//0//3972bp//98%/AF093097  
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED  
 PROTEIN).//1.7E-72//254aa//45%/P54352  
 C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%  
 //P35526  
 C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.9E-51//335aa  
 //37%/Q64375  
 C-NT2RP4000078//Homo sapiens mRNA for KIA0850 protein, complete c  
 ds.//0//3013bp//99%/AB020657  
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161  
 bp//99%/AB011538  
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 1  
 00 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%/Q10568  
 C-NT2RP4000129  
 C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activ  
 ating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%  
 //AF011427  
 C-NT2RP4000150  
 C-NT2RP4000151  
 C-NT2RP4000159  
 C-NT2RP4000185  
 C-NT2RP4000210//Homo sapiens mRNA for KIA0700 protein, partial cd  
 s.//0//4149bp//99%/AB014600  
 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//  
 5.9E-15//104aa//40%/P15287  
 C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein  
 (CASP).//0//1932bp//99%/AJ006470  
 C-NT2RP4000246//MPC DERIVED PROLINE RICH PROTEIN 1 (MDPP-1).//2.7  
 E-84//208aa//76%/Q03173  
 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//  
 153aa//43%/Q23968  
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOS  
 OME 1.//3.5E-297//1024aa//55%/P87115  
 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-  
 LYASE) (ADENYL CYCLASE).//1.5E-26//237aa//28%/Q01631  
 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KER  
 ATIN).//0.000003//101aa//32%/P26372  
 C-NT2RP4000355  
 C-NT2RP4000360//Homo sapiens mRNA for KIA0738 protein, complete c  
 ds.//0//4074bp//99%/AB018281  
 C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated pro  
 tein (IKAP) mRNA, complete cds.//0//4782bp//99%/AF044195  
 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECU  
 RSOR (MRF-1).//2.6E-77//262aa//54%/Q75570  
 C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating  
 protein.//0//2412bp//99%/AJ238243  
 C-NT2RP4000381  
 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%/PS  
 2738  
 C-NT2RP4000415  
 C-NT2RP4000417//MANNOsyl-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC  
 3.2.1.113) (MAN (9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//  
 /33%/P45701  
 C-NT2RP4000448//Homo sapiens mRNA: cDNA DKFp566C0746 (from clone  
 DKFp566C0746).//0//3991bp//99%/AL050078  
 C-NT2RP4000449  
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.//0.0000  
 003//175aa//27%/P09309  
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.  
 2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING  
 PROTEASE 15) (DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%/PS  
 0101  
 C-NT2RP4000480  
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT RE  
 GULATOR NTR4).//1.9E-67//721aa//29%/Q09475  
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%  
 //P40484  
 C-NT2RP4000500  
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//  
 /45%/P45818  
 C-NT2RP4000524  
 C-NT2RP4000541  
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%  
 //P40319  
 C-NT2RP4000560  
 C-NT2RP4000588  
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, c  
 omplete cds.//2.9E-188//863bp//99%/AF067730  
 C-NT2RP4000638  
 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.//0.0000  
 003//175aa//27%/P09309  
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPS  
 E.//1.1E-32//350aa//30%/P39625  
 C-NT2RP4000704  
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME  
 X.//1.1E-13//295aa//27%/Q11073  
 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199  
 aa//78%/P10267  
 C-NT2RP4000728//Homo sapiens mRNA for KIA0931 protein, partial cd  
 s.//0//3392bp//95%/AB023148  
 C-NT2RP4000737  
 C-NT2RP4000739//Homo sapiens mRNA for KIA0102 protein, complete c  
 ds.//0//3574bp//99%/AB023229  
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGE  
 NIC REGION.//0.00000032//67aa//31%/P53915  
 C-NT2RP4000817//Homo sapiens mRNA for KIA0470 protein, complete c  
 ds.//0//1927bp//99%/AB007939  
 C-NT2RP4000833  
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//  
 4.3E-94//810bp//65%/Y18265  
 C-NT2RP4000839//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5  
 E-21//271aa//28%/Q00808  
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTI  
 DASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).  
 //5.7E-82//324aa//48%/Q09175  
 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//1  
 74aa//55%/P16415  
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%  
 /Q35682  
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.  
 6E-96//513aa//42%/P22314  
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 K  
 D PROTEIN).//2.6E-26//227aa//36%/Q06828

【0952】

【表649】

C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.5E-76//346aa//43%/Q61058	C-NT2RP4001373
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%/Y16521	C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.2E-17//146aa//35%/P18160
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%/Q58900	C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOM E 1.//2E-53//436aa//30%/Q10085
C-NT2RP4000955	C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete c ds.//0//2716bp//99%/AB023140
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//90aa//42%/P38660	C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%/Q14141
C-NT2RP4000975	C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%/Q99676
C-NT2RP4000979	C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%/AF129131
C-NT2RP4000984	C-NT2RP4001483//2-OXOGlutARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%/Q02218
C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%/P34579	C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%/P39010
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%/P70700	C-NT2RP4001502
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%/P39968	C-NT2RP4001507
C-NT2RP4001006	C-NT2RP4001524
C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete c ds.//0//2482bp//99%/AB023181	C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INT ERGENIC REGION.//5.7E-54//242aa//38%/P25656
C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUC INE--TRNA LIGASE).//1.5E-92//443aa//44%/Q09996	C-NT2RP4001551//Homo sapiens chromatin-specific transcription elon gation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%/AF152961
C-NT2RP4001057	C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%/P96902
C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%/Q64375	C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26%/Q02453
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//563aa//46%/P13586	C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%/P35197
C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%/AB023967	C-NT2RP4001571
C-NT2RP4001086	C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%/AF100756
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//21aa//36%/P51400	C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%/AJ223830
C-NT2RP4001100	C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN E--TRNA LIGASE) (ILERS).//1.7E-141//373aa//47%/P73505
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%/P38378	C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cd s.//0//1897bp//99%/AB020676
C-NT2RP4001122//TIPO PROTEIN.//1.4E-65//253aa//41%/Q15736	C-NT2RP4001614
C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%/Q07283	C-NT2RP4001634
C-NT2RP4001138	C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%/P40469
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP).//0.00000021//93aa//33%/P44514	C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%/P25323
C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%/P33750	C-NT2RP4001677
C-NT2RP4001149	C-NT2RP4001679
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (N R-CAM) (BRAVO).//3.4E-29//385aa//29%/P35331	C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4E-10//243aa//25%/Q10568
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR ECURSOR (CTPT).//4.7E-29//227aa//35%/P52178	C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%/Q10282
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA A, complete cds.//4.4E-104//1460bp//65%/U95760	C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECU RSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%/Q09332
C-NT2RP4001207	C-NT2RP4001739
C-NT2RP4001210	C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%/P51523
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%/P38660	C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTO R (RHO/RAC CEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%/P98174
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%/Q04652	C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete c ds.//0//3144bp//99%/AB023232
C-NT2RP4001235	C-NT2RP4001803
C-NT2RP4001256	C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%/Q35566
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cd s.//0//2876bp//99%/AB020682	C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%/P55083
C-NT2RP4001274//Human transporter protein (glt) mRNA, complete cd s.//4.4E-58//1196bp//61%/U49082	C-NT2RP4001828
C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%/Q07283	C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complet e cds.//6.3E-99//555bp//73%/AF155595
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MON38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%/P24391	C-NT2RP4001861//TRICHOHYALIN.//1E-35//307aa//34%/P37709
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%/AJ001119	C-NT2RP4001893//Homo sapiens mRNA: cDNA DKFZp5640043 (from clone D KFZp5640043).//0//1306bp//98%/AL050390
C-NT2RP4001339//Homo sapiens mRNA for AMMERCI protein.//9.2E-160//736bp//99%/AJ007014	C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00000014//345aa//25%/Q0808
C-NT2RP4001343	C-NT2RP4001901
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%/AB017494	C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy ch ain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%/U53445	
C-NT2RP4001353	
C-NT2RP4001372//IRREGULAR CHIASM C-ROUHEST PROTEIN PRECURSOR (IRR EC PROTEIN).//1.6E-19//222aa//30%/Q08180	

【0953】

【表650】

aa//32%/Q12024	C-OVARC1000443//Homo sapiens mRNA: cDNA DKF2p434A073 (from clone O
C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//3	KF2p434A073).//0//1216bp//99%/AL080126
8%/P49711	C-OVARC1000461
C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.	C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//2
1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEI	5%/P11075
N L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL	C-OVARC1000466
METHYLTRANSFERASE).//1.5E-13//211aa//28%/Q43209	C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.4
C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//35	8) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.1
6aa//27%/P13816	E-10//125aa//35%/P51452
C-NT2RP4001953	C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cd
C-NT2RP4001966	s.//0//1919bp//99%/AB020636
C-NT2RP4001975	C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2
C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370a	E-157//892bp//91%/AF051850
a//27%/Q04652	C-OVARC1000564
C-NT2RP4002052	C-OVARC1000576
C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DE	C-OVARC1000588
AH BOX PROTEIN 13).//1E-137//679aa//40%/Q43143	C-OVARC1000605
C-NT2RP4002071	C-OVARC1000640
C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10)	C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA fo
(HPF7).//3E-150//722aa//39%/Q05481	r GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%/D43772
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA	C-OVARC1000661
CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIA).//0.00000	C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%/P
67//250aa//31%/P52655	08866
C-NT2RP4002298	C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%/
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//	Q58343
53%/P38938	C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//11
C-NT2RP4002791	13bp//86%/AF001533
C-NT2RP4002888//Homo sapiens mRNA: cDNA DKF2p434F172 (from clone O	C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172b
KF2p434F172).//0//2557bp//99%/AL080202	p//97%/AJ130978
C-NT2RP4002905	C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1
C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%/P53552	E-215//1027bp//98%/AF132946
C-NT2RP5003477//VEGETABLE INCOMPATIBILITY PROTEIN MET-E-1.//5.5	C-OVARC1001162
E-15//280aa//27%/Q00808	C-OVARC1001243
C-NT2RP5003492	C-OVARC1001296
C-NT2RP5003500	C-OVARC1001360
C-NT2RP5003506	C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor i
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR	nvolved in B-CLL.//6E-148//683bp//99%/AJ224819
).//3.3E-23//219aa//40%/P37116	C-OVARC1001425
C-NT2RP5003524	C-PLACE1000005
C-NT2RP5003534	C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%/P53538
C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%/P02262	C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CR
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//	OTOMASE).//2.8E-29//134aa//43%/P52046
0.000042//102aa//32%/Q14727	C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete c
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6	ds.//5.5E-312//1411bp//99%/AB020639
E-295//1393bp//97%/AF058922	C-PLACE1000185
C-OVARC1000035	C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete c
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.2	ds.//0//1904bp//99%/AB023194
7.1) (RNASE LE).//0.0000032//60aa//45%/P80022	C-PLACE1000347
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.5E-12//174aa//26%/Q02874	C-PLACE1000374
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN)	C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cd
(HFC1) (VCAF) (CFF).//8.4E-14//259aa//30%/P51610	s.//0//2208bp//99%/AB020660
C-OVARC1000113	C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99
C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0	%//AJ224979
//1562bp//99%/AF132955	C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.
C-OVARC1000148	7E-30//352aa//31%/P15151
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38	C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//3
interacting with transcription factor Spl.//2.5E-95//461bp//98%/	34aa//72%/P23246
AJ242975	C-PLACE1000420//7, 8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.
C-OVARC1000168	-) (8-OXO-DGTPASE).//0.0000028//134aa//29%/P53368
C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA,	C-PLACE1000435
complete cds.//1.8E-32//511bp//85%/AF068332	C-PLACE1000444
C-OVARC1000212	C-PLACE1000562
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (AR	C-PLACE1000564
NT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALP	C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GU
HA).//8.2E-120//351aa//54%/Q16665	ANINE NUCLEOTIDE- BINDING PROTEIN 1).//1.6E-270//437aa//86%/P3245
C-OVARC1000288//VACUOLAR AMINOPEPTIDASE 1 PRECURSOR (EC 3.4.11.22)	5
(POLYPEPTIDASE) (LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDAS	C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete c
E III) (AMINOPEPTIDASE YSC1).//5.4E-53//384aa//30%/P14904	ds.//0//2393bp//99%/AB020657
C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%/P23249	C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA,
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//	complete cds.//2E-55//779bp//67%/AF044201
38%/P29363	C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%/Q0
C-OVARC1000321	8891
C-OVARC1000326	C-PLACE1000716
C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGEN	C-PLACE1000748
IC REGION.//5.9E-14//200aa//27%/P40004	C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds./
C-OVARC1000347	/4.5E-250//1189bp//97%/AB028449
C-OVARC1000384	C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cd
C-OVARC1000411	s.//0//2002bp//99%/AB014548
C-OVARC1000420	C-PLACE1000798
C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%/Q04205	C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR14

【表651】

8W. //2.5E-49//181aa//54%/P32899	//6.9E-206//396aa//86%/P51522
C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%/P39010	C-PLACE1003334
C-PLACE1000948	C-PLACE1003342
C-PLACE1000972	C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%/U92715
C-PLACE1000977//BETA-CHIMAEIN (BETA-CHIMERIN).//4.4E-22//129aa//35%/Q03070	C-PLACE1003369
C-PLACE1001000	C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%/D83200
C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%/AF055485	C-PLACE1003611
C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%/Q04652	C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%/P18824
C-PLACE1001383//ZINC-FINGER PROTEIN UBI-04 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM).//3E-33//138aa//42%/Q61103	C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//209aa//34%/Q08170
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//132aa//46%/Q12929	C-PLACE1003711
C-PLACE1001399//Homo sapiens chromosome 17, clone hPK.22_M.12, complete sequence.//0//2118bp//99%/AC005412	C-PLACE1003723
C-PLACE1001412	C-PLACE1003762
C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22. WORKING DRAFT SEQUENCE, in unordered pieces.//0//1440bp//99%/AL031660	C-PLACE1003771
C-PLACE1001503	C-PLACE1003784
C-PLACE1001570	C-PLACE1003923
C-PLACE1001610	C-PLACE1003936
C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4E-81//263aa//56%/P08635	C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.4E-124//326aa//73%/P80385
C-PLACE1001729	C-PLACE1004104
C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//3.5E-75//439aa//41%/P16381	C-PLACE1004114
C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%/Q57290	C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.1E-181//340aa//96%/P29387
C-PLACE1001810	C-PLACE1004149
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%/AF058953	C-PLACE1004156
C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%/P94524	C-PLACE1004161
C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%/AF131737	C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%/AJ010071
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%/AF099935	C-PLACE1004197//BUTYROPHEIN PRECURSOR (BT).//4.5E-10//208aa//27%/Q62556
C-PLACE1001928	C-PLACE1004203//Homo sapiens GPI-anchored membrane protein Cdw108 precursor, mRNA, complete cds.//0//1882bp//99%/AF069493
C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%/Q49091	C-PLACE1004258
C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%/Q61211	C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%/O15393
C-PLACE1002072	C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%/AF084830
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATASE) (ADENYLATE CYCLASE).//0.0000053//188aa//29%/P49606	C-PLACE1004289
C-PLACE1002140	C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%/P33750
C-PLACE1002163	C-PLACE1004316//H. sapiens mRNA for apoptosis specific protein.//0//1767bp//99%/Y11588
C-PLACE1002170	C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%/AF100153
C-PLACE1002433	C-PLACE1004376
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%/Q13105	C-PLACE1004388
C-PLACE1002465	C-PLACE1004405
C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%/AB018256	C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%/Q63448
C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%/AF068180	C-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%/U49283
C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%/Q15391	C-PLACE1004451
C-PLACE1002794	C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.000002//218aa//23%/P25823
C-PLACE1002815	C-PLACE1004473
C-PLACE1002839	C-PLACE1004510//Homo sapiens cofactor of initiator function (C1F150) mRNA, complete//1.3E-209//954bp//99%/AF026445
C-PLACE1002851	C-PLACE1004516
C-PLACE1002941	C-PLACE1004548
C-PLACE1002996	C-PLACE1004584//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%/Q10568
C-PLACE1003045	C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%/Q13438
C-PLACE1003092	C-PLACE1004645
C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%/Q13268	C-PLACE1004646//B. taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%/X66277
C-PLACE1003108	C-PLACE1004664
C-PLACE1003145	C-PLACE1004672
C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PUB42).//3.8E-37//143aa//51%/P42743	C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALC-2 (PMP41) (ALG-257).//1.6E-95//191aa//96%/P12815
C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%/P33750	C-PLACE1004691
C-PLACE1003200	C-PLACE1004722
C-PLACE1003296//Homo sapiens mRNA: cDNA DKFp434G173 (from clone D KF2p434G173).//0//1706bp//99%/AL080133	C-PLACE1004736
C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//52	C-PLACE1004740

【0955】



【表652】

C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase S T3Gal VI, complete cds.//1.1E-224//790bp//98%/AB022918  
 C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%/P30337  
 C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHAT- LYASE) (ADENYL CYCLASE).//4.7E-65//695aa//29%/Q01631  
 C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%/Q08170  
 C-PLACE1004824  
 C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%/Q0 8891  
 C-PLACE1004885  
 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RN A HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%/Q42643  
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LD H-A).//4.9E-48//198aa//44%/P06151  
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds //0//1853bp//98%/AF099936  
 C-PLACE1004934  
 C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%/Q93794  
 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%/Q11073  
 C-PLACE1004982  
 C-PLACE1005026  
 C-PLACE1005027  
 C-PLACE1005046  
 C-PLACE1005077  
 C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.// 1E-209//1031bp//96%/L40401  
 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565a a//30%/Q04652  
 C-PLACE1005111  
 C-PLACE1005181  
 C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%/P05636  
 C-PLACE1005206  
 C-PLACE1005232  
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-). //1.3E-27//349aa//32%/Q01577  
 C-PLACE1005261  
 C-PLACE1005266  
 C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cd s.//3.2E-297//1341bp//100%/AB011182  
 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa //28%/P53352  
 C-PLACE1005305//CTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7. 4.10) (AK3).//2E-111//226aa//92%/P08760  
 C-PLACE1005308  
 C-PLACE1005313  
 C-PLACE1005327  
 C-PLACE1005335  
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PS155 SYNTHASE) (PSEUDOURIDYLATE SYNTH ASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%/Q33335  
 C-PLACE1005374  
 C-PLACE1005480  
 C-PLACE1005481  
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%/AJ006276  
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOM E 111.//5.6E-52//173aa//57%/Q09251  
 C-PLACE1005550  
 C-PLACE1005554  
 C-PLACE1005623  
 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, co mplete cds.//0//2130bp//99%/AF083255  
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE W2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%/P3135 0  
 C-PLACE1005730  
 C-PLACE1005755  
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CH AIN (EC 3.1.2.14) (THIOESTERASE II).//2.5E-79//209aa//53%/P08635  
 C-PLACE1005803  
 C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, comple te cds.//1.1E-217//994bp//99%/AF027156  
 C-PLACE1005851  
 C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%/P54120  
 C-PLACE1005923  
 C-PLACE1005925  
 C-PLACE1005934  
 C-PLACE1005936  
 C-PLACE1005951  
 C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30// 98aa//37%/P43636  
 C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE).//5.4E-54//455aa//32%/P14904  
 C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNI T (TAFII-90).//0.0000014//254aa//25%/P38129  
 C-PLACE1005990  
 C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase- 2.//0//1564bp//99%/AJ236876  
 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161 //744bp//99%/X99906  
 C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%/AF039023  
 C-PLACE1006139  
 C-PLACE1006159  
 C-PLACE1006167  
 C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cd s.//4.5E-293//953bp//99%/AB020706  
 C-PLACE1006195  
 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7 E-116//496aa//48%/Q09747  
 C-PLACE1006225  
 C-PLACE1006236  
 C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN)./ /2E-16//244aa//31%/P28675  
 C-PLACE1006246  
 C-PLACE1006325//Homo sapiens mRNA: cDNA DKFp564J142 (from clone D KFP564J142).//3.8E-278//1271bp//99%/AL080066  
 C-PLACE1006335  
 C-PLACE1006357  
 C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168 bp//99%/AF062085  
 C-PLACE1006412  
 C-PLACE1006414  
 C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%/P49 910  
 C-PLACE1006445  
 C-PLACE1006470  
 C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%/Q 90595  
 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68). //1.1E-229//367aa//96%/Q00004  
 C-PLACE1006492  
 C-PLACE1006531  
 C-PLACE1006552  
 C-PLACE1006598//Homo sapiens clone MH0310K15, WORKING DRAFT SEQUEN CE, 4 unordered pieces.//0//2182bp//99%/AC007383  
 C-PLACE1006615  
 C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partia: cd s.//0//1760bp//99%/AB023145  
 C-PLACE1006673  
 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, co mplete cds, clone:HP10328.//5.8E-24//734bp//62%/AB015630  
 C-PLACE1006704  
 C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FM N ADENYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SY NTHETASE).//6.9E-13//177aa//33%/Q59263  
 C-PLACE1006782  
 C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//2 32aa//80%/P08547  
 C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2. 15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PRO TEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN). //2E-15//188aa//29%/P35123  
 C-PLACE1006883  
 C-PLACE1006901  
 C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%/Q99181  
 C-PLACE1006932  
 C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME 111.//6.7E-48//278aa//41%/Q10000  
 C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%/ P97998  
 C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, co mplete cds.//0//1770bp//99%/AB023421  
 C-PLACE1006961  
 C-PLACE1006962  
 C-PLACE1006966  
 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPO

【0956】

【表653】

NSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%/Q14542  
 C-PLACE1007021  
 C-PLACE1007105  
 C-PLACE1007178  
 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III  
 OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)./  
 /1E-42//370aa//31%/P54304  
 C-PLACE1007238  
 C-PLACE1007239//Homo sapiens mRNA for transcription elongation fac  
 tor S-II, hS-II-TI, complete cds.//6.5E-216//1068bp//96%/D50495  
 C-PLACE1007242  
 C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%/P34579  
 C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp/  
 /99%/Y15908  
 C-PLACE1007274  
 C-PLACE1007282  
 C-PLACE1007301  
 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, comp  
 lete cds.//4.1E-17//1037bp//56%/AF117649  
 C-PLACE1007342  
 C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EB  
 BP) mRNA, complete cds.//0//2366bp//99%/AF096870  
 C-PLACE1007367  
 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-1  
 3.//0.0000044//127aa//30%/P27715  
 C-PLACE1007386  
 C-PLACE1007402  
 C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%/Q17320  
 C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-  
 CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEX  
 ING-PROTEIN-2) (ADABP).//8.8E-25//140aa//35%/P27487  
 C-PLACE1007450  
 C-PLACE1007452  
 C-PLACE1007460  
 C-PLACE1007484  
 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTO  
 R (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53  
 //426aa//33%/P52734  
 C-PLACE1007507  
 C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19)  
 (K19) (CK 19).//1.4E-85//385aa//45%/P08728  
 C-PLACE1007524  
 C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein AS  
 B-2 mRNA, complete cds.//8.9E-316//1485bp//98%/AF159164  
 C-PLACE1007544  
 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME  
 111.//1E-49//361aa//36%/P34537  
 C-PLACE1007583  
 C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666  
 aa//44%/Q99676  
 C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete c  
 ds.//0//713bp//99%/AB023194  
 C-PLACE1007621  
 C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.000001//228aa//  
 31%/P32506  
 C-PLACE1007645  
 C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete c  
 ds.//0//1952bp//99%/AB023194  
 C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTO  
 ANTIGEN HOMOLOG).//8.7E-09//279aa//28%/Q26457  
 C-PLACE1007690  
 C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%/P43535  
 C-PLACE1007706//Homo sapiens metalloprotease 1 (MPI) mRNA, complet  
 e cds.//0//3431bp//99%/AF061243  
 C-PLACE1007725  
 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-4  
 4//231aa//42%/P10265  
 C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete c  
 ds.//9.2E-294//1504bp//94%/AB014585  
 C-PLACE1007746  
 C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp  
 //99%/AB019602  
 C-PLACE1007810  
 C-PLACE1007843  
 C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome  
 region, segment 3/13.//0//1751bp//99%/AP000010  
 C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete c  
 ds.//0//3112bp//99%/AB018309  
 C-PLACE1007897  
 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (M  
 YOSIN 11).//2.6E-14//370aa//25%/Q99323  
 C-PLACE1007954  
 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRN  
 A, complete cds.//0//2252bp//99%/AF084530  
 C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (P  
 DE8B) mRNA, partial cds.//0//2300bp//99%/AF079529  
 C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP  
 M).//1.1E-36//202aa//48%/P52272  
 C-PLACE1007990  
 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSY  
 N-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%/Q6  
 3622  
 C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUEN  
 CE, 4 unordered pieces.//0//1833bp//99%/AC005628  
 C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN N  
 UP107) (107 KD NUCLEOPORIN) (P105).//4.6E-318//613aa//94%/P52590  
 C-PLACE1008095  
 C-PLACE1008122  
 C-PLACE1008129  
 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOM  
 E 111.//1.3E-24//395aa//31%/Q09531  
 C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%/P37709  
 C-PLACE1008209  
 C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMM  
 A-COP).//1.3E-283//671aa//77%/P53620  
 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//16  
 2aa//37%/P12689  
 C-PLACE1008280  
 C-PLACE1008309  
 C-PLACE1008329  
 C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial co  
 s.//0//1853bp//100%/AB014579  
 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%/P05432  
 C-PLACE1008401  
 C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTO  
 SIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%/P41541  
 C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%/Q  
 06527  
 C-PLACE1008457  
 C-PLACE1008465  
 C-PLACE1008488  
 C-PLACE1008524//Human DNA sequence from clone 34821 on chromosome  
 6p12.1-21.1. Contains part of a gene for a novel protein with ZUS  
 domain similar to part of Tight Junction Protein ZO1 (TJPI) and UM  
 C5 Homologs, the gene for a novel B2RP (peripheral benzodiazepine  
 recepto//0//1980bp//99%/AL031778  
 C-PLACE1008531  
 C-PLACE1008532  
 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT  
 ANTIGEN).//1.1E-09//52aa//48%/P22620  
 C-PLACE1008568  
 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN N  
 UP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%/P37199  
 C-PLACE1008621  
 C-PLACE1008626  
 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1  
 850bp//99%/AJ006591  
 C-PLACE1008629  
 C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA,  
 complete cds.//0//1548bp//100%/AF044333  
 C-PLACE1008693  
 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S pr  
 otein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitoch  
 ondrial protein, complete cds.//0//3002bp//99%/AF038406  
 C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBU  
 NIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%/O35345  
 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protei  
 n rad1A.//2.3E-269//1225bp//99%/AJ004974  
 C-PLACE1008813  
 C-PLACE1008854  
 C-PLACE1008867  
 C-PLACE1008887  
 C-PLACE1008902  
 C-PLACE1008925  
 C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%/P12623  
 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99  
 %//AJ003112  
 C-PLACE1009045  
 C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%/P48582  
 C-PLACE1009090

【0957】

【表654】

C-PLACE1009091	//Q62571
C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FU RIN 2).//1.9E-44//480aa//30%/P30432	C-PLACE1010102
C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452a a//67%/P51814	C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537 aa//44%/Q04652
C-PLACE1009110	C-PLACE1010106//Homo sapiens mRNA: cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//99%/AL049385
C-PLACE1009111	C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COM PLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%/P22082
C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGEN IC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%/Q05086	C-PLACE1010148//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.000000 46//431aa//23%/P35662
C-PLACE1009158	C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).// 9.8E-11//95aa//49%/Q01130
C-PLACE1009166	C-PLACE1010202
C-PLACE1009174	C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62 %/P25722
C-PLACE1009186	C-PLACE1010274//Homo sapiens mRNA: cDNA DKFZp5640123 (from clone D KFZp5640123).//0//1964bp//99%/AL080122
C-PLACE1009190	C-PLACE1010293
C-PLACE1009230	C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR ECURSOR (CTPT).//1.1E-09//350aa//22%/P52178
C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) m RNA, complete cds: nuclear gene for mitochondrial product.//2.1E-1 32//1229bp//75%/AF107295	C-PLACE1010324
C-PLACE1009328	C-PLACE1010329
C-PLACE1009335	C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (P I-PLC).//0.00000002//126aa//29%/P34024
C-PLACE1009338	C-PLACE1010364
C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29 %/Q12067	C-PLACE1010383
C-PLACE1009375	C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cd s.//0//2121bp//99%/AB020643
C-PLACE1009388	C-PLACE1010491
C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOS OME 1.//0.000000047//165aa//33%/Q09820	C-PLACE1010492
C-PLACE1009434	C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induc ed by progesterone), complete cds.//0//1981bp//99%/AB022718
C-PLACE1009443	C-PLACE1010529
C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%/ P42356	C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0 0000012//616aa//24%/P25386
C-PLACE1009459	C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane a nchor protein, complete cds.//0//1904bp//99%/AB017546
C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1 E-289//550aa//93%/P54319	C-PLACE1010616
C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CH ROMOSOME 111.//3.9E-40//179aa//37%/P34580	C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.000 00016//120aa//28%/P02642
C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%/Q99418	C-PLACE1010629
C-PLACE1009542	C-PLACE1010630
C-PLACE1009571	C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39 %/Q01755
C-PLACE1009581	C-PLACE1010714
C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1 E-54//291aa//40%/Q00808	C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polype ptide-C, complete cds.//4E-299//1091bp//99%/AB019987
C-PLACE1009607	C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRN A, partial cds.//8.9E-91//668bp//82%/AF020267
C-PLACE1009621	C-PLACE1010771//M. musculus HCMGP mRNA.//7.4E-168//966bp//89%/X680 61
C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa// 41%/P25159	C-PLACE1010786
C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).// 1.5E-285//538aa//99%/P55161	C-PLACE1010800
C-PLACE1009665	C-PLACE1010811
C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0// 1854bp//100%/AF062534	C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%/Q05481
C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING P ROTEIN C12G12.13C IN CHROMOSOME 1.//7E-33//166aa//43%/Q09876	C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cd s.//0//1885bp//99%/AB011182
C-PLACE1009721//NSF1 PROTEIN.//1.7E-22//176aa//33%/P35200	C-PLACE1010900
C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%/P54120	C-PLACE2000050
C-PLACE1009763//Homo sapiens mRNA for Medd8-activating enzyme HUBa 3, complete cds.//4.3E-294//1329bp//100%/AB012190	C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (NOTCH PROTEIN).//2.4E-191//828aa//48%/P21783
C-PLACE1009794	C-PLACE4000590
C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete c ds.//0//2685bp//99%/AB020712	C-PLACE4000638
C-PLACE1009886	C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).// 7.9E-177//201aa//34%/P49816
C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INT ERGENIC REGION.//1.9E-108//277aa//43%/P53145	C-Y79AA1001647
C-PLACE1009971	
C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84 )//4.6E-59//450aa//34%/P28175	
C-PLACE1009995//Homo sapiens mRNA: cDNA DKFZp5640123 (from clone D KFZp5640123).//0//1962bp//99%/AL080122	
C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70//736bp//73%/U48288	
C-PLACE1010023	
C-PLACE1010031	
C-PLACE1010053//M. musculus Snpr mRNA for RNA binding protein.//6E- 279//1402bp//94%/U84692	
C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%/AF065482	
C-PLACE1010076	
C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%	

## 【0229】

全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データ

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長  
さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

C-HEMBA1000005/DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%/  
Q61712  
C-HEMBA1000030

【表655】

C-HEMBA1000046	C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//
C-HEMBA1000050	0.0000002//198aa//29%/Q60401
C-HEMBA1000076	C-HEMBA1001303
C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%/P08553	C-HEMBA1001310
C-HEMBA1000158//HEPATOCTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5E-16//166aa//36%/P35584	C-HEMBA1001326
C-HEMBA1000168//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%/P35662	C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds.//1.4E-13//614bp//99%/AF057358
C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%/P48555	C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%/P17081
C-HEMBA1000193	C-HEMBA1001388
C-HEMBA1000227	C-HEMBA1001398
C-HEMBA1000288	C-HEMBA1001405
C-HEMBA1000302	C-HEMBA1001407
C-HEMBA1000304	C-HEMBA1001413
C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91%/Q35594	C-HEMBA1001415
C-HEMBA1000359//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%/AL049654	C-HEMBA1001446
C-HEMBA1000387	C-HEMBA1001450
C-HEMBA1000392	C-HEMBA1001455
C-HEMBA1000460	C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%/P18850
C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%/Q04652	C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%/P29166
C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%/P22279	C-HEMBA1001533
C-HEMBA1000501	C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%/AB020657
C-HEMBA1000508	C-HEMBA1001581
C-HEMBA1000520	C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%/Q14141
C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%/P02826	C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSG A).//1.6E-10//155aa//28%/Q63679
C-HEMBA1000534	C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROEIN).//4.6E-35//365aa//33%/P33450
C-HEMBA1000555	C-HEMBA1001702
C-HEMBA1000568	C-HEMBA1001714//Homo sapiens mRNA: cDNA DKFp564G0422 (from clone DKFp564G0422).//0//1845bp//99%/AL050386
C-HEMBA1000588	C-HEMBA1001731
C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%/Q43295	C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%/P53009
C-HEMBA1000636	C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%/P11675
C-HEMBA1000682	C-HEMBA1001815
C-HEMBA1000686	C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%/Q99676
C-HEMBA1000719	C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%/Q07230
C-HEMBA1000727	C-HEMBA1001864
C-HEMBA1000752	C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%/P20659
C-HEMBA1000817	C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.9.9.2) (ME2GLYOH).//9.3E-36//395aa//26%/Q63342
C-HEMBA1000851	C-HEMBA1001987
C-HEMBA1000867	C-HEMBA1002018
C-HEMBA1000869	C-HEMBA1002049
C-HEMBA1000872	C-HEMBA1002084
C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN).//1.6E-30//127aa//40%/P43366	C-HEMBA1002125
C-HEMBA1000918	C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%/P79293
C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN FOZE8.5 IN CHROMOSOME X.//1E-10//288aa//23%/Q19124	C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%/P43694
C-HEMBA1000946	C-HEMBA1002191
C-HEMBA1000968	C-HEMBA1002199
C-HEMBA1000971	C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%/P18161
C-HEMBA1000975	C-HEMBA1002237
C-HEMBA1001009	C-HEMBA1002265
C-HEMBA1001022	C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%/AF125537
C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN 8) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//1.4E-12//131aa//38%/Q01485	C-HEMBA1002349
C-HEMBA1001052	C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%/AF092563
C-HEMBA1001080	C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%/P22793
C-HEMBA1001085	C-HEMBA1002430
C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%/P48059	C-HEMBA1002439
C-HEMBA1001109	C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%/Q00994
C-HEMBA1001122	C-HEMBA1002460
C-HEMBA1001133	C-HEMBA1002462
C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX3 1) (KIAA0865) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%/Q06730	C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%/P98175
C-HEMBA1001140	C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEC PROTEIN).//1.1E-12//285aa//31%/P17437
C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%/P51646	C-HEMBA1002477
C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%/AB020678	
C-HEMBA1001235	
C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%/AJ130733	
C-HEMBA1001281	

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C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//35%/P48732	ds.//0//1732bp//98%/AB020712
C-HEMBA1002515	C-HEMBA1003417//Homo sapiens mRNA: cDNA DKFZp586C021 (from clone O KfZp586C021).//1.6E-312//1414bp//99%/AL050287
C-HEMBA1002542	C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%/P37709
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%/AF075587	C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%/AB013139
C-HEMBA1002583	C-HEMBA1003447
C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%/AB011169	C-HEMBA1003461
C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%/AB018351	C-HEMBA1003463
C-HEMBA1002688	C-HEMBA1003528
C-HEMBA1002696	C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%/P50480
C-HEMBA1002750	C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%/P53384
C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%/AJ000414	C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.2E-31//71aa//100%/P16874
C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%/AB020636	C-HEMBA1003568//52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-49//279aa//32%/P19474
C-HEMBA1002777	C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%/Q13330
C-HEMBA1002794	C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%/P26039
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2E-314//1437bp//99%/AF071185	C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa//35%/P19682
C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2E-304//1383bp//99%/AJ132819	C-HEMBA1003615
C-HEMBA1002850	C-HEMBA1003617//Homo sapiens HRHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%/AB015344
C-HEMBA1002863	C-HEMBA1003621
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EED8.8 IN CHROMOSOME 11.//1.5E-44//188aa//52%/Q09297	C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%/Q13207
C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%/AB011148	C-HEMBA1003690//HISTONE DEACETYLASE HDAC1.//2.1E-59//249aa//47%/P53973
C-HEMBA1002937	C-HEMBA1003711
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%/P16157	C-HEMBA1003807
C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%/AB020710	C-HEMBA1003864
C-HEMBA1002954	C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//89aa//46%/P16372
C-HEMBA1002971	C-HEMBA1003959
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%/P14646	C-HEMBA1003989
C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa//74%/Q02224	C-HEMBA1004074
C-HEMBA1003033	C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.5E-221//1188bp//78%/AF091234
C-HEMBA1003035	C-HEMBA1004146
C-HEMBA1003041	C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1893bp//98%/AB023145
C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%/Q75439	C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%/U05048
C-HEMBA1003067	C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.7E-217//1217bp//88%/AF095927
C-HEMBA1003096	C-HEMBA1004246
C-HEMBA1003117	C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.8E-257//738bp//99%/AF092094
C-HEMBA1003129	C-HEMBA1004289
C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%/P41940	C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%/AF132955
C-HEMBA1003148//Homo sapiens mRNA full length insert cDNA clone EU ROIMAGE 381801.//0//1583bp//99%/AL079278	C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2E-316//1445bp//99%/AF089841
C-HEMBA1003175	C-HEMBA1004596
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%/P44551	C-HEMBA1004693
C-HEMBA1003199	C-HEMBA1004736
C-HEMBA1003222	C-HEMBA1004753
C-HEMBA1003235//TROPOMYOSIN.//0.000023//109aa//33%/Q02088	C-HEMBA1004756//Human transporter protein (glt7) mRNA, complete cds.//9.1E-34//515bp//66%/U49082
C-HEMBA1003250//PROTEIN KINASE APKIA (EC 2.7.1.-).//7.2E-41//245aa//42%/Q06548	C-HEMBA1004758//Homo sapiens transcription factor SLI mRNA, complete cds.//2.6E-246//1249bp//94%/L39060
C-HEMBA1003257	C-HEMBA1004763
C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%/P32506	C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%/P08547
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229//1043bp//99%/AB024436	C-HEMBA1004771
C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%/AB011109	C-HEMBA1004776
C-HEMBA1003322	C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%/P50851
C-HEMBA1003327	C-HEMBA1004806
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0000002//248aa//23%/Q02224	C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%/Q00004
C-HEMBA1003370	C-HEMBA1004850
C-HEMBA1003380	C-HEMBA1004863//Homo sapiens mRNA: cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//100%/AL080114
C-HEMBA1003395	C-HEMBA1004923
C-HEMBA1003402	C-HEMBA1004929
C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%/AB020712	C-HEMBA1004930//26S PROTEASOME SUBUNIT 55B (KIAA0072) (HA1357).//

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3.3E-27//65aa//100%/Q16401	C-HEMBA1004933	C-HEMBA1004954	C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%/P12036	C-HEMBA1005475	C-HEMBA1005581//Homo sapiens SLIT2 (SLIT2) mRNA, complete cds.//0//1721bp//100%/AF133270	C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%/P16372	C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1 a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%/AF076183	C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%/P26043	C-HEMBA1006377	C-HEMBA1006467	C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%/Q01552	C-HEMBA1006530	C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//0.00000043//111aa//40%/Q01485	C-HEMBA1006795	C-HEMBA1006877//OXISTEROL-BINDING PROTEIN.//2E-59//378aa//39%/P16258	C-HEMBA1006936	C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%/AF078849	C-HEMBA1007342	C-HEMBA1000008	C-HEMBA1000018	C-HEMBA1000024	C-HEMBA1000025	C-HEMBA1000036	C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%/AF084928	C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%/P11799	C-HEMBA1000103	C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%/Y15521	C-HEMBA1000136	C-HEMBA1000215	C-HEMBA1000226//PUTATIVE PRE-mRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEDD5.//2.7E-12//112aa//47%/Q09530	C-HEMBA1000244	C-HEMBA1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%/Q23256	C-HEMBA1000338	C-HEMBA1000339	C-HEMBA1000391	C-HEMBA1000438	C-HEMBA1000449	C-HEMBA1000589	C-HEMBA1000591	C-HEMBA1000623	C-HEMBA1000630	C-HEMBA1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//232aa//28%/P78970	C-HEMBA1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%/P27671	C-HEMBA1000671	C-HEMBA1000673	C-HEMBA1000705	C-HEMBA1000706	C-HEMBA1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%/U53475	C-HEMBA1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%/AF151847	C-HEMBA1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.2E-126//613bp//97%/AF111105	C-HEMBA1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-54//232aa//43%/P39956	C-HEMBA1000807	C-HEMBA1000810	C-HEMBA1000848	C-HEMBA1000852	C-HEMBA1000870	C-HEMBA1000887	C-HEMBA1000908	C-HEMBA1000927//Homo sapiens caldesinin mRNA, complete cds.//1.1E-70//595bp//76%/AF120102	C-HEMBA1000947//Homo sapiens clone HAW100 putative ribonuclease II I mRNA, complete cds.//0//2292bp//99%/AF116910	C-HEMBA1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%/AF099974	C-HEMBA1000975	C-HEMBA1000985//M1PP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-18//178aa//30%/P28575	C-HEMBA1000991	C-HEMBA1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%/P51523	C-HEMBA1001014	C-HEMBA1001024	C-HEMBA1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%/P46087	C-HEMBA1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//80%/AF010144	C-HEMBA1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%/AF034803	C-HEMBA1001096	C-HEMBA1001105	C-HEMBA1001117	C-HEMBA1001126	C-HEMBA1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%/AB019435	C-HEMBA1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%/AF110267	C-HEMBA1001153	C-HEMBA1001169	C-HEMBA1001175//ANKYRIN.//6.9E-11//169aa//31%/Q02357	C-HEMBA1001182	C-HEMBA1001199	C-HEMBA1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%/AB023187	C-HEMBA1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%/AF089897	C-HEMBA1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%/AF132966	C-HEMBA1001289	C-HEMBA1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%/P17081	C-HEMBA1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%/U92703	C-HEMBA1001331	C-HEMBA1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%/P98175	C-HEMBA1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%/AF097441	C-HEMBA1001369	C-HEMBA1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%/AF100757	C-HEMBA1001387	C-MAMMA1002117	C-MAMMA1002319	C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%/Q02926	C-NT2RM1000080//LINC-1 PROTEIN.//5.9E-25//211aa//31%/Q21190	C-NT2RM1000242	C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%/P49028	C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%/P39942	C-NT2RM1000669	C-NT2RM1000781	C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%/AF092138	C-NT2RM1001008	C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.00000002//980bp//95%/AF085360	C-NT2RM1001074	C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000055//239aa//27%/P39942	C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSS s. complete sequence.//0//1740bp//99%/AL031291	C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%/P25167	C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DM IC) (CYTO
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【0961】

【表658】

PLASMIC DYNEIN INTERMEDIATE CHAIN). //0.0000043//136aa//31%/P54703	P). //9.5E-279//545aa//98%/P23514
C-NT2RM2000032	C-NT2RM20000837
C-NT2RM2000042	C-NT2RM20000951//Homo sapiens XYLK mRNA for xylulokinase, complete cds. //1.7E-200//927bp//99%/AB015046
C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8). //1.3E-36//160aa//40%/P50102	C-NT2RM20000952
C-NT2RM2000093	C-NT2RM20000984
C-NT2RM2000101	C-NT2RM2001004
C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds. //0//1574bp//99%/AF067223	C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1). //8.2E-154//285aa//99%/Q60809
C-NT2RM2000192	C-NT2RM2001065
C-NT2RM2000239	C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOM E III. //2.4E-15//266aa//26%/P46577
C-NT2RM2000250//Homo sapiens mRNA: cDNA DKFZp564L232 (from clone D KFZp564L232). //4.2E-314//1416bp//100%/AL080069	C-NT2RM2001131
C-NT2RM2000259	C-NT2RM2001141
C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN). //3.6E-19//181aa//34%/P14918	C-NT2RM2001152
C-NT2RM2000287	C-NT2RM2001177//Homo sapiens mRNA: cDNA DKFZp586G1822 (from clone DKFZp586G1822). //2.1E-293//1335bp//99%/AL080109
C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds. //3.4E-294//863bp//99%/AB020666	C-NT2RM2001194
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds. //0//1637bp//99%/AB011132	C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT). //1.3E-20//267aa//35%/P05143
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN. //1.8E-14//245aa//29%/P11274	C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5). //0.0000015//95aa//35%/P48724
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK 7 mRNA, partial cds. //0//1506bp//99%/U48251	C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (C-PIP10). //3.6E-10//177aa//32%/P97924
C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE). //1.7E-68//419aa//36%/P50849	C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE). //1.3E-180//328aa//99%/P13264
C-NT2RM2000374	C-NT2RM2001243
C-NT2RM2000395	C-NT2RM2001247
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LAT E ENDOCYTIC INTERMEDIATE COMPONENT). //1.6E-54//344aa//33%/P32802	C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR). //1.6E-166//312aa//98%/P53995
C-NT2RM2000407	C-NT2RM2001291
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73. //1E-222//237aa//89%/Q08469	C-NT2RM2001306//Homo sapiens mRNA: cDNA DKFZp564I052 (from clone D KFZp564I052). //0//1694bp//99%/AL080063
C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-CGN3 INTERGENIC REGION. //0.0000001//157aa//28%/P36113	C-NT2RM2001312
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-). //0.0000089//377aa//24%/P22211	C-NT2RM2001319
C-NT2RM2000490//SYNAPTOTAGMIN (P65). //1.8E-13//166aa//34%/P41823	C-NT2RM2001324//ZYXIN. //6.8E-55//200aa//41%/Q04584
C-NT2RM2000502	C-NT2RM2001345//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1. //0.0000029//334aa//22%/Q00808
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MPI) mRNA, complete cds. //0//1673bp//99%/AF061243	C-NT2RM2001370
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN). //1.3E-12//282aa//32%/P17437	C-NT2RM2001393
C-NT2RM2000540	C-NT2RM2001420
C-NT2RM2000567	C-NT2RM2001424//Homo sapiens mRNA: cDNA DKFZp586D0920 (from clone DKFZp586D0920). //0//1621bp//100%/AL050146
C-NT2RM2000569	C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2). //7.4E-121//437aa//57%/P52569
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN E-TRNA LIGASE) (ILERS). //1.7E-187//741aa//46%/P73505	C-NT2RM2001504
C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds. //0//3001bp//99%/D86987	C-NT2RM2001524
C-NT2RM2000588//HISTONE DEACETYLASE HDAC1. //2.8E-60//384aa//40%/P53973	C-NT2RM2001544
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds. //0//2712bp//99%/AF156487	C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1). //6.9E-27//90aa//42%/P38660
C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds. //4.9E-70//838bp//69%/AF179221	C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //4.3E-61//312aa//44%/P19474
C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //4.4E-32//319aa//35%/Q08170	C-NT2RM2001582
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds. //0//3791bp//99%/AB018272	C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds. //0//1000bp//100%/AB014610
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds. //0//2530bp//99%/AB014558	C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ. //5.1E-26//204aa//34%/P28692
C-NT2RM2000639	C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds. //0//2390bp//99%/AB007931
C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds. //0//1543bp//99%/AB014576	C-NT2RM2001930
C-NT2RM2000669	C-NT2RM2001935
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2). //3.7E-142//285aa//90%/P32391	C-NT2RM2001936//32.3 KD PROTEIN IN CWPI-MBR1 INTERGENIC REGION. //2.7E-27//216aa//34%/P28320
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1). //3.8E-23//184aa//36%/Q15404	C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION. //0.0000001//212aa//23%/P38250
C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds. //4.4E-231//1065bp//99%/AB015342	C-NT2RM2001982
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L. //5.7E-53//266aa//43%/P41877	C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77). //1.9E-39//253aa//35%/P37838
C-NT2RM2000795	C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PD1) (EC 5.3.4.1). //1.3E-10//232aa//28%/Q12730
C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-CO	C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOM E I. //3.1E-12//206aa//30%/Q09782

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//0.0000099//338aa//24%/Q07878	C-NT2RP1000259
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HWRNP X) (CBP).//5E-62//104aa//57%/Q61990	C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%/AF067730
C-NT2RM2002091	C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%/AF053551
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840	C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%/P32447
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%/AF030435	C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%/P25343
C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKNA (EC 2.7.1.-).//4.9E-13//487aa//26%/P49695	C-NT2RP1000357
C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805	C-NT2RP1000376//Homo sapiens mRNA: cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%/AL080187
C-NT2RM2002178//Homo sapiens mRNA: cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%/AL117402	C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%/AB011159
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%/P25167	C-NT2RP1000416
C-NT2RM40000061	C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCA P-G mRNA, complete cds.//1.8E-94//1019bp//63%/AF111423
C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%/P52742	C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%/Q08257
C-NT2RM4000139//R. norvegicus trg mRNA.//2.3E-114//1161bp//72%/X68101	C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%/P34580
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//4.8E-13//686aa//23%/P25386	C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%/P09653
C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%/P16381	C-NT2RP1000481
C-NT2RM4000197	C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%/D87686
C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%/AB018255	C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%/P49020
C-NT2RM4000229//Callus gallus actin filament-associated protein (A FAP-110) mRNA, complete cds.//1.1E-27//633bp//64%/L20303	C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%/P97367
C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%/M99438	C-NT2RP1000581
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%/AJ132637	C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%/P25233
C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%/AF083246	C-NT2RP1000688
C-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%/Q24371	C-NT2RP1000695
C-NT2RM4000386//Mus musculus mRNA for Ten-3. complete cds.//0//2156bp//86%/AB025412	C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%/E14379
C-NT2RM4000395	C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%/AF101434
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769	C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
C-NT2RM4000457//HYPOTHETICAL III.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8E-20//393aa//24%/Q10297	C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%/Q07960
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds.//0//2092bp//99%/AF097025	C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%/AF067223
C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 18-6; PEPTIDE P-H].//4.8E-11//242aa//31%/P04280	C-NT2RP1000846
C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%/P39955	C-NT2RP1000851
C-NT2RM4000511	C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%/P16884	C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%/Q13823
C-NT2RM4000520	C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.6E-105//504bp//99%/U39317
C-NT2RM4000585	C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%/Q04652
C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%/AF186273	C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%/Q13823
C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%/AB014587	C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//956bp//99%/M17885
C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%/AB020657	C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%/P19338
C-NT2RP1000040	C-NT2RP1000980
C-NT2RP1000063	C-NT2RP1000988
C-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%/X98834	C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (T H1) mRNA, complete cds.//2.2E-78//1529bp//61%/L01790
C-NT2RP1000101	C-NT2RP1001014
C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%/P93471	C-NT2RP1001395
C-NT2RP1000112	C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%/P91917
C-NT2RP1000124	C-NT2RP1001424
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%/P51859	C-NT2RP1001449
C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%/AB023165	C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%/AJ005257
C-NT2RP1000170	C-NT2RP1001466
C-NT2RP1000191	C-NT2RP1001475
C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%/Q02357	C-NT2RP1001482
C-NT2RP1000243	C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%/Q08891
	C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IP

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S). //1.6E-166//506aa//60%/P42803	C-NT2RP2000503
C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN). //1.6E-30//232aa//30%/O35566	C-NT2RP2000510
C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA). //5.8E-121//271aa//89%/P47758	C-NT2RP2000516
C-NT2RP1001616	C-NT2RP2000603
C-NT2RP1001665//CALMODULIN. //0.0000051//83aa//30%/P02594	C-NT2RP2000617
C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40). //9.8E-17//79aa//55%/O34136	C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cd s. //0//2482bp//99%/AB014514
C-NT2RP2000007	C-NT2RP2000656
C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2). //2.4E-177//726aa//47%/P51523	C-NT2RP2000658
C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1). //1.8E-22//184aa//34%/Q01730	C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-). //1.3E-27//349aa//32%/Q01577
C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (Tid1) mRNA, complete cds. //0//1390bp//98%/AF061749	C-NT2RP2000704
C-NT2RP2000054	C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) //2.7E-100//488aa//44%/O32038
C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON). //9.4E-16//45aa//100%/P49446	C-NT2RP2000764//NIFS PROTEIN. //6.6E-36//252aa//42%/P12623
C-NT2RP2000067	C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cd s. //0//3347bp//99%/AB020680
C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROEIN). //3.4E-51//383aa//32%/P33450	C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A). //0.00000056//179aa//29%/Q99104
C-NT2RP2000079	C-NT2RP2000814//GELATIN FACTOR (ACTIN BINDING PROTEIN 120) (ABP-1 20). //0.0000011//96aa//29%/P13466
C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cd s. //0//2286bp//100%/AB018338	C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT. //0.00000079//172aa//28%/P26174
C-NT2RP2000091	C-NT2RP2000819
C-NT2RP2000097	C-NT2RP2000841
C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds. //0//2244bp//99%/AB018356	C-NT2RP2000845
C-NT2RP2000120	C-NT2RP2000863
C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SMF2L. //2.5E-117//541aa//42%/P41877	C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2. //0//694aa//99%/O60841
C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cd s. //0//2286bp//99%/AB023206	C-NT2RP2000892
C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN). //4.4E-226//423aa//99%/P35585	C-NT2RP2000931//MATRIN 3. //2.4E-289//467aa//95%/P43244
C-NT2RP2000153//GAR2 PROTEIN. //9.8E-23//311aa//28%/P41891	C-NT2RP2000932//Homo sapiens mRNA: cDNA DKFZp5640043 (from clone D KfZp5640043). //0//2487bp//99%/AL050390
C-NT2RP2000157//MLD2 PROTEIN. //2.6E-11//62aa//40%/Q09329	C-NT2RP2000938
C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete c ds. //3.4E-315//1430bp//99%/AB023225	C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete c ds. //0//3458bp//99%/AB018298
C-NT2RP2000173	C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds. //0//1989bp//96%/AB024704
C-NT2RP2000175	C-NT2RP2000985
C-NT2RP2000195	C-NT2RP2001036
C-NT2RP2000205	C-NT2RP2001044
C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cd s. //0//2898bp//99%/AB020699	C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0488. //0//2749bp//99%/AB007957
C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1). //0.000043//103aa//28%/P35568	C-NT2RP2001065
C-NT2RP2000232	C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE). //5.8E-46//222aa//45%/Q20939
C-NT2RP2000233	C-NT2RP2001081//SYNAPTOTAGMIN IV. //4.2E-118//430aa//54%/P50232
C-NT2RP2000239	C-NT2RP2001094
C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMI NYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P 110 SUBUNIT). //3.4E-21//210aa//33%/P56558	C-NT2RP2001119
C-NT2RP2000270	C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein. //0//2514bp//99%/AJ132440
C-NT2RP2000274	C-NT2RP2001218
C-NT2RP2000283	C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEA VY CHAIN) (NMHC). //2.2E-10//366aa//28%/P14105
C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMO SOME 1. //1.6E-27//576aa//25%/Q10297	C-NT2RP2001381
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT). //3.3E-186//255aa//60%/Q99676	C-NT2RP2001397//Homo sapiens mRNA: cDNA DKFZp434B174 (from clone D KfZp434B174). //0//1495bp//100%/AL080146
C-NT2RP2000298	C-NT2RP2001427
C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PROD H) mRNA, complete cds. //4.3E-279//1193bp//99%/U82381	C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cd s. //0//1748bp//99%/AB018340
C-NT2RP2000328	C-NT2RP2001675
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3). //2E-111//226aa//92%/P08760	C-NT2RP2001721
C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN M YD116. //6.3E-115//674aa//46%/P17564	C-NT2RP2001907
C-NT2RP2000369	C-NT2RP2001969
C-NT2RP2000412	C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha 1) mRNA, complete cds. //4.7E-177//1538bp//74%/AF062378
C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F). //4.3E-228//415aa//100%/P52597	C-NT2RP2002046
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds. //0//1757bp//99%/AF102265	C-NT2RP2002154
C-NT2RP2000438	C-NT2RP2002208
C-NT2RP2000448//XES1 PROTEIN. //8.7E-54//392aa//38%/P35844	C-NT2RP2002270//AF-9 PROTEIN. //0.0000012//74aa//36%/P42568
	C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein. //0//2333bp//99%/Y16521
	C-NT2RP2002325//Homo sapiens mRNA for Pax1lp, complete cds. //8.4E-254//1158bp//99%/AB015594
	C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced var iant mRNA, complete cds. //4.3E-240//1105bp//99%/AF038958
	C-NT2RP2002426
	C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, c omplete cds. //0//2180bp//99%/AB005289
	C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME

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X.//6.2E-19//288aa//26%/Q11073	C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.0000095//297aa//20%/P13692
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815	C-NT2RP2004999
C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345	C-NT2RP2005000
C-NT2RP2002621	C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%/AB014515
C-NT2RP2002672	C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%/AJ011779
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME 11.//1.9E-14//210aa//30%/O14345	C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%/P32447
C-NT2RP2002769	C-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%/X98743
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764	C-NT2RP2005140
C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%/AF038392	C-NT2RP2005147
C-NT2RP2002954	C-NT2RP2005159
C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%/P51669	C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds.//0//2087bp//99%/AF097025
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.0000001//98aa//36%/P10129	C-NT2RP2005270
C-NT2RP2002985//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%/AB026190	C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%/D89053
C-NT2RP2003108	C-NT2RP2005293
C-NT2RP2003117	C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%/AB014576
C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.3E-82//642bp//68%/AF079765	C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MB03 (MBD3) mRNA, complete cds.//0//2199bp//99%/AF072247
C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%/Q04652	C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%/Q13823
C-NT2RP2003177	C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%/Q08170
C-NT2RP2003194	C-NT2RP2005441
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%/AF151811	C-NT2RP2005453
C-NT2RP2003295//Homo sapiens RBP mRNA for RPB5 mediating protein, complete cds.//0//1526bp//99%/AB006572	C-NT2RP2005464
C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%/P26337	C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%/P38127
C-NT2RP2003367	C-NT2RP2005472
C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%/P38378	C-NT2RP2005495
C-NT2RP2003446	C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PP55).//5.2E-81//166aa//88%/P36876
C-NT2RP2003533	C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%/AF151803
C-NT2RP2003543//HYPOTHETICAL TRNA/RNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%/P74261	C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%/AF092563
C-NT2RP2003596	C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%/AF035526
C-NT2RP2003629	C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%/AB007963
C-NT2RP2003687	C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-O-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%/Q39366
C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%/Q05481	C-NT2RP2005555
C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%/P51669	C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%/AF062529
C-NT2RP2003793	C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9E-313//1455bp//98%/AF062085
C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%/O09175	C-NT2RP2005622
C-NT2RP2003986	C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%/P47623
C-NT2RP2004042	C-NT2RP2005637
C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%/AL096820	C-NT2RP2005640
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%/P38120	C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%/P56101
C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%/P36044	C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%/AJ010973
C-NT2RP2004463	C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%/AF089814
C-NT2RP2004602	C-NT2RP2005683
C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%/AB023139	C-NT2RP2005690
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%/AJ006291	C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%/AB018342
C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1.//5.6E-64//616aa//33%/Q92355	C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODPI PROTEIN).//0.00000003//169aa//28%/P38074
C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%/Q10490	C-NT2RP2005748
C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%/P53588	C-NT2RP2005752//Homo sapiens TMFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%/AF068868
C-NT2RP2004802	C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%/AF082516
C-NT2RP2004841	C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%/P47943
C-NT2RP2004936	

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【表662】

C-NT2RP2005767//G. gallus PBI gene.//5E-163//1158bp//81%/X90849	C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DE AM BOX PROTEIN 13)//1.7E-139//679aa//41%/043143
C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase iso form (P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%/AF151351	C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%/AF071185
C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%/Q02038	C-NT2RP3000484
C-NT2RP2005781	C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//72%/P28160
C-NT2RP2005804	C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%/P15151
C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%/P34223	C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%/Q07283
C-NT2RP2005853	C-NT2RP3000599
C-NT2RP2005868	C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%/P51523
C-NT2RP2005886	C-NT2RP3000644
C-NT2RP2005890	C-NT2RP3000661
C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%/AB023188	C-NT2RP3000665
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%/P48837	C-NT2RP3000690
C-NT2RP2006038	C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%/Q94650
C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%/Q08170	C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%/Q61982
C-NT2RP2006052	C-NT2RP3000836
C-NT2RP2006069	C-NT2RP3000841
C-NT2RP2006071	C-NT2RP3000850
C-NT2RP2006100//Homo sapiens mRNA: cDNA OKFZp5648102 (from clone D KF2p5648102).//0//1759bp//99%/AL049970	C-NT2RP3000852
C-NT2RP2006106	C-NT2RP3000859
C-NT2RP2006141	C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.9E-69//1611bp//61%/U53445
C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%/AB014554	C-NT2RP3000869
C-NT2RP2006196	C-NT2RP3000901
C-NT2RP2006200	C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds.//0//3199bp//99%/AF064257
C-NT2RP2006219//H. sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%/X96484	C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.7E-185//585bp//88%/AF015264
C-NT2RP2006237	C-NT2RP3000980
C-NT2RP2006238	C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B (CONTAINS: LIGHT CHAIN LC1).//2E-59//388aa//32%/P46821	C-NT2RP3001004
C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%/AF035262	C-NT2RP3001081
C-NT2RP2006333	C-NT2RP3001084
C-NT2RP2006365	C-NT2RP3001096//Rattus norvegicus leprecan (leprel) mRNA, complete cds.//1.7E-94//787bp//66%/AF087433
C-NT2RP2006393	C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%/P55201
C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOME BOX).//0.00000034//50aa//50%/Q61658	C-NT2RP3001109
C-NT2RP2006456	C-NT2RP3001116
C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%/AJ006266	C-NT2RP3001119
C-NT2RP2006467	C-NT2RP3001133
C-NT2RP2006472	C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%/AB018305
C-NT2RP2006565//Sus scrofa mRNA for SCAP1 protein.//0//1276bp//84%/Y15710	C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%/AJ006266
C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P45, 0-KMB) (OLFACTIVE).//4.2E-134//486aa//50%/P24461	C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.7E-10//196aa//27%/P53154
C-NT2RP2006573//2'-3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%/P09543	C-NT2RP3001214
C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%/AB020708	C-NT2RP3001216//CYCLICIN 1 (MULTIPLE-BAND POLYPEPTIDE 1) (FRAGMENT).//0.0000023//137aa//33%/P35663
C-NT2RP3000072	C-NT2RP3001221//GAMMA-BUTYROBETAIN, 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAIN HYDROXYLASE).//1.9E-31//353aa//30%/P80193
C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%/AB011164	C-NT2RP3001236
C-NT2RP3000220	C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%/P14873
C-NT2RP3000251	C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%/AB020718
C-NT2RP3000252//Homo sapiens GTP-binding protein NCB mRNA, complete cds.//0//2388bp//99%/AF120334	C-NT2RP3001307
C-NT2RP3000312	C-NT2RP3001325
C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%/AJ242978	C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%/AB025905
C-NT2RP3000333	C-NT2RP3001392
C-NT2RP3000348	C-NT2RP3001396
C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303.//0.000000028//185aa//31%/Q25074	C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%/P49711
C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760	C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%/P53009
C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%/AB019219	C-NT2RP3001420
C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%/P35293	C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%/Q33529
	C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%/Q09053

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【表663】

C-NT2RP3001457	ATIN)../0.000003//101aa//32%/P26372
C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A../9.1E-13//87aa//43%/P11632	C-NT2RP4000355
C-NT2RP3001495//Human oxidoreductase (HMCMA56) mRNA, complete cds../0//1475bp//99%/U13395	C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds../0//4074bp//99%/AB018281
C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor 1 RCB (TRCB) mRNA, complete cds../0//2295bp//99%/AF064801	C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds../0//4782bp//99%/AF044195
C-NT2RP3001529//SPO08-ASSOCIATED GTP-BINDING PROTEIN../1E-61//345aa//42%/P20964	C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1)../2.6E-77//262aa//54%/Q75570
C-NT2RP3001621	C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein../0//2412bp//99%/AJ238243
C-NT2RP3001629	C-NT2RP4000381
C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210../6.8E-18//91aa//38%/Q92609	C-NT2RP4000398//ZINC FINGER PROTEIN 140../2.9E-110//435aa//50%/P52738
C-NT2RP3001646//WD-40 REPEAT PROTEIN MS12../8.8E-09//132aa//31%/Q22468	C-NT2RP4000415
C-NT2RP3001676	C-NT2RP4000417//MANNOsyl-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT)../2.6E-51//438aa//33%/P45701
C-NT2RP3001679	C-NT2RP4000448//Homo sapiens mRNA: cDNA DKFZp566G0746 (from clone DKFZp566G0746)../0//3991bp//99%/AL050078
C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE../1.6E-11//348aa//27%/P24733	C-NT2RP4000449
C-NT2RP3001819//RING CANAL PROTEIN (XELCH PROTEIN)../7.4E-18//249aa//30%/Q04652	C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0../0.000003//175aa//27%/P09309
C-NT2RP3001896	C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15)../2.5E-37//291aa//38%/P50101
C-NT2RP3001915	C-NT2RP4000480
C-NT2RP3001929	C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (mRNA TRANSPORT REGULATOR NTR4)../1.9E-67//721aa//29%/Q09475
C-NT2RP3003193//ZINC FINGER PROTEIN 135../7.3E-98//269aa//62%/P52742	C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1)../8.8E-50//214aa//50%/P40484
C-NT2RP3004466	C-NT2RP4000500
C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35../3.3E-113//466aa//42%/P34110	C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1../1.5E-106//495aa//45%/P45818
C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds../0//1520bp//99%/AB014532	C-NT2RP4000524
C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds../0//974bp//95%/AB011126	C-NT2RP4000541
C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NON ERYTHROID)../0.00000038//150aa//28%/Q01484	C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN)../7.4E-14//233aa//31%/P40319
C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15 D) mRNA, complete cds../0//1770bp//99%/AF026445	C-NT2RP4000560
C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds../0//1639bp//99%/AB007946	C-NT2RP4000588
C-NT2RP3004594//Homo sapiens mRNA for AMD-1 protein../0//1807bp//99%/AJ006266	C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds../2.9E-188//863bp//99%/AF067730
C-NT2RP3004617//ZINC-BINDING PROTEIN A33../7.2E-75//464aa//35%/Q02084	C-NT2RP4000638
C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA A, complete cds../0//3972bp//98%/AF093097	C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0../0.0000037//175aa//27%/P09309
C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN)../1.7E-72//254aa//45%/P54352	C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPS E../1.1E-32//350aa//30%/P39625
C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64../2.6E-98//239aa//64%/P35526	C-NT2RP4000704
C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65../4.9E-51//335aa//37%/Q64375	C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X../1.1E-13//295aa//27%/Q11073
C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds../0//3013bp//99%/AB020657	C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN../3.2E-191//199aa//78%/P10267
C-NT2RP4000109//Homo sapiens mRNA for MECF5, partial cds../0//2161bp//99%/AB011538	C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds../0//3392bp//95%/AB023148
C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)../0//728aa//99%/Q10568	C-NT2RP4000737
C-NT2RP4000129	C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds../0//3574bp//99%/AB023229
C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds../3.8E-28//528bp//67%/AF011427	C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION../0.00000032//67aa//31%/P53915
C-NT2RP4000150	C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds../0//1927bp//99%/AB007939
C-NT2RP4000151	C-NT2RP4000833
C-NT2RP4000159	C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1../4.3E-94//810bp//65%/Y18265
C-NT2RP4000185	C-NT2RP4000839//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1../8.5E-21//271aa//28%/Q00808
C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds../0//4149bp//99%/AB014600	C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)../5.7E-82//324aa//48%/Q09175
C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA)../5.9E-15//104aa//40%/P15287	C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)../4.1E-85//174aa//55%/P16415
C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)../0//1932bp//99%/AJ006470	C-NT2RP4000878//MYELOID UPREGULATED PROTEIN../6.2E-91//173aa//87%/Q03582
C-NT2RP4000246//MPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1)../2.7E-84//208aa//76%/Q03173	C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN)../9.6E-96//513aa//42%/P22314
C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9)../5.5E-29//153aa//43%/Q23968	C-NT2RP4000925//FIBRINOMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)../2.6E-26//227aa//36%/Q06828
C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1../3.5E-297//1024aa//55%/P87115	C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1)../1.5E-76//346aa//

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/43%/Q61068	0
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%	C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOM E 1.//2E-53//436aa//30%/Q10085
X//Y16521	C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete c ds.//0//2716bp//99%/AB023140
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%/Q58900	C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%/Q14141
C-NT2RP4000955	C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%/Q99676
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//90aa//42%/P38660	C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%/AF129131
C-NT2RP4000975	C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%/Q02218
C-NT2RP4000979	C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%/P39010
C-NT2RP4000984	C-NT2RP4001502
C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%/P34579	C-NT2RP4001507
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%/P70700	C-NT2RP4001524
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%/P39968	C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INT ERGENIC REGION.//5.7E-54//742aa//38%/P25656
C-NT2RP4001006	C-NT2RP4001551//Homo sapiens chromatin-specific transcription elon gation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%/AF152961
C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete c ds.//0//2482bp//99%/AB023181	C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%/P96902
C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUC INE--TRNA LIGASE).//1.5E-92//443aa//44%/Q09996	C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.0000054//213aa//26%/Q02453
C-NT2RP4001057	C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%/P35197
C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%/Q64375	C-NT2RP4001571
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//563aa//46%/P13586	C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%/AF100756
C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%/AB023967	C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%/AJ223830
C-NT2RP4001086	C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN E--TRNA LIGASE) (ILERS).//1.7E-141//373aa//47%/P73505
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%/P51400	C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cd s.//0//1897bp//99%/AB020676
C-NT2RP4001100	C-NT2RP4001614
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%/P38378	C-NT2RP4001634
C-NT2RP4001122//TIPO PROTEIN.//1.4E-65//253aa//41%/Q15736	C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/HMS19.//5.1E-46//234aa//32%/P40469
C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%/Q07283	C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%/P25323
C-NT2RP4001138	C-NT2RP4001677
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAISE (EC 3.5.1.18) (SDAP).//0.0000021//93aa//33%/P44514	C-NT2RP4001679
C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%/P33750	C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4E-10//243aa//25%/Q10568
C-NT2RP4001149	C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%/Q10282
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (N R-CAM) (BRAVO).//3.4E-29//385aa//29%/P35331	C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECU RSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%/Q09332
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR ECURSOR (CTPT).//4.7E-29//227aa//35%/P52178	C-NT2RP4001739
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRN A, complete cds.//4.4E-104//1460bp//65%/J95760	C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%/P51523
C-NT2RP4001207	C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTO R (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%/P98174
C-NT2RP4001210	C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete c ds.//0//3144bp//99%/AB023232
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%/P38660	C-NT2RP4001803
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%/Q04652	C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%/Q35566
C-NT2RP4001235	C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%/P55083
C-NT2RP4001256	C-NT2RP4001828
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cd s.//0//2876bp//99%/AB020682	C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complet e cds.//6.3E-99//555bp//73%/AF155595
C-NT2RP4001274//Human transporter protein (glr) mRNA, complete cd s.//4.4E-58//1196bp//61%/U49082	C-NT2RP4001861//TRICHOHYALIN.//1E-35//307aa//34%/P37709
C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%/Q07283	C-NT2RP4001893//Homo sapiens mRNA: cDNA DKFp5640043 (from clone D KFp5640043).//0//1306bp//98%/AL050390
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MON38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%/P24391	C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00000014//345aa//25%/Q08088
C-NT2RP4001315//Bos taurus mRNA for Rab5 GTP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%/AJ001119	C-NT2RP4001901
C-NT2RP4001339//Homo sapiens mRNA for AMMERCI protein.//9.2E-160//736bp//99%/AJ007014	C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%/Q12024
C-NT2RP4001343	C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%/P49711
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%/AB017494	
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy ch ain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%/U53445	
C-NT2RP4001353	
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRR EC PROTEIN).//1.6E-19//222aa//30%/Q08180	
C-NT2RP4001373	
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.2E-17//146aa//35%/P1816	

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C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) //1.5E-13//211aa//28%/Q43209	C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%/P11075
C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//355aa//27%/P13816	C-OVARC1000466
C-NT2RP4001953	C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.4)
C-NT2RP4001966	8) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VMR) //3.1E-10//125aa//35%/P51452
C-NT2RP4001975	C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%/AB020636
C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN) //6.9E-24//370aa//27%/Q04652	C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-15//782bp//91%/AF051850
C-NT2RP4002052	C-OVARC1000564
C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13) //1E-13//679aa//40%/Q43143	C-OVARC1000576
C-NT2RP4002071	C-OVARC1000588
C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //3E-150//722aa//39%/Q05481	C-OVARC1000605
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL) //0.0000067//250aa//31%/P52655	C-OVARC1000640
C-NT2RP4002298	C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%/D43772
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-) //1.5E-63//159aa//53%/P38938	C-OVARC1000661
C-NT2RP4002791	C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%/P08886
C-NT2RP4002888//Homo sapiens mRNA: cDNA DKFZp434F172 (from clone D KFZp434F172) //0//2557bp//99%/AL080202	C-OVARC1000959//HYPOTHETICAL PROTEIN NJ0933.//1.2E-17//127aa//33%/Q58343
C-NT2RP4002905	C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//113bp//86%/AF001533
C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%/P53552	C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%/AJ130978
C-NT2RP5003477//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%/Q00808	C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%/AF132946
C-NT2RP5003492	C-OVARC1001162
C-NT2RP5003500	C-OVARC1001243
C-NT2RP5003506	C-OVARC1001296
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) //3.3E-23//219aa//40%/P37116	C-OVARC1001360
C-NT2RP5003524	C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6E-148//683bp//99%/AJ224819
C-NT2RP5003534	C-OVARC1001425
C-OVARC1000008//HISTONE H2A.1.//1.1E-55//117aa//99%/P02262	C-PLACE1000005
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1) //0.0000042//102aa//32%/Q14727	C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%/P53538
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%/AF058922	C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CR OTOMASE) //2.8E-29//134aa//43%/P52046
C-OVARC1000035	C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5E-312//1411bp//99%/AB020639
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.2.7.1) (RNASE LE) //0.0000032//60aa//45%/P80022	C-PLACE1000185
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%/Q02874	C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%/AB023194
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF) //8.4E-14//259aa//30%/P51610	C-PLACE1000347
C-OVARC1000113	C-PLACE1000374
C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%/AF132955	C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%/AB020660
C-OVARC1000148	C-PLACE1000383//Homo sapiens mRNA for WTBR1 protein.//0//753bp//99%/AJ224979
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.//2.5E-95//461bp//98%/AJ242975	C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN) //2.7E-30//352aa//31%/P5151
C-OVARC1000168	C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF) //1.2E-132//334aa//72%/P23246
C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%/AF068332	C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANYL TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) //0.000028//134aa//29%/P53368
C-OVARC1000212	C-PLACE1000435
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (AR NT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALP HA) //8.2E-120//351aa//54%/Q16665	C-PLACE1000444
C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE) (LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE I11) (AMINOPEPTIDASE YSC1) //5.4E-53//384aa//30%/P14904	C-PLACE1000562
C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%/P23249	C-PLACE1000564
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2) //2.7E-40//154aa//38%/P29363	C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GU ANINE NUCLEOTIDE-BINDING PROTEIN 1) //1.6E-270//437aa//86%/P32455
C-OVARC1000321	C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%/AB020657
C-OVARC1000326	C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//87%/AF044201
C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCNA-WBP1 INTERGENIC REGION.//5.9E-14//200aa//27%/P40004	C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%/Q08891
C-OVARC1000347	C-PLACE1000716
C-OVARC1000384	C-PLACE1000748
C-OVARC1000411	C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.6E-250//1189bp//97%/AB028449
C-OVARC1000420	C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%/AB014548
C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%/Q04205	C-PLACE1000798
C-OVARC1000443//Homo sapiens mRNA: cDNA DKFZp434A073 (from clone D KFZp434A073) //0//1216bp//99%/AL080126	C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148.//2.5E-49//181aa//54%/P32899
C-OVARC1000461	C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%/P39010

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C-PLACE1000948	C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%/U92715
C-PLACE1000972	C-PLACE1003369
C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%/Q03070	C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%/D83200
C-PLACE1001000	C-PLACE1003611
C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%/AF065485	C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%/P18824
C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%/Q04652	C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//209aa//34%/Q08170
C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM).//3E-33//138aa//42%/Q61103	C-PLACE1003711
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//132aa//46%/Q12929	C-PLACE1003723
C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N.12, complete sequence.//0//2118bp//99%/ACD05412	C-PLACE1003762
C-PLACE1001412	C-PLACE1003771
C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered pieces.//0//1440bp//99%/AL031660	C-PLACE1003784
C-PLACE1001503	C-PLACE1003923
C-PLACE1001570	C-PLACE1003936
C-PLACE1001610	C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.4E-124//326aa//73%/P80385
C-PLACE1001692//5-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4E-81//263aa//56%/P08635	C-PLACE1004104
C-PLACE1001729	C-PLACE1004114
C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//3.5E-75//439aa//41%/P16381	C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.1E-181//340aa//96%/P29387
C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMN).//5.4E-63//427aa//35%/Q57290	C-PLACE1004149
C-PLACE1001810	C-PLACE1004156
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%/AF058953	C-PLACE1004161
C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%/P94524	C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%/AJ010071
C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%/AF131737	C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%/Q62556
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%/AF099935	C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//0//1862bp//99%/AF069493
C-PLACE1001928	C-PLACE1004258
C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%/Q49091	C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%/D15393
C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%/Q61211	C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%/AF084830
C-PLACE1002072	C-PLACE1004289
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//0.00000053//188aa//29%/P49606	C-PLACE1004302//SQF1 PROTEIN.//1.9E-110//325aa//48%/P33750
C-PLACE1002140	C-PLACE1004316//H. sapiens mRNA for apoptosis specific protein.//0//1767bp//99%/Y11588
C-PLACE1002163	C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%/AF100153
C-PLACE1002170	C-PLACE1004376
C-PLACE1002433	C-PLACE1004388
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%/Q13105	C-PLACE1004405
C-PLACE1002465	C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%/Q63448
C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%/AB018256	C-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%/U49283
C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%/AF068180	C-PLACE1004451
C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%/Q15391	C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%/P25823
C-PLACE1002794	C-PLACE1004473
C-PLACE1002815	C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete.//1.3E-209//954bp//99%/AF026445
C-PLACE1002839	C-PLACE1004516
C-PLACE1002851	C-PLACE1004548
C-PLACE1002941	C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%/Q10568
C-PLACE1002996	C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%/Q13438
C-PLACE1003045	C-PLACE1004645
C-PLACE1003092	C-PLACE1004646//B. taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%/X66277
C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%/Q13268	C-PLACE1004664
C-PLACE1003108	C-PLACE1004672
C-PLACE1003145	C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//96%/P12815
C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%/P42743	C-PLACE1004691
C-PLACE1003190//SQF1 PROTEIN.//1.9E-110//325aa//48%/P33750	C-PLACE1004722
C-PLACE1003200	C-PLACE1004736
C-PLACE1003296//Homo sapiens mRNA: cDNA DKFp434G173 (from clone D DKFp434G173).//0//1706bp//99%/AL080133	C-PLACE1004740
C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%/P51522	C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N-RECOGNIN).//4.4E-35//578aa//27%/Q60152
C-PLACE1003334	C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase S T3Gal VI, complete cds.//7.1E-224//790bp//98%/AB022918
C-PLACE1003342	C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-

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CHIMAERIN).//1.9E-32//259aa//32%/P30337	98aa//37%/P43636
C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//4.7E-65//695aa//29%/Q01631	C-PLACE1005955//VACUOLAR AMINOPEPTIDASE 1 PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-54//455aa//32%/P14904
C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%/Q08170	C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//254aa//25%/P38129
C-PLACE1004824	C-PLACE1005990
C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%/Q08891	C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%/AJ236876
C-PLACE1004885	C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%/X99906
C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%/Q42643	C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%/AF039023
C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.9E-48//198aa//44%/P06151	C-PLACE1006139
C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%/AF099936	C-PLACE1006159
C-PLACE1004934	C-PLACE1006167
C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%/Q93794	C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%/AB020706
C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%/Q11073	C-PLACE1006195
C-PLACE1004982	C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%/Q09747
C-PLACE1005026	C-PLACE1006225
C-PLACE1005027	C-PLACE1006236
C-PLACE1005046	C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-52) (DECORIN).//2E-16//244aa//31%/P28675
C-PLACE1005077	C-PLACE1006246
C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%/L40401	C-PLACE1006325//Homo sapiens mRNA: cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//1271bp//99%/AL080066
C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%/Q04652	C-PLACE1006335
C-PLACE1005111	C-PLACE1006357
C-PLACE1005181	C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%/AF062085
C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%/P05636	C-PLACE1006412
C-PLACE1005206	C-PLACE1006414
C-PLACE1005232	C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%/P49910
C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%/Q01577	C-PLACE1006445
C-PLACE1005261	C-PLACE1006470
C-PLACE1005266	C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%/Q90595
C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%/AB011182	C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%/Q00004
C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%/P53352	C-PLACE1006492
C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760	C-PLACE1006531
C-PLACE1005308	C-PLACE1006552
C-PLACE1005313	C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//2182bp//99%/AC007383
C-PLACE1005327	C-PLACE1006615
C-PLACE1005335	C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%/AB023145
C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PS155 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%/Q33335	C-PLACE1006673
C-PLACE1005374	C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//734bp//62%/AB015630
C-PLACE1005480	C-PLACE1006704
C-PLACE1005481	C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%/Q59263
C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%/AJ006276	C-PLACE1006782
C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME 11.//5.6E-52//173aa//57%/Q09251	C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%/P08547
C-PLACE1005550	C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%/P35123
C-PLACE1005554	C-PLACE1006883
C-PLACE1005623	C-PLACE1006901
C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%/AF083255	C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%/Q99181
C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%/P31350	C-PLACE1006932
C-PLACE1005730	C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME 11.//6.7E-48//278aa//41%/Q10000
C-PLACE1005755	C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%/P97998
C-PLACE1005763//5-ACYL FATTY ACID SYNTHASE THIOLESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOLESTERASE 1).//2.5E-79//209aa//53%/P08635	C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%/AB023421
C-PLACE1005803	C-PLACE1006961
C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%/AF027156	C-PLACE1006962
C-PLACE1005851	C-PLACE1006966
C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%/P54120	C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%/Q14542
C-PLACE1005923	C-PLACE1007021
C-PLACE1005925	C-PLACE1007105
C-PLACE1005934	
C-PLACE1005936	
C-PLACE1005951	
C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//1	

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C-PLACE1007178	A, complete cds. //0//2252bp//99%/AF084530
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE). //1E-42//370aa//31%/PS4304	C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds. //0//2300bp//99%/AF079529
C-PLACE1007238	C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M). //1E-36//202aa//48%/PS2272
C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds. //6.5E-216//1068bp//96%/D50495	C-PLACE1007990
C-PLACE1007242	C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSY N-110) (SYNAPTIC DENSITY PROTEIN PSD-93). //6.1E-14//128aa//39%/Q63622
C-PLACE1007243//UNC-47 PROTEIN. //0.0000017//211aa//27%/P34579	C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0//1833bp//99%/AC005628
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein. //0//2052bp//99%/Y15908	C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105). //4.6E-318//613aa//94%/PS2590
C-PLACE1007274	C-PLACE1008095
C-PLACE1007282	C-PLACE1008122
C-PLACE1007301	C-PLACE1008129
C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds. //4.1E-17//1037bp//56%/AF117649	C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III. //1.3E-24//395aa//31%/Q09531
C-PLACE1007342	C-PLACE1008177//TRICHOHYALIN. //2.3E-29//487aa//26%/P37709
C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds. //0//2366bp//99%/AF096870	C-PLACE1008209
C-PLACE1007367	C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP). //1.3E-283//671aa//77%/PS3620
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13. //0.00000044//127aa//30%/P27715	C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-). //2.3E-18//162aa//37%/P12689
C-PLACE1007386	C-PLACE1008280
C-PLACE1007402	C-PLACE1008309
C-PLACE1007409//WHITE PROTEIN. //1.1E-64//428aa//32%/Q17320	C-PLACE1008329
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP). //8.8E-25//140aa//35%/P27487	C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds. //0//1853bp//100%/AB014579
C-PLACE1007450	C-PLACE1008398//GENE 33 POLYPEPTIDE. //7.3E-114//243aa//87%/P05432
C-PLACE1007452	C-PLACE1008401
C-PLACE1007460	C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP). //0//698aa//95%/P41541
C-PLACE1007484	C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR. //3.1E-11//189aa//32%/Q06527
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG). //5.4E-53//426aa//33%/PS2734	C-PLACE1008457
C-PLACE1007507	C-PLACE1008465
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19). //1.4E-85//385aa//45%/P08728	C-PLACE1008488
C-PLACE1007524	C-PLACE1008524//Human DNA sequence from clone 34821 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazepine receptor). //0//1980bp//99%/AL031778
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds. //8.9E-316//1485bp//98%/AF159164	C-PLACE1008531
C-PLACE1007544	C-PLACE1008532
C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R0503.4 IN CHROMOSOME III. //1E-49//361aa//36%/P34537	C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN). //1.1E-09//62aa//48%/P22620
C-PLACE1007583	C-PLACE1008568
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT). //1.6E-143//666aa//44%/Q99676	C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140). //7.8E-236//453aa//96%/P37199
C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds. //0//713bp//99%/AB023194	C-PLACE1008621
C-PLACE1007621	C-PLACE1008626
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR. //0.0000001//228aa//31%/P32506	C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein. //0//1850bp//99%/AJ006591
C-PLACE1007645	C-PLACE1008629
C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds. //0//1952bp//99%/AB023194	C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds. //0//1548bp//100%/AF044333
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG). //8.7E-09//279aa//28%/Q26457	C-PLACE1008693
C-PLACE1007690	C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds. //0//3002bp//99%/AF038406
C-PLACE1007697//CCN20 PROTEIN. //7.6E-119//717aa//38%/P43535	C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2). //3.1E-280//533aa//98%/Q35345
C-PLACE1007706//Homo sapiens metalloprotease 1 (MPI) mRNA, complete cds. //0//3431bp//99%/AF061243	C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A. //2.3E-269//1225bp//99%/AJ004974
C-PLACE1007725	C-PLACE1008813
C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-). //1.5E-44//231aa//42%/P10265	C-PLACE1008854
C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds. //9.2E-294//1504bp//94%/AB014585	C-PLACE1008867
C-PLACE1007746	C-PLACE1008887
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds. //0//1836bp//99%/AB019602	C-PLACE1008902
C-PLACE1007810	C-PLACE1008925
C-PLACE1007843	C-PLACE1009020//NIFS PROTEIN. //3.9E-55//279aa//41%/P12623
C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13. //0//1751bp//99%/AP000010	C-PLACE1009027//Homo sapiens mRNA for doublecortin. //0//1919bp//99%/AJ003112
C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds. //0//3112bp//99%/AB018309	C-PLACE1009045
C-PLACE1007897	C-PLACE1009060//BRO1 PROTEIN. //6.7E-19//567aa//24%/P48582
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II). //2.6E-14//370aa//25%/Q99323	C-PLACE1009090
C-PLACE1007954	C-PLACE1009091
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA	C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2). //1.9E-44//480aa//30%/P30432

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【表669】

C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452a  
 a//67%/P51814  
 C-PLACE1009110  
 C-PLACE1009111  
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENE  
 IC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%/Q05086  
 C-PLACE1009158  
 C-PLACE1009166  
 C-PLACE1009174  
 C-PLACE1009186  
 C-PLACE1009190  
 C-PLACE1009230  
 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) m  
 RNA, complete cds; nuclear gene for mitochondrial product.//2.1E-1  
 32//1229bp//75%/AF107295  
 C-PLACE1009328  
 C-PLACE1009335  
 C-PLACE1009338  
 C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29  
 %//Q12067  
 C-PLACE1009375  
 C-PLACE1009388  
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOS  
 OME 1.//0.00000047//165aa//33%/Q09820  
 C-PLACE1009434  
 C-PLACE1009443  
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67)  
 (P14-KINASE) (PTDINS-4-KINASE) (P14K-ALPHA).//7.8E-71//82aa//89%/P  
 42356  
 C-PLACE1009459  
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1  
 E-289//550aa//93%/P54319  
 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CH  
 ROMOSOME 111.//3.9E-40//179aa//37%/P34580  
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN)  
 (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%/Q99418  
 C-PLACE1009542  
 C-PLACE1009571  
 C-PLACE1009581  
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1  
 E-54//291aa//40%/Q0808  
 C-PLACE1009607  
 C-PLACE1009621  
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//  
 41%/P25159  
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//  
 1.5E-285//538aa//99%/P55161  
 C-PLACE1009665  
 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//  
 1854bp//100%/AF062534  
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING P  
 ROTEIN C12G12.13C IN CHROMOSOME 1.//7E-33//166aa//43%/Q09876  
 C-PLACE1009721//WSF1 PROTEIN.//1.7E-22//176aa//33%/P35200  
 C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%/P54120  
 C-PLACE1009763//Homo sapiens mRNA for Wdd8-activating enzyme huba  
 3, complete cds.//4.3E-294//1329bp//100%/AB012190  
 C-PLACE1009794  
 C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete c  
 ds.//0//2685bp//99%/AB070712  
 C-PLACE1009866  
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEMI-PRP20 INT  
 ERGENIC REGION.//1.9E-108//277aa//43%/P53145  
 C-PLACE1009971  
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84  
 ).//4.6E-59//450aa//34%/P28175  
 C-PLACE1009995//Homo sapiens mRNA: cDNA DKFp5640123 (from clone D  
 KFp5640123).//0//1962bp//99%/AL080122  
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP  
 220 mRNA, complete cds.//5.2E-70//736bp//73%/U48288  
 C-PLACE1010023  
 C-PLACE1010031  
 C-PLACE1010053//M. musculus Spnr mRNA for RNA binding protein.//6E-  
 279//1402bp//94%/X84692  
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete  
 cds.//0//2019bp//99%/AF065482  
 C-PLACE1010076  
 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%  
 //Q62671  
 C-PLACE1010102  
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537  
 aa//44%/Q04652  
 C-PLACE1010106//Homo sapiens mRNA: cDNA DKFp568M1418 (from clone  
 DKFp568M1418).//0//1974bp//99%/AL049385  
 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COM  
 PLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN  
 GAM1) (TRANSCRIPTION FACTOR TFE3).//1.7E-20//156aa//42%/P22082  
 C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.000000  
 46//431aa//23%/P35662  
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING  
 FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//  
 9.8E-11//95aa//49%/Q01130  
 C-PLACE1010202  
 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62  
 %//P25722  
 C-PLACE1010274//Homo sapiens mRNA: cDNA DKFp5640123 (from clone D  
 KFp5640123).//0//1964bp//99%/AL080122  
 C-PLACE1010293  
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR  
 ECURSOR (CTPT).//1.1E-09//350aa//22%/P52178  
 C-PLACE1010324  
 C-PLACE1010329  
 C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR  
 (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (P  
 I-PLC).//0.000000002//126aa//29%/P34024  
 C-PLACE1010364  
 C-PLACE1010383  
 C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cd  
 s.//0//2121bp//99%/AB020643  
 C-PLACE1010491  
 C-PLACE1010492  
 C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induc  
 ed by progesterone), complete cds.//0//1981bp//99%/AB022718  
 C-PLACE1010529  
 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0  
 000012//616aa//24%/P25386  
 C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane a  
 nchor protein, complete cds.//0//1904bp//99%/AB017546  
 C-PLACE1010616  
 C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.000  
 00016//120aa//28%/P02642  
 C-PLACE1010629  
 C-PLACE1010630  
 C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39  
 %//Q01755  
 C-PLACE1010714  
 C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polype  
 ptide-C, complete cds.//4E-299//1091bp//99%/AB019987  
 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRN  
 A, partial cds.//8.9E-91//668bp//82%/AF020267  
 C-PLACE1010771//M. musculus HCNGP mRNA.//7.4E-168//966bp//89%/X680  
 61  
 C-PLACE1010786  
 C-PLACE1010800  
 C-PLACE1010811  
 C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10)  
 (HPF7).//1.3E-143//407aa//58%/Q05481  
 C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cd  
 s.//0//1885bp//99%/AB011182  
 C-PLACE1010900  
 C-PLACE2000050  
 C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR  
 (XOTCH PROTEIN).//2.4E-191//828aa//48%/P21783  
 C-PLACE4000590  
 C-PLACE4000638  
 C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//  
 7.9E-17//201aa//34%/P49816  
 C-Y79AA1001647

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【配列表】

【図面の簡単な説明】

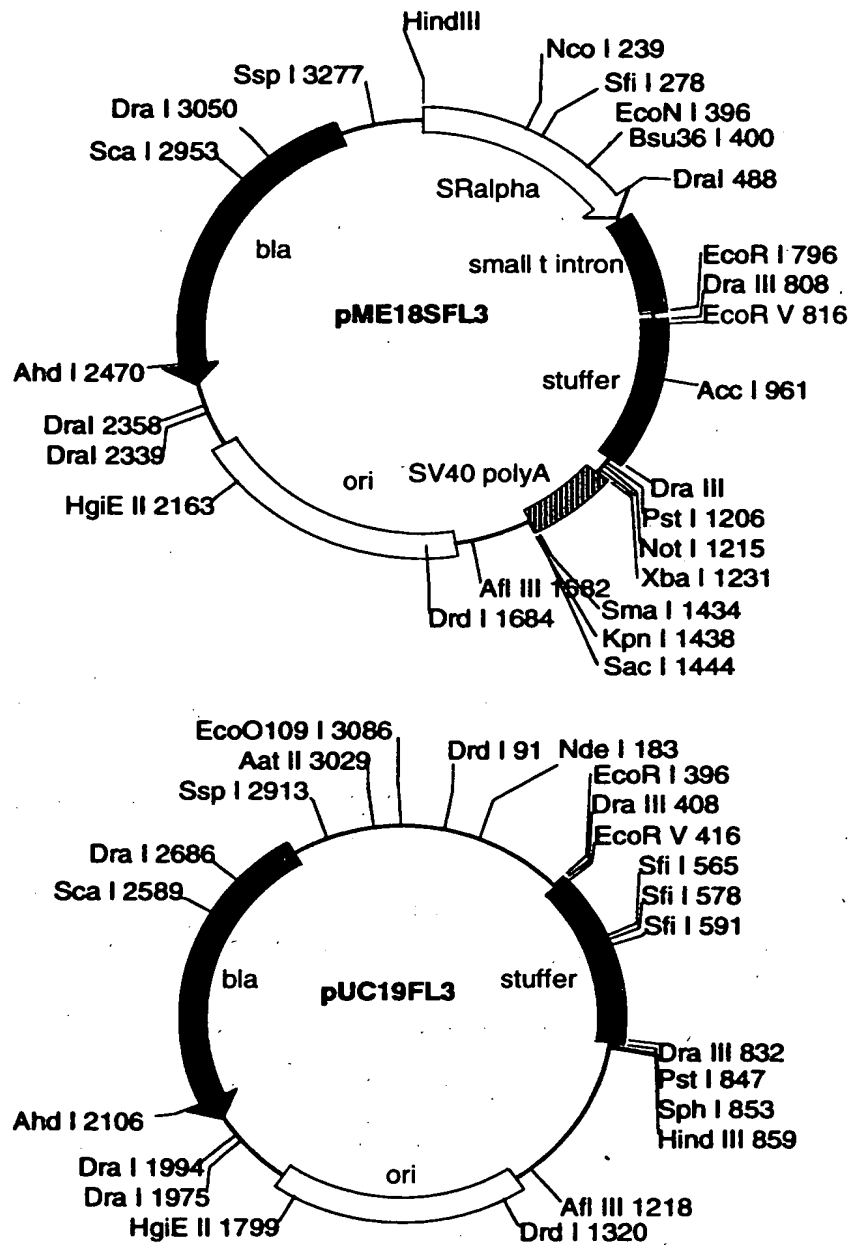
【図 1】 pME18SFL3とpUC19FL3のベクターのマップ

【図 2】 遺伝子発現解析の再現性を示すグラフ。縦軸と横軸はそれぞれ異なる実験によって得られた発現強度を示している。

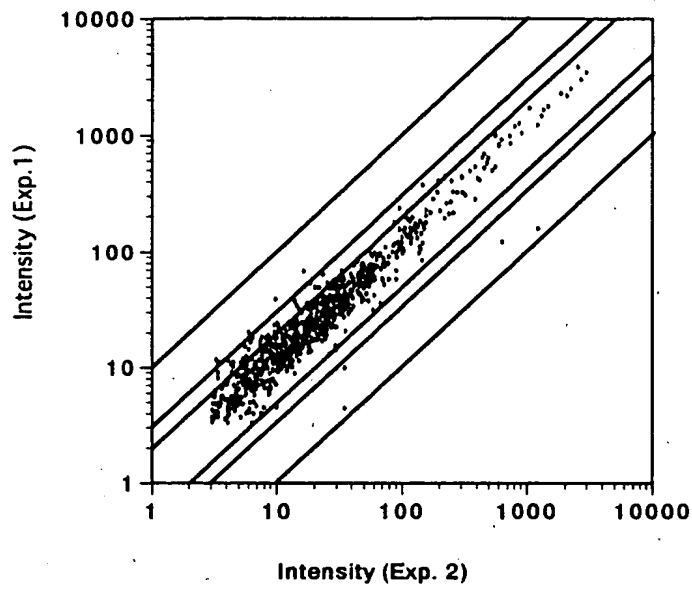
【図 3】 遺伝子発現解析における検出感度を示すグラフ。縦軸は発現強度を、横軸はプローブの濃度 ( $\mu\text{g/ml}$ ) を示す。

【書類名】 図面

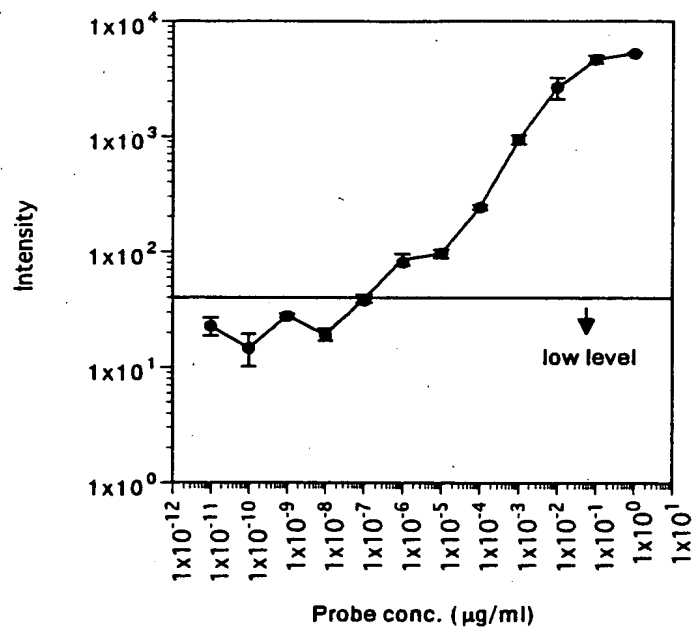
【図1】



【図2】



【図3】



【書類名】 要約書

【要約】

【課題】 全長cDNAを合成することができるプライマーとその用途の提供。

【解決手段】 ヒトのタンパク質をコードする5547のcDNAを単離した。そしてこのcDNAの5'側、および3'側の塩基配列を明らかにした。得られた塩基配列に基づいて、全長cDNA合成用プライマーを提供するとともに、cDNAによってコードされるタンパク質の機能を明らかにした。本発明のcDNAは全長であるため、翻訳開始点を含み、タンパク質の機能解析において有用な情報を与える。

【選択図】 なし

職権訂正履歴（書類修正）

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<修正内容>

- ・「物件電子化フラグ（X083）」：' 2'（物件電子化無し・返還無し）
- ・「提出物件名（X081）」：' CD-R DNA配列表' としてください。

出 願 人 履 歴 情 報

識別番号 [597059742]

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